MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Fri Mar 26 00:26:45 2010
Length of input sequence	577 amino acids
Number of nanomers from input sequence	569
Number of nanomers with obligatory P1 anchor residue	168
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	57

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	WQPQPAAEL	559	2.1000	35.00
2	VHLICPQII	141	2.0000	33.33
3	IRLADTNLL	20	1.6000	26.67
4	VHFVAPQSI	498	1.2500	20.83
5	FFGVRPHVV	448	1.1500	19.17
6	LVVGPSTEI	116	1.0900	18.17
7	YTICPAIAH	416	1.0000	16.67
8	IVTAGTVDC	131	0.6000	10.00

9	FGAAAATAA	486	0.5900	9.83
10	IGAIAGRSI	266	0.4900	8.17
11	YAQLYGPTT	8	0.4700	7.83
12	VRRYIAKYT	409	0.4000	6.67
13	FVAPQSIDA	500	0.2000	3.33
14	WQTAHVMKA	381	0.1900	3.17
15	LESLDGWPV	187	0.1200	2.00
16	LHDMGAISM	354	-0.0200	0
17	VNRGLAPVA	516	-0.1300	0
18	VRAVGKTDL	526	-0.2600	0
19	WGIIKADIG	83	-0.3000	0
20	IVEALAAGT	149	-0.3000	0
21	LVLWEPAFF	441	-0.3000	0
22	VVLKGGAIA	455	-0.3000	0
23	WPVNFALLG	193	-0.4600	0
24	LPLNDALPS	534	-0.4600	0
25	ICPAIAHGM	418	-0.5200	0
26	YWGIIKADI	82	-0.7000	0
27	WEQLRGGAS	212	-0.7000	0
28	MIGSDSQAM	362	-0.7200	0
29	VRPHVVLKG	451	-0.8000	0
30	IGKAGNPDI	100	-0.8300	0
31	VLWEPAFFG	442	-0.9000	0
32	IITVAAQPN	290	-0.9500	0
33	IGIRDGRIV	90	-1.0100	0
34	MGRVGEVVL	370	-1.0500	0
35	IRDGRIVGI	92	-1.3000	0
36	VEALAAGTT	150	-1.3000	0
37	LAVADVAGV	239	-1.3000	0
38	MGQGRASRA	58	-1.4000	0
39	IVGIGKAGN	97	-1.4000	0
40	FALLGKGNT	197	-1.4000	0
41	YHTEGAGGG	277	-1.5000	0
42	MGAISMIGS	357	-1.5000	0

43	LRTWQTAHV	378	-1.5000	0
44	VGKLADLVL	435	-1.5000	0
45	VLKGGAIAW	456	-1.5000	0
46	LAVNRGLAP	514	-1.5600	0
47	VADVAGVQV	241	-1.6500	0
48	FKLHEDWGS	222	-1.6800	0
49	VVGPSTEII	117	-1.7000	0
50	VLPSSTNPT	299	-1.7000	0
51	LAFAESRIR	336	-1.7100	0
52	YGPTTGDRI	12	-1.8000	0
53	LRESMGQGR	54	-1.8000	0
54	ICPQIIVEA	144	-1.8000	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	VHLICPQII	141	3.0000	50.00
2	IRLADTNLL	20	2.6000	43.33
3	VHFVAPQSI	498	2.2500	37.50
4	LVVGPSTEI	116	2.0900	34.83
5	IVTAGTVDC	131	1.6000	26.67
6	IGAIAGRSI	266	1.4900	24.83
7	VRRYIAKYT	409	1.4000	23.33
8	FFGVRPHVV	448	1.1500	19.17
9	LESLDGWPV	187	1.1200	18.67
10	WQPQPAAEL	559	1.1000	18.33
11	MFGAAAATA	485	1.0000	16.67
12	LHDMGAISM	354	0.9800	16.33
13	VNRGLAPVA	516	0.8700	14.50
14	VRAVGKTDL	526	0.7400	12.33
15	IVEALAAGT	149	0.7000	11.67
16	LVLWEPAFF	441	0.7000	11.67
17	VVLKGGAIA	455	0.7000	11.67

18	FGAAAATAA	486	0.5900	9.83
19	LPLNDALPS	534	0.5400	9.00
20	ICPAIAHGM	418	0.4800	8.00
21	MIGSDSQAM	362	0.2800	4.67
22	VRPHVVLKG	451	0.2000	3.33
23	FVAPQSIDA	500	0.2000	3.33
24	IGKAGNPDI	100	0.1700	2.83
25	VLWEPAFFG	442	0.1000	1.67
26	IITVAAQPN	290	0.0500	0.83
27	IGIRDGRIV	90	-0.0100	0
28	MGRVGEVVL	370	-0.0500	0
29	IRDGRIVGI	92	-0.3000	0
30	VEALAAGTT	150	-0.3000	0
31	LAVADVAGV	239	-0.3000	0
32	MGQGRASRA	58	-0.4000	0
33	IVGIGKAGN	97	-0.4000	0
34	MGAISMIGS	357	-0.5000	0
35	LRTWQTAHV	378	-0.5000	0
36	VGKLADLVL	435	-0.5000	0
37	VLKGGAIAW	456	-0.5000	0
38	YAQLYGPTT	8	-0.5300	0
39	LAVNRGLAP	514	-0.5600	0
40	VADVAGVQV	241	-0.6500	0
41	VVGPSTEII	117	-0.7000	0
42	VLPSSTNPT	299	-0.7000	0
43	LAFAESRIR	336	-0.7100	0
44	LRESMGQGR	54	-0.8000	0
45	ICPQIIVEA	144	-0.8000	0
46	IISGNRRIV	124	-0.8100	0
47	WQTAHVMKA	381	-0.8100	0
48	VCHHLNPRI	324	-0.8300	0
49	VGIGKAGNP	98	-0.9000	0
50	VQVALHSDT	247	-0.9000	0
51	LPMTQRYFL	567	-0.9000	0

52	ITVAAQPNV	291	-0.9300	0
53	MLMVCHHLN	321	-0.9500	0
54	WHLARMLES	181	-1.0000	0
55	IGSVEVGKL	430	-1.0500	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	VRIDGQVWQ	552	5.7000	60.00
2	VHRDLVVGP	112	4.9000	51.58
3	VRPHVVLKG	451	4.3000	45.26
4	VIIDYWGII	78	4.2000	44.21
5	VLHDMGAIS	353	3.9000	41.05
6	IRLADTNLL	20	3.8700	40.74
7	FVEDTIGAI	261	3.6000	37.89
8	IRPSTIAAE	343	3.6000	37.89
9	VFGGGKVLR	47	3.5000	36.84
10	IVGIGKAGN	97	3.5000	36.84
11	LVVGPSTEI	116	3.5000	36.84
12	LVLWEPAFF	441	3.5000	36.84
13	VRAVGKTDL	526	3.3600	35.37
14	VHLICPQII	141	3.3000	34.74
15	LAGDEAVFG	41	3.1000	32.63
16	IVTAGTVDC	131	3.1000	32.63
17	IGSDSQAMG	363	3.1000	32.63
18	LHSDTLNET	251	2.9100	30.63
19	IRDGRIVGI	92	2.9000	30.53
20	MIGSDSQAM	362	2.9000	30.53
21	VNPDALWEQ	206	2.8000	29.47
22	MVCHHLNPR	323	2.7100	28.53
23	IIGGGTGPA	160	2.7000	28.42
24	LRGGASGFK	215	2.7000	28.42
25	VNRGLAPVA	516	2.7000	28.42

26	VITGAVIID	73	2.6000	27.37
27	VHFVAPQSI	498	2.6000	27.37
28	IKADIGIRD	86	2.5000	26.32
29	VVGPSTEII	117	2.5000	26.32
30	WQTAHVMKA	381	2.5000	26.32
31	LKGGAIAWA	457	2.5000	26.32
32	IIKADIGIR	85	2.4000	25.26
33	LEGDPSGSQ	394	2.4000	25.26
34	VGIGKAGNP	98	2.3000	24.21
35	VNFALLGKG	195	2.3000	24.21
36	LRTWQTAHV	378	2.3000	24.21
37	VLPSSTNPT	299	2.2100	23.26
38	IISGNRRIV	124	2.2000	23.16
39	VMKARRGAL	386	2.1600	22.74
40	LAVADVAGV	239	2.0000	21.05
41	LPLNDALPS	534	2.0000	21.05
42	IGSVEVGKL	430	1.9600	20.63
43	MARLSRERY	0	1.8000	18.95
44	LAAGTTTII	153	1.8000	18.95
45	LGKGNTVNP	200	1.7000	17.89
46	LLVEVTEDR	27	1.6000	16.84
47	ITGAVIIDY	74	1.6000	16.84
48	VGPSTEIIS	118	1.6000	16.84
49	MGAISMIGS	357	1.6000	16.84
50	LYGPTTGDR	11	1.5000	15.79
51	YWGIIKADI	82	1.5000	15.79
52	LRESMGQGR	54	1.4000	14.74
53	LMVCHHLNP	322	1.4000	14.74
54	VVLKGGAIA	455	1.4000	14.74
55	FGGGKVLRE	48	1.3000	13.68
56	WGIIKADIG	83	1.3000	13.68
57	VEVGKLADL	433	1.2600	13.26

ALLELE: DRB1_0305	Threshold for 3 % with score: 1.7	Highest Score achievable by any peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	VRIDGQVWQ	552	5.4000	59.34
2	FVEDTIGAI	261	3.7000	40.66
3	WQTAHVMKA	381	3.5000	38.46
4	VHRDLVVGP	112	2.9000	31.87
5	VNPDALWEQ	206	2.5000	27.47
6	VLHDMGAIS	353	2.5000	27.47
7	VIIDYWGII	78	2.3000	25.27
8	IVTAGTVDC	131	2.1000	23.08
9	LEGDPSGSQ	394	2.1000	23.08
10	YTICPAIAH	416	1.9800	21.76
11	IRLADTNLL	20	1.9100	20.99
12	VRPHVVLKG	451	1.9000	20.88
13	WHLARMLES	181	1.8000	19.78
14	IVGIGKAGN	97	1.7000	18.68
15	IIGGGTGPA	160	1.7000	18.68
16	VNRGLAPVA	516	1.7000	18.68
17	YWGIIKADI	82	1.6000	17.58
18	LVVGPSTEI	116	1.6000	17.58
19	LRGGASGFK	215	1.6000	17.58
20	LKGGAIAWA	457	1.5000	16.48
21	VHLICPQII	141	1.4000	15.38
22	FVAPQSIDA	500	1.4000	15.38
23	VRAVGKTDL	526	1.4000	15.38
24	LHSDTLNET	251	1.2100	13.30
25	FALLGKGNT	197	1.2000	13.19
26	IRPSTIAAE	343	1.2000	13.19
27	VFGGGKVLR	47	1.0000	10.99
28	IRDGRIVGI	92	1.0000	10.99
29	FGGGKVLRE	48	0.9000	9.89
30	WGIIKADIG	83	0.9000	9.89
31	LAGDEAVFG	41	0.7000	7.69

32	IGSDSQAMG	363	0.7000	7.69
33	VHFVAPQSI	498	0.7000	7.69
34	VVGPSTEII	117	0.6000	6.59
35	LVLWEPAFF	441	0.6000	6.59
36	LPLNDALPS	534	0.6000	6.59
37	VLPSSTNPT	299	0.5100	5.60
38	VITGAVIID	73	0.5000	5.49
39	WQPQPAAEL	559	0.5000	5.49
40	VAGVQVALH	244	0.4800	5.27
41	IKADIGIRD	86	0.4000	4.40
42	ISMIGSDSQ	360	0.4000	4.40
43	MIGSDSQAM	362	0.4000	4.40
44	VVLKGGAIA	455	0.4000	4.40
45	FGAAAATAA	486	0.4000	4.40
46	LDMLMVCHH	319	0.3800	4.18
47	VGIGKAGNP	98	0.3000	3.30
48	LRTWQTAHV	378	0.3000	3.30
49	MVCHHLNPR	323	0.2100	2.31
50	VGPSTEIIS	118	0.2000	2.20
51	IISGNRRIV	124	0.2000	2.20
52	ICPQIIVEA	144	0.2000	2.20
53	WEQLRGGAS	212	0.2000	2.20
54	MGAISMIGS	357	0.2000	2.20
55	VMKARRGAL	386	0.2000	2.20
56	VTAGTVDCH	132	0.1800	1.98
57	MGQGRASRA	58	0.0700	0.77

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	VRIDGQVWQ	552	6.2800	71.36
2	VHRDLVVGP	112	3.7800	42.95
3	IRLADTNLL	20	3.6000	40.91

4	VLHDMGAIS	353	3.5000	39.77
5	VRPHVVLKG	451	3.4000	38.64
6	IVTAGTVDC	131	2.9800	33.86
7	LHSDTLNET	251	2.9000	32.95
8	IVGIGKAGN	97	2.7000	30.68
9	VNPDALWEQ	206	2.7000	30.68
10	LVVGPSTEI	116	2.6000	29.55
11	VHLICPQII	141	2.5000	28.41
12	LKGGAIAWA	457	2.5000	28.41
13	VRAVGKTDL	526	2.4000	27.27
14	VLPSSTNPT	299	2.2000	25.00
15	IRPSTIAAE	343	2.2000	25.00
16	WQTAHVMKA	381	2.2000	25.00
17	LPLNDALPS	534	2.1000	23.86
18	VVGPSTEII	117	2.0000	22.73
19	VIIDYWGII	78	1.9000	21.59
20	MVCHHLNPR	323	1.9000	21.59
21	VFGGGKVLR	47	1.8800	21.36
22	IRDGRIVGI	92	1.8800	21.36
23	VHFVAPQSI	498	1.8000	20.45
24	ISMIGSDSQ	360	1.7000	19.32
25	IGSDSQAMG	363	1.7000	19.32
26	LEGDPSGSQ	394	1.7000	19.32
27	LVLWEPAFF	441	1.6000	18.18
28	LAGDEAVFG	41	1.5800	17.95
29	MIGSDSQAM	362	1.5000	17.05
30	VTAGTVDCH	132	1.4800	16.82
31	VAGVQVALH	244	1.4800	16.82
32	VVLKGGAIA	455	1.4000	15.91
33	LDMLMVCHH	319	1.3800	15.68
34	IIGGGTGPA	160	1.3000	14.77
35	WHLARMLES	181	1.3000	14.77
36	FVEDTIGAI	261	1.3000	14.77
37	LRTWQTAHV	378	1.3000	14.77

38	VNRGLAPVA	516	1.3000	14.77
39	LRGGASGFK	215	1.2000	13.64
40	VITGAVIID	73	1.1800	13.41
41	IKADIGIRD	86	1.0800	12.27
42	ICPQIIVEA	144	1.0800	12.27
43	LAVADVAGV	239	1.0000	11.36
44	MFGAAAATA	485	1.0000	11.36
45	MARLSRERY	0	0.9000	10.23
46	IISGNRRIV	124	0.9000	10.23
47	LAAGTTTII	153	0.9000	10.23
48	MLMVCHHLN	321	0.9000	10.23
49	LMVCHHLNP	322	0.9000	10.23
50	VGPSTEIIS	118	0.8800	10.00
51	MGAISMIGS	357	0.8800	10.00
52	MGQGRASRA	58	0.8000	9.09
53	IHAYHTEGA	274	0.8000	9.09
54	VVLRTWQTA	376	0.7000	7.95
55	YTICPAIAH	416	0.6600	7.50
56	YWGIIKADI	82	0.6000	6.82
57	LGKGNTVNP	200	0.5800	6.59

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	VRIDGQVWQ	552	6.2800	71.36
2	VHRDLVVGP	112	3.7800	42.95
3	IRLADTNLL	20	3.6000	40.91
4	VLHDMGAIS	353	3.5000	39.77
5	VRPHVVLKG	451	3.4000	38.64
6	IVTAGTVDC	131	2.9800	33.86
7	LHSDTLNET	251	2.9000	32.95
8	IVGIGKAGN	97	2.7000	30.68
9	VNPDALWEQ	206	2.7000	30.68

10	LVVGPSTEI	116	2.6000	29.55
11	VHLICPQII	141	2.5000	28.41
12	LKGGAIAWA	457	2.5000	28.41
13	VRAVGKTDL	526	2.4000	27.27
14	VLPSSTNPT	299	2.2000	25.00
15	IRPSTIAAE	343	2.2000	25.00
16	WQTAHVMKA	381	2.2000	25.00
17	LPLNDALPS	534	2.1000	23.86
18	VVGPSTEII	117	2.0000	22.73
19	VIIDYWGII	78	1.9000	21.59
20	MVCHHLNPR	323	1.9000	21.59
21	VFGGGKVLR	47	1.8800	21.36
22	IRDGRIVGI	92	1.8800	21.36
23	VHFVAPQSI	498	1.8000	20.45
24	ISMIGSDSQ	360	1.7000	19.32
25	IGSDSQAMG	363	1.7000	19.32
26	LEGDPSGSQ	394	1.7000	19.32
27	LVLWEPAFF	441	1.6000	18.18
28	LAGDEAVFG	41	1.5800	17.95
29	MIGSDSQAM	362	1.5000	17.05
30	VTAGTVDCH	132	1.4800	16.82
31	VAGVQVALH	244	1.4800	16.82
32	VVLKGGAIA	455	1.4000	15.91
33	LDMLMVCHH	319	1.3800	15.68
34	IIGGGTGPA	160	1.3000	14.77
35	WHLARMLES	181	1.3000	14.77
36	FVEDTIGAI	261	1.3000	14.77
37	LRTWQTAHV	378	1.3000	14.77
38	VNRGLAPVA	516	1.3000	14.77
39	LRGGASGFK	215	1.2000	13.64
40	VITGAVIID	73	1.1800	13.41
41	IKADIGIRD	86	1.0800	12.27
42	ICPQIIVEA	144	1.0800	12.27
43	LAVADVAGV	239	1.0000	11.36

44	MFGAAAATA	485	1.0000	11.36
45	MARLSRERY	0	0.9000	10.23
46	IISGNRRIV	124	0.9000	10.23
47	LAAGTTTII	153	0.9000	10.23
48	MLMVCHHLN	321	0.9000	10.23
49	LMVCHHLNP	322	0.9000	10.23
50	VGPSTEIIS	118	0.8800	10.00
51	MGAISMIGS	357	0.8800	10.00
52	MGQGRASRA	58	0.8000	9.09
53	IHAYHTEGA	274	0.8000	9.09
54	VVLRTWQTA	376	0.7000	7.95
55	YTICPAIAH	416	0.6600	7.50
56	YWGIIKADI	82	0.6000	6.82
57	LGKGNTVNP	200	0.5800	6.59

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	VRIDGQVWQ	552	6.2800	71.36
2	VHRDLVVGP	112	3.7800	42.95
3	IRLADTNLL	20	3.6000	40.91
4	VLHDMGAIS	353	3.5000	39.77
5	VRPHVVLKG	451	3.4000	38.64
6	IVTAGTVDC	131	2.9800	33.86
7	LHSDTLNET	251	2.9000	32.95
8	IVGIGKAGN	97	2.7000	30.68
9	VNPDALWEQ	206	2.7000	30.68
10	LVVGPSTEI	116	2.6000	29.55
11	VHLICPQII	141	2.5000	28.41
12	LKGGAIAWA	457	2.5000	28.41
13	VRAVGKTDL	526	2.4000	27.27
14	VLPSSTNPT	299	2.2000	25.00
15	IRPSTIAAE	343	2.2000	25.00

16	WQTAHVMKA	381	2.2000	25.00
17	LPLNDALPS	534	2.1000	23.86
18	VVGPSTEII	117	2.0000	22.73
19	VIIDYWGII	78	1.9000	21.59
20	MVCHHLNPR	323	1.9000	21.59
21	VFGGGKVLR	47	1.8800	21.36
22	IRDGRIVGI	92	1.8800	21.36
23	VHFVAPQSI	498	1.8000	20.45
24	ISMIGSDSQ	360	1.7000	19.32
25	IGSDSQAMG	363	1.7000	19.32
26	LEGDPSGSQ	394	1.7000	19.32
27	LVLWEPAFF	441	1.6000	18.18
28	LAGDEAVFG	41	1.5800	17.95
29	MIGSDSQAM	362	1.5000	17.05
30	VTAGTVDCH	132	1.4800	16.82
31	VAGVQVALH	244	1.4800	16.82
32	VVLKGGAIA	455	1.4000	15.91
33	LDMLMVCHH	319	1.3800	15.68
34	IIGGGTGPA	160	1.3000	14.77
35	WHLARMLES	181	1.3000	14.77
36	FVEDTIGAI	261	1.3000	14.77
37	LRTWQTAHV	378	1.3000	14.77
38	VNRGLAPVA	516	1.3000	14.77
39	LRGGASGFK	215	1.2000	13.64
40	VITGAVIID	73	1.1800	13.41
41	IKADIGIRD	86	1.0800	12.27
42	ICPQIIVEA	144	1.0800	12.27
43	LAVADVAGV	239	1.0000	11.36
44	MFGAAAATA	485	1.0000	11.36
45	MARLSRERY	0	0.9000	10.23
46	IISGNRRIV	124	0.9000	10.23
47	LAAGTTTII	153	0.9000	10.23
48	MLMVCHHLN	321	0.9000	10.23
49	LMVCHHLNP	322	0.9000	10.23

50	VGPSTEIIS	118	0.8800	10.00
51	MGAISMIGS	357	0.8800	10.00
52	MGQGRASRA	58	0.8000	9.09
53	IHAYHTEGA	274	0.8000	9.09
54	VVLRTWQTA	376	0.7000	7.95
55	YTICPAIAH	416	0.6600	7.50
56	YWGIIKADI	82	0.6000	6.82
57	LGKGNTVNP	200	0.5800	6.59

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	VRIDGQVWQ	552	4.7000	49.47
2	FVEDTIGAI	261	4.6000	48.42
3	VHRDLVVGP	112	3.9000	41.05
4	WQTAHVMKA	381	3.5000	36.84
5	VRPHVVLKG	451	3.3000	34.74
6	VIIDYWGII	78	3.2000	33.68
7	VLHDMGAIS	353	2.9000	30.53
8	IRLADTNLL	20	2.8700	30.21
9	IRPSTIAAE	343	2.6000	27.37
10	VFGGGKVLR	47	2.5000	26.32
11	YWGIIKADI	82	2.5000	26.32
12	IVGIGKAGN	97	2.5000	26.32
13	LVVGPSTEI	116	2.5000	26.32
14	LVLWEPAFF	441	2.5000	26.32
15	VRAVGKTDL	526	2.3600	24.84
16	FGGGKVLRE	48	2.3000	24.21
17	WGIIKADIG	83	2.3000	24.21
18	VHLICPQII	141	2.3000	24.21
19	WHLARMLES	181	2.2000	23.16
20	LAGDEAVFG	41	2.1000	22.11
21	IVTAGTVDC	131	2.1000	22.11

22	IGSDSQAMG	363	2.1000	22.11
23	LHSDTLNET	251	1.9100	20.11
24	IRDGRIVGI	92	1.9000	20.00
25	FALLGKGNT	197	1.9000	20.00
26	MIGSDSQAM	362	1.9000	20.00
27	VNPDALWEQ	206	1.8000	18.95
28	MVCHHLNPR	323	1.7100	18.00
29	IIGGGTGPA	160	1.7000	17.89
30	LRGGASGFK	215	1.7000	17.89
31	VNRGLAPVA	516	1.7000	17.89
32	VITGAVIID	73	1.6000	16.84
33	VHFVAPQSI	498	1.6000	16.84
34	IKADIGIRD	86	1.5000	15.79
35	VVGPSTEII	117	1.5000	15.79
36	LKGGAIAWA	457	1.5000	15.79
37	WQPQPAAEL	559	1.4600	15.37
38	IIKADIGIR	85	1.4000	14.74
39	LEGDPSGSQ	394	1.4000	14.74
40	YTICPAIAH	416	1.4000	14.74
41	FVAPQSIDA	500	1.4000	14.74
42	VGIGKAGNP	98	1.3000	13.68
43	VNFALLGKG	195	1.3000	13.68
44	LRTWQTAHV	378	1.3000	13.68
45	VLPSSTNPT	299	1.2100	12.74
46	IISGNRRIV	124	1.2000	12.63
47	VMKARRGAL	386	1.1600	12.21
48	LAVADVAGV	239	1.0000	10.53
49	YIAKYTICP	412	1.0000	10.53
50	FFGVRPHVV	448	1.0000	10.53
51	LPLNDALPS	534	1.0000	10.53
52	IGSVEVGKL	430	0.9600	10.11
53	MARLSRERY	0	0.8000	8.42
54	LAAGTTTII	153	0.8000	8.42
55	WPVNFALLG	193	0.8000	8.42

56	LGKGNTVNP	200	0.7000	7.37
57	LLVEVTEDR	27	0.6000	6.32

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	VRIDGQVWQ	552	6.2800	71.36
2	VHRDLVVGP	112	3.7800	42.95
3	IRLADTNLL	20	3.6000	40.91
4	VLHDMGAIS	353	3.5000	39.77
5	VRPHVVLKG	451	3.4000	38.64
6	IVTAGTVDC	131	2.9800	33.86
7	LHSDTLNET	251	2.9000	32.95
8	IVGIGKAGN	97	2.7000	30.68
9	VNPDALWEQ	206	2.7000	30.68
10	LVVGPSTEI	116	2.6000	29.55
11	VHLICPQII	141	2.5000	28.41
12	LKGGAIAWA	457	2.5000	28.41
13	VRAVGKTDL	526	2.4000	27.27
14	VLPSSTNPT	299	2.2000	25.00
15	IRPSTIAAE	343	2.2000	25.00
16	WQTAHVMKA	381	2.2000	25.00
17	LPLNDALPS	534	2.1000	23.86
18	VVGPSTEII	117	2.0000	22.73
19	VIIDYWGII	78	1.9000	21.59
20	MVCHHLNPR	323	1.9000	21.59
21	VFGGGKVLR	47	1.8800	21.36
22	IRDGRIVGI	92	1.8800	21.36
23	VHFVAPQSI	498	1.8000	20.45
24	ISMIGSDSQ	360	1.7000	19.32
25	IGSDSQAMG	363	1.7000	19.32
26	LEGDPSGSQ	394	1.7000	19.32
27	LVLWEPAFF	441	1.6000	18.18

28	LAGDEAVFG	41	1.5800	17.95
29	MIGSDSQAM	362	1.5000	17.05
30	VTAGTVDCH	132	1.4800	16.82
31	VAGVQVALH	244	1.4800	16.82
32	VVLKGGAIA	455	1.4000	15.91
33	LDMLMVCHH	319	1.3800	15.68
34	IIGGGTGPA	160	1.3000	14.77
35	WHLARMLES	181	1.3000	14.77
36	FVEDTIGAI	261	1.3000	14.77
37	LRTWQTAHV	378	1.3000	14.77
38	VNRGLAPVA	516	1.3000	14.77
39	LRGGASGFK	215	1.2000	13.64
40	VITGAVIID	73	1.1800	13.41
41	IKADIGIRD	86	1.0800	12.27
42	ICPQIIVEA	144	1.0800	12.27
43	LAVADVAGV	239	1.0000	11.36
44	MFGAAAATA	485	1.0000	11.36
45	MARLSRERY	0	0.9000	10.23
46	IISGNRRIV	124	0.9000	10.23
47	LAAGTTTII	153	0.9000	10.23
48	MLMVCHHLN	321	0.9000	10.23
49	LMVCHHLNP	322	0.9000	10.23
50	VGPSTEIIS	118	0.8800	10.00
51	MGAISMIGS	357	0.8800	10.00
52	MGQGRASRA	58	0.8000	9.09
53	IHAYHTEGA	274	0.8000	9.09
54	VVLRTWQTA	376	0.7000	7.95
55	YTICPAIAH	416	0.6600	7.50
56	YWGIIKADI	82	0.6000	6.82
57	LGKGNTVNP	200	0.5800	6.59

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	IRLADTNLL	20	3.7000	43.02
2	VRPHVVLKG	451	3.2000	37.21
3	VRIDGQVWQ	552	3.1800	36.98
4	LLVEVTEDR	27	3.1000	36.05
5	IVTAGTVDC	131	3.0800	35.81
6	WQTAHVMKA	381	2.9000	33.72
7	VLPSSTNPT	299	2.4000	27.91
8	WHLARMLES	181	2.1000	24.42
9	ISMIGSDSQ	360	2.1000	24.42
10	LPLNDALPS	534	1.8000	20.93
11	MIGSDSQAM	362	1.7000	19.77
12	YTICPAIAH	416	1.6600	19.30
13	VHRDLVVGP	112	1.5800	18.37
14	FVAPQSIDA	500	1.5800	18.37
15	WGIIKADIG	83	1.5000	17.44
16	VVGPSTEII	117	1.5000	17.44
17	FKLHEDWGS	222	1.4000	16.28
18	VHLICPQII	141	1.3000	15.12
19	WQPQPAAEL	559	1.3000	15.12
20	LRTWQTAHV	378	1.2000	13.95
21	LEGDPSGSQ	394	0.9000	10.47
22	LDMLMVCHH	319	0.8800	10.23
23	VLHDMGAIS	353	0.8000	9.30
24	MVCHHLNPR	323	0.7000	8.14
25	LVVGPSTEI	116	0.6000	6.98
26	WPVNFALLG	193	0.6000	6.98
27	FVEDTIGAI	261	0.6000	6.98
28	VCHHLNPRI	324	0.6000	6.98
29	IRPSTIAAE	343	0.5000	5.81
30	VIIDYWGII	78	0.4000	4.65
31	IAAEDVLHD	348	0.4000	4.65
32	FGAAAATAA	486	0.4000	4.65
33	IHAYHTEGA	274	0.3000	3.49

34	ICPQIIVEA	144	0.0800	0.93
35	YIAKYTICP	412	0.0800	0.93
36	MGAISMIGS	357	-0.0200	0
37	LVLWEPAFF	441	-0.1000	0
38	VAAQPNVLP	293	-0.1200	0
39	VLRTWQTAH	377	-0.1200	0
40	IGKAGNPDI	100	-0.2000	0
41	WAAMGDANA	464	-0.2000	0
42	WGSTPAAID	228	-0.3000	0
43	LAVADVAGV	239	-0.3000	0
44	LHSDTLNET	251	-0.3000	0
45	LAGDEAVFG	41	-0.3200	0
46	VNPDALWEQ	206	-0.5000	0
47	VLWEPAFFG	442	-0.5000	0
48	YGPTTGDRI	12	-0.6000	0
49	FFGVRPHVV	448	-0.6000	0
50	VHFVAPQSI	498	-0.6000	0
51	IIGGGTGPA	160	-0.7000	0
52	VAGVQVALH	244	-0.7200	0
53	LRGGASGFK	215	-0.8000	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	LRTWQTAHV	378	5.0000	52.08
2	IRLADTNLL	20	4.7000	48.96
3	VRPHVVLKG	451	4.6000	47.92
4	IVTAGTVDC	131	4.2000	43.75
5	VVLRTWQTA	376	4.2000	43.75
6	LVLWEPAFF	441	3.7000	38.54
7	FKLHEDWGS	222	3.3000	34.38
8	LVVGPSTEI	116	2.7000	28.13
9	VHLICPQII	141	2.6800	27.92

10	IGIRDGRIV	90	2.5000	26.04
11	LAFAESRIR	336	2.5000	26.04
12	LDGWPVNFA	190	2.0000	20.83
13	MIGSDSQAM	362	2.0000	20.83
14	WQTAHVMKA	381	1.9000	19.79
15	MVCHHLNPR	323	1.8000	18.75
16	LPLNDALPS	534	1.8000	18.75
17	VVLKGGAIA	455	1.7000	17.71
18	VLPRPMFGA	480	1.7000	17.71
19	VHFVAPQSI	498	1.7000	17.71
20	VLPSSTNPT	299	1.6000	16.67
21	IDYWGIIKA	80	1.5000	15.62
22	VVGPSTEII	117	1.4000	14.58
23	WHLARMLES	181	1.4000	14.58
24	VCHHLNPRI	324	1.4000	14.58
25	LLGKGNTVN	199	1.3000	13.54
26	VRRYIAKYT	409	1.3000	13.54
27	YIAKYTICP	412	1.3000	13.54
28	FVAPQSIDA	500	1.3000	13.54
29	IHAYHTEGA	274	1.1000	11.46
30	YTICPAIAH	416	1.0800	11.25
31	LAAGTTTII	153	1.0000	10.42
32	MFGAAAATA	485	1.0000	10.42
33	LAVADVAGV	239	0.7000	7.29
34	MGAISMIGS	357	0.6800	7.08
35	LGKGNTVNP	200	0.6000	6.25
36	IAGRSIHAY	269	0.6000	6.25
37	VRIDGQVWQ	552	0.6000	6.25
38	ISMIGSDSQ	360	0.5800	6.04
39	IGKAGNPDI	100	0.5000	5.21
40	LKGGAIAWA	457	0.5000	5.21
41	VAGVQVALH	244	0.4800	5.00
42	IGAIAGRSI	266	0.4800	5.00
43	LDMLMVCHH	319	0.4800	5.00

44	IIGGGTGPA	160	0.4000	4.17
45	ICPAIAHGM	418	0.4000	4.17
46	LRGGASGFK	215	0.3000	3.12
47	LHDMGAISM	354	0.2000	2.08
48	VITGAVIID	73	0.1000	1.04
49	IITVAAQPN	290	0.1000	1.04
50	LMVCHHLNP	322	-0.1000	0
51	LNPRIPEDL	328	-0.1000	0
52	VLRTWQTAH	377	-0.1200	0
53	VALHSDTLN	249	-0.2000	0
54	VAAQPNVLP	293	-0.2000	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	IRLADTNLL	20	4.8000	54.55
2	IVTAGTVDC	131	3.9000	44.32
3	LRTWQTAHV	378	3.3500	38.07
4	ISMIGSDSQ	360	2.5000	28.41
5	VHLICPQII	141	2.4000	27.27
6	LDMLMVCHH	319	2.0800	23.64
7	LVLWEPAFF	441	2.0500	23.30
8	VLPSSTNPT	299	2.0000	22.73
9	VVGPSTEII	117	1.9000	21.59
10	WQTAHVMKA	381	1.8000	20.45
11	VRPHVVLKG	451	1.7000	19.32
12	VAGVQVALH	244	1.6800	19.09
13	IHAYHTEGA	274	1.6000	18.18
14	VHFVAPQSI	498	1.6000	18.18
15	VRIDGQVWQ	552	1.5000	17.05
16	LVVGPSTEI	116	1.3000	14.77
17	MGAISMIGS	357	1.2800	14.55
18	MIGSDSQAM	362	1.0000	11.36

19	MFGAAAATA	485	1.0000	11.36
20	LHDMGAISM	354	0.9800	11.14
21	FVAPQSIDA	500	0.8800	10.00
22	LPLNDALPS	534	0.8000	9.09
23	WHLARMLES	181	0.7000	7.95
24	LAVADVAGV	239	0.7000	7.95
25	YTICPAIAH	416	0.6600	7.50
26	LLVEVTEDR	27	0.6000	6.82
27	IGKAGNPDI	100	0.5000	5.68
28	LDGWPVNFA	190	0.4500	5.11
29	ICPQIIVEA	144	0.1000	1.14
30	VVLKGGAIA	455	0.1000	1.14
31	WGIIKADIG	83	-0.1000	0
32	VHRDLVVGP	112	-0.1000	0
33	VAAQPNVLP	293	-0.1000	0
34	LAFAESRIR	336	-0.1000	0
35	IGSVEVGKL	430	-0.1000	0
36	FGAAAATAA	486	-0.1000	0
37	VLRTWQTAH	377	-0.2200	0
38	IVEALAAGT	149	-0.3000	0
39	MLMVCHHLN	321	-0.3000	0
40	MVCHHLNPR	323	-0.3000	0
41	VGKLADLVL	435	-0.3000	0
42	WAAMGDANA	464	-0.3000	0
43	VRAVGKTDL	526	-0.3000	0
44	IVGIGKAGN	97	-0.4000	0
45	LAAGTTTII	153	-0.4000	0
46	IIGGGTGPA	160	-0.4000	0
47	VQVALHSDT	247	-0.4000	0
48	LAPVADVRA	520	-0.4000	0
49	LYGPTTGDR	11	-0.5000	0
50	LRGGASGFK	215	-0.5000	0
51	VVLRTWQTA	376	-0.5000	0
52	LEGDPSGSQ	394	-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	IRLADTNLL	20	4.8000	51.06
2	IVTAGTVDC	131	2.9000	30.85
3	YTICPAIAH	416	2.8800	30.64
4	WQTAHVMKA	381	2.8000	29.79
5	LRTWQTAHV	378	2.6500	28.19
6	LDMLMVCHH	319	2.3000	24.47
7	ISMIGSDSQ	360	2.3000	24.47
8	WGIIKADIG	83	2.2000	23.40
9	IRPSTIAAE	343	2.0000	21.28
10	VRPHVVLKG	451	2.0000	21.28
11	LVLWEPAFF	441	1.9500	20.74
12	VAGVQVALH	244	1.9000	20.21
13	VLPSSTNPT	299	1.9000	20.21
14	FVAPQSIDA	500	1.8800	20.00
15	WHLARMLES	181	1.7000	18.09
16	VHLICPQII	141	1.6000	17.02
17	WQPQPAAEL	559	1.5000	15.96
18	VRIDGQVWQ	552	1.3000	13.83
19	VVGPSTEII	117	1.1000	11.70
20	MIGSDSQAM	362	1.1000	11.70
21	LHDMGAISM	354	1.0800	11.49
22	LLGKGNTVN	199	1.0000	10.64
23	IITVAAQPN	290	1.0000	10.64
24	FGAAAATAA	486	0.9000	9.57
25	FGGGKVLRE	48	0.8000	8.51
26	WGSTPAAID	228	0.8000	8.51
27	VHFVAPQSI	498	0.8000	8.51
28	MLMVCHHLN	321	0.7000	7.45
29	FFGVRPHVV	448	0.7000	7.45
30	WAAMGDANA	464	0.7000	7.45

31	YIAKYTICP	412	0.6800	7.23
32	IVGIGKAGN	97	0.6000	6.38
33	LARMLESLD	183	0.6000	6.38
34	IHAYHTEGA	274	0.6000	6.38
35	LVVGPSTEI	116	0.5000	5.32
36	LPSIEVDPD	540	0.5000	5.32
37	LNDALPSIE	536	0.3000	3.19
38	MGAISMIGS	357	0.2800	2.98
39	IAAEDVLHD	348	0.1000	1.06
40	LICPQIIVE	143	0.0800	0.85
41	WPVNFALLG	193	-0.1000	0
42	VRRYIAKYT	409	-0.1000	0
43	IGSVEVGKL	430	-0.1000	0
44	LPLNDALPS	534	-0.2000	0
45	IGKAGNPDI	100	-0.3000	0
46	VGKLADLVL	435	-0.3000	0
47	VRAVGKTDL	526	-0.3000	0
48	VITGAVIID	73	-0.3200	0
49	LLVEVTEDR	27	-0.4000	0
50	IVEALAAGT	149	-0.4000	0
51	ICPAIAHGM	418	-0.4000	0
52	VQVALHSDT	247	-0.5000	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	IRLADTNLL	20	3.8000	43.18
2	IVTAGTVDC	131	2.9000	32.95
3	WQTAHVMKA	381	2.8000	31.82
4	LRTWQTAHV	378	2.3500	26.70
5	FVAPQSIDA	500	1.8800	21.36
6	WHLARMLES	181	1.7000	19.32
7	YTICPAIAH	416	1.6600	18.86

8	ISMIGSDSQ	360	1.5000	17.05
9	VHLICPQII	141	1.4000	15.91
10	LDMLMVCHH	319	1.0800	12.27
11	LVLWEPAFF	441	1.0500	11.93
12	VLPSSTNPT	299	1.0000	11.36
13	WGIIKADIG	83	0.9000	10.23
14	VVGPSTEII	117	0.9000	10.23
15	FGAAAATAA	486	0.9000	10.23
16	VRPHVVLKG	451	0.7000	7.95
17	WAAMGDANA	464	0.7000	7.95
18	VAGVQVALH	244	0.6800	7.73
19	IHAYHTEGA	274	0.6000	6.82
20	VHFVAPQSI	498	0.6000	6.82
21	VRIDGQVWQ	552	0.5000	5.68
22	WQPQPAAEL	559	0.5000	5.68
23	FFGVRPHVV	448	0.4000	4.55
24	LVVGPSTEI	116	0.3000	3.41
25	MGAISMIGS	357	0.2800	3.18
26	YIAKYTICP	412	0.2800	3.18
27	LHDMGAISM	354	-0.0200	0
28	LPLNDALPS	534	-0.2000	0
29	LAVADVAGV	239	-0.3000	0
30	LLVEVTEDR	27	-0.4000	0
31	IGKAGNPDI	100	-0.5000	0
32	LDGWPVNFA	190	-0.5500	0
33	ICPQIIVEA	144	-0.9000	0
34	WEQLRGGAS	212	-0.9000	0
35	VVLKGGAIA	455	-0.9000	0
36	LLGKGNTVN	199	-1.0000	0
37	IITVAAQPN	290	-1.0000	0
38	IRPSTIAAE	343	-1.0000	0
39	VRRYIAKYT	409	-1.0000	0
40	VHRDLVVGP	112	-1.1000	0
41	VAAQPNVLP	293	-1.1000	0

42	LAFAESRIR	336	-1.1000	0
43	IGSVEVGKL	430	-1.1000	0
44	VLRTWQTAH	377	-1.2200	0
45	IVEALAAGT	149	-1.3000	0
46	MLMVCHHLN	321	-1.3000	0
47	MVCHHLNPR	323	-1.3000	0
48	VGKLADLVL	435	-1.3000	0
49	VRAVGKTDL	526	-1.3000	0
50	IVGIGKAGN	97	-1.4000	0
51	LAAGTTTII	153	-1.4000	0
52	IIGGGTGPA	160	-1.4000	0
53	WPVNFALLG	193	-1.4000	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	IRLADTNLL	20	5.8000	61.70
2	IVTAGTVDC	131	3.9000	41.49
3	LRTWQTAHV	378	3.6500	38.83
4	LDMLMVCHH	319	3.3000	35.11
5	ISMIGSDSQ	360	3.3000	35.11
6	IRPSTIAAE	343	3.0000	31.91
7	VRPHVVLKG	451	3.0000	31.91
8	LVLWEPAFF	441	2.9500	31.38
9	VAGVQVALH	244	2.9000	30.85
10	VLPSSTNPT	299	2.9000	30.85
11	VHLICPQII	141	2.6000	27.66
12	VRIDGQVWQ	552	2.3000	24.47
13	VVGPSTEII	117	2.1000	22.34
14	MIGSDSQAM	362	2.1000	22.34
15	LHDMGAISM	354	2.0800	22.13
16	LLGKGNTVN	199	2.0000	21.28
17	IITVAAQPN	290	2.0000	21.28

18	YTICPAIAH	416	1.8800	20.00
19	WQTAHVMKA	381	1.8000	19.15
20	VHFVAPQSI	498	1.8000	19.15
21	MLMVCHHLN	321	1.7000	18.09
22	IVGIGKAGN	97	1.6000	17.02
23	LARMLESLD	183	1.6000	17.02
24	IHAYHTEGA	274	1.6000	17.02
25	LVVGPSTEI	116	1.5000	15.96
26	LPSIEVDPD	540	1.5000	15.96
27	LNDALPSIE	536	1.3000	13.83
28	MGAISMIGS	357	1.2800	13.62
29	WGIIKADIG	83	1.2000	12.77
30	IAAEDVLHD	348	1.1000	11.70
31	LICPQIIVE	143	1.0800	11.49
32	LAVADVAGV	239	1.0000	10.64
33	VLRTWQTAH	377	1.0000	10.64
34	MFGAAAATA	485	1.0000	10.64
35	VRRYIAKYT	409	0.9000	9.57
36	IGSVEVGKL	430	0.9000	9.57
37	FVAPQSIDA	500	0.8800	9.36
38	LPLNDALPS	534	0.8000	8.51
39	IGKAGNPDI	100	0.7000	7.45
40	WHLARMLES	181	0.7000	7.45
41	VGKLADLVL	435	0.7000	7.45
42	VRAVGKTDL	526	0.7000	7.45
43	VITGAVIID	73	0.6800	7.23
44	LLVEVTEDR	27	0.6000	6.38
45	IVEALAAGT	149	0.6000	6.38
46	ICPAIAHGM	418	0.6000	6.38
47	VQVALHSDT	247	0.5000	5.32
48	WQPQPAAEL	559	0.5000	5.32
49	LDGWPVNFA	190	0.4500	4.79
50	VHRDLVVGP	112	0.3000	3.19
51	VAAQPNVLP	293	0.3000	3.19

52	LEGDPSGSQ	394	0.3000	3.19
53	ITGAVIIDY	74	0.2800	2.98
54	MDHLIGSVE	426	0.2000	2.13
55	VLWEPAFFG	442	0.1500	1.60
56	ICPQIIVEA	144	0.1000	1.06
57	VVLKGGAIA	455	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	IRLADTNLL	20	4.6600	51.78
2	LLVEVTEDR	27	4.6000	51.11
3	VRPHVVLKG	451	4.6000	51.11
4	MIGSDSQAM	362	3.2000	35.56
5	VLPSSTNPT	299	3.1000	34.44
6	IVTAGTVDC	131	3.0800	34.22
7	WGIIKADIG	83	2.9000	32.22
8	WQTAHVMKA	381	2.9000	32.22
9	VHRDLVVGP	112	2.5800	28.67
10	WHLARMLES	181	2.5000	27.78
11	VRIDGQVWQ	552	2.4800	27.56
12	VVGPSTEII	117	2.4000	26.67
13	WQPQPAAEL	559	2.2600	25.11
14	VHLICPQII	141	2.2000	24.44
15	MVCHHLNPR	323	2.2000	24.44
16	LRTWQTAHV	378	2.2000	24.44
17	LPLNDALPS	534	2.2000	24.44
18	WPVNFALLG	193	2.0000	22.22
19	IRPSTIAAE	343	1.9000	21.11
20	FKLHEDWGS	222	1.8000	20.00
21	LVLWEPAFF	441	1.8000	20.00
22	FVAPQSIDA	500	1.5800	17.56
23	LVVGPSTEI	116	1.5000	16.67

24	FVEDTIGAI	261	1.5000	16.67
25	VCHHLNPRI	324	1.5000	16.67
26	IAAEDVLHD	348	1.5000	16.67
27	IIVEALAAG	148	1.4000	15.56
28	YHTEGAGGG	277	1.4000	15.56
29	ISMIGSDSQ	360	1.4000	15.56
30	VIIDYWGII	78	1.3000	14.44
31	VLHDMGAIS	353	1.2000	13.33
32	LAGDEAVFG	41	1.0800	12.00
33	YIAKYTICP	412	1.0800	12.00
34	YTICPAIAH	416	1.0800	12.00
35	VLWEPAFFG	442	0.9000	10.00
36	VAAQPNVLP	293	0.8800	9.78
37	WGSTPAAID	228	0.8000	8.89
38	IGKAGNPDI	100	0.7000	7.78
39	LAVADVAGV	239	0.7000	7.78
40	LPSSTNPTR	300	0.6000	6.67
41	LHDMGAISM	354	0.5800	6.44
42	FGGGKVLRE	48	0.4000	4.44
43	LHSDTLNET	251	0.4000	4.44
44	ICPAIAHGM	418	0.4000	4.44
45	FFGVRPHVV	448	0.4000	4.44
46	FGAAAATAA	486	0.4000	4.44
47	MGAISMIGS	357	0.3800	4.22
48	YGPTTGDRI	12	0.3000	3.33
49	IHAYHTEGA	274	0.3000	3.33
50	LDMLMVCHH	319	0.3000	3.33
51	VHFVAPQSI	498	0.3000	3.33
52	VLRESMGQG	53	0.2000	2.22
53	LEGDPSGSQ	394	0.2000	2.22
54	VAPQSIDAR	501	0.2000	2.22
55	LAFAESRIR	336	0.1000	1.11
56	ICPQIIVEA	144	0.0800	0.89

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	IRLADTNLL	20	4.8000	54.55
2	IVTAGTVDC	131	3.9000	44.32
3	LRTWQTAHV	378	3.3500	38.07
4	ISMIGSDSQ	360	2.5000	28.41
5	VHLICPQII	141	2.4000	27.27
6	LDMLMVCHH	319	2.0800	23.64
7	LVLWEPAFF	441	2.0500	23.30
8	VLPSSTNPT	299	2.0000	22.73
9	VVGPSTEII	117	1.9000	21.59
10	WQTAHVMKA	381	1.8000	20.45
11	VRPHVVLKG	451	1.7000	19.32
12	VAGVQVALH	244	1.6800	19.09
13	IHAYHTEGA	274	1.6000	18.18
14	VHFVAPQSI	498	1.6000	18.18
15	VRIDGQVWQ	552	1.5000	17.05
16	LVVGPSTEI	116	1.3000	14.77
17	MGAISMIGS	357	1.2800	14.55
18	MIGSDSQAM	362	1.0000	11.36
19	MFGAAAATA	485	1.0000	11.36
20	LHDMGAISM	354	0.9800	11.14
21	FVAPQSIDA	500	0.8800	10.00
22	LPLNDALPS	534	0.8000	9.09
23	WHLARMLES	181	0.7000	7.95
24	LAVADVAGV	239	0.7000	7.95
25	YTICPAIAH	416	0.6600	7.50
26	LLVEVTEDR	27	0.6000	6.82
27	IGKAGNPDI	100	0.5000	5.68
28	LDGWPVNFA	190	0.4500	5.11
29	ICPQIIVEA	144	0.1000	1.14
30	VVLKGGAIA	455	0.1000	1.14

31	WGIIKADIG	83	-0.1000	0
32	VHRDLVVGP	112	-0.1000	0
33	VAAQPNVLP	293	-0.1000	0
34	LAFAESRIR	336	-0.1000	0
35	IGSVEVGKL	430	-0.1000	0
36	FGAAAATAA	486	-0.1000	0
37	VLRTWQTAH	377	-0.2200	0
38	IVEALAAGT	149	-0.3000	0
39	MLMVCHHLN	321	-0.3000	0
40	MVCHHLNPR	323	-0.3000	0
41	VGKLADLVL	435	-0.3000	0
42	WAAMGDANA	464	-0.3000	0
43	VRAVGKTDL	526	-0.3000	0
44	IVGIGKAGN	97	-0.4000	0
45	LAAGTTTII	153	-0.4000	0
46	IIGGGTGPA	160	-0.4000	0
47	VQVALHSDT	247	-0.4000	0
48	LAPVADVRA	520	-0.4000	0
49	LYGPTTGDR	11	-0.5000	0
50	LRGGASGFK	215	-0.5000	0
51	VVLRTWQTA	376	-0.5000	0
52	LEGDPSGSQ	394	-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	IRLADTNLL	20	3.7000	43.02
2	VRPHVVLKG	451	3.2000	37.21
3	VRIDGQVWQ	552	3.1800	36.98
4	LLVEVTEDR	27	3.1000	36.05
5	IVTAGTVDC	131	3.0800	35.81
6	WQTAHVMKA	381	2.9000	33.72
7	VLPSSTNPT	299	2.4000	27.91

8	WHLARMLES	181	2.1000	24.42
9	ISMIGSDSQ	360	2.1000	24.42
10	LPLNDALPS	534	1.8000	20.93
11	MIGSDSQAM	362	1.7000	19.77
12	YTICPAIAH	416	1.6600	19.30
13	VHRDLVVGP	112	1.5800	18.37
14	FVAPQSIDA	500	1.5800	18.37
15	WGIIKADIG	83	1.5000	17.44
16	VVGPSTEII	117	1.5000	17.44
17	FKLHEDWGS	222	1.4000	16.28
18	VHLICPQII	141	1.3000	15.12
19	WQPQPAAEL	559	1.3000	15.12
20	LRTWQTAHV	378	1.2000	13.95
21	LEGDPSGSQ	394	0.9000	10.47
22	LDMLMVCHH	319	0.8800	10.23
23	VLHDMGAIS	353	0.8000	9.30
24	MVCHHLNPR	323	0.7000	8.14
25	LVVGPSTEI	116	0.6000	6.98
26	WPVNFALLG	193	0.6000	6.98
27	FVEDTIGAI	261	0.6000	6.98
28	VCHHLNPRI	324	0.6000	6.98
29	IRPSTIAAE	343	0.5000	5.81
30	VIIDYWGII	78	0.4000	4.65
31	IAAEDVLHD	348	0.4000	4.65
32	FGAAAATAA	486	0.4000	4.65
33	IHAYHTEGA	274	0.3000	3.49
34	ICPQIIVEA	144	0.0800	0.93
35	YIAKYTICP	412	0.0800	0.93
36	MGAISMIGS	357	-0.0200	0
37	LVLWEPAFF	441	-0.1000	0
38	VAAQPNVLP	293	-0.1200	0
39	VLRTWQTAH	377	-0.1200	0
40	IGKAGNPDI	100	-0.2000	0
41	WAAMGDANA	464	-0.2000	0

42	WGSTPAAID	228	-0.3000	0
43	LAVADVAGV	239	-0.3000	0
44	LHSDTLNET	251	-0.3000	0
45	LAGDEAVFG	41	-0.3200	0
46	VNPDALWEQ	206	-0.5000	0
47	VLWEPAFFG	442	-0.5000	0
48	YGPTTGDRI	12	-0.6000	0
49	FFGVRPHVV	448	-0.6000	0
50	VHFVAPQSI	498	-0.6000	0
51	IIGGGTGPA	160	-0.7000	0
52	VAGVQVALH	244	-0.7200	0
53	LRGGASGFK	215	-0.8000	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	IRLADTNLL	20	6.9200	59.66
2	VHLICPQII	141	5.9000	50.86
3	MIGSDSQAM	362	5.5000	47.41
4	VHFVAPQSI	498	5.5000	47.41
5	LVVGPSTEI	116	5.4000	46.55
6	VRAVGKTDL	526	5.3000	45.69
7	LPMTQRYFL	567	5.3000	45.69
8	VVGPSTEII	117	4.3200	37.24
9	FFGVRPHVV	448	4.3000	37.07
10	IGAIAGRSI	266	4.1000	35.34
11	IGSVEVGKL	430	4.1000	35.34
12	FGVRPHVVL	449	4.1000	35.34
13	FVAPQSIDA	500	3.9000	33.62
14	YGPTTGDRI	12	3.7000	31.90
15	YTICPAIAH	416	3.7000	31.90
16	MGRVGEVVL	370	3.6000	31.03
17	VLPSSTNPT	299	3.5200	30.34

18	YWGIIKADI	82	3.5000	30.17
19	WQPQPAAEL	559	3.4000	29.31
20	IRDGRIVGI	92	3.3000	28.45
21	VRPHVVLKG	451	3.3000	28.45
22	WQTAHVMKA	381	3.1000	26.72
23	WHLARMLES	181	2.9000	25.00
24	LNPRIPEDL	328	2.8000	24.14
25	IVTAGTVDC	131	2.6200	22.59
26	LVLWEPAFF	441	2.6000	22.41
27	VIIDYWGII	78	2.5000	21.55
28	LHDMGAISM	354	2.5000	21.55
29	VMKARRGAL	386	2.4000	20.69
30	IMTGVHRDL	108	2.3000	19.83
31	ITGAVIIDY	74	2.2000	18.97
32	FVEDTIGAI	261	2.2000	18.97
33	IRPSTIAAE	343	2.2000	18.97
34	ICPAIAHGM	418	2.2000	18.97
35	LAAGTTTII	153	2.1200	18.28
36	IGKAGNPDI	100	2.1000	18.10
37	VLKGGAIAW	456	2.1000	18.10
38	LRTWQTAHV	378	2.0200	17.41
39	IGIRDGRIV	90	2.0000	17.24
40	MLMVCHHLN	321	1.9000	16.38
41	VCHHLNPRI	324	1.9000	16.38
42	MGAISMIGS	357	1.9000	16.38
43	VRRYIAKYT	409	1.9000	16.38
44	VGKLADLVL	435	1.8000	15.52
45	VLRTWQTAH	377	1.7000	14.66
46	FGGGKVLRE	48	1.6000	13.79
47	LAVADVAGV	239	1.6000	13.79
48	VADVAGVQV	241	1.6000	13.79
49	IITVAAQPN	290	1.6000	13.79
50	YIAKYTICP	412	1.5200	13.10
51	LMVCHHLNP	322	1.4000	12.07

52	FGAAAATAA	486	1.4000	12.07
53	LESLDGWPV	187	1.3000	11.21
54	LRESMGQGR	54	1.2000	10.34
55	WGIIKADIG	83	1.2000	10.34
56	VVLRTWQTA	376	1.2000	10.34
57	VEVGKLADL	433	1.0000	8.62

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	IRLADTNLL	20	6.9200	59.66
2	VHLICPQII	141	5.9000	50.86
3	MIGSDSQAM	362	5.5000	47.41
4	VHFVAPQSI	498	5.5000	47.41
5	LVVGPSTEI	116	5.4000	46.55
6	VRAVGKTDL	526	5.3000	45.69
7	LPMTQRYFL	567	5.3000	45.69
8	VVGPSTEII	117	4.3200	37.24
9	FFGVRPHVV	448	4.3000	37.07
10	IGAIAGRSI	266	4.1000	35.34
11	IGSVEVGKL	430	4.1000	35.34
12	FGVRPHVVL	449	4.1000	35.34
13	FVAPQSIDA	500	3.9000	33.62
14	YGPTTGDRI	12	3.7000	31.90
15	YTICPAIAH	416	3.7000	31.90
16	MGRVGEVVL	370	3.6000	31.03
17	VLPSSTNPT	299	3.5200	30.34
18	YWGIIKADI	82	3.5000	30.17
19	WQPQPAAEL	559	3.4000	29.31
20	IRDGRIVGI	92	3.3000	28.45
21	VRPHVVLKG	451	3.3000	28.45
22	WQTAHVMKA	381	3.1000	26.72
23	WHLARMLES	181	2.9000	25.00

24	LNPRIPEDL	328	2.8000	24.14
25	IVTAGTVDC	131	2.6200	22.59
26	LVLWEPAFF	441	2.6000	22.41
27	VIIDYWGII	78	2.5000	21.55
28	LHDMGAISM	354	2.5000	21.55
29	VMKARRGAL	386	2.4000	20.69
30	IMTGVHRDL	108	2.3000	19.83
31	ITGAVIIDY	74	2.2000	18.97
32	FVEDTIGAI	261	2.2000	18.97
33	IRPSTIAAE	343	2.2000	18.97
34	ICPAIAHGM	418	2.2000	18.97
35	LAAGTTTII	153	2.1200	18.28
36	IGKAGNPDI	100	2.1000	18.10
37	VLKGGAIAW	456	2.1000	18.10
38	LRTWQTAHV	378	2.0200	17.41
39	IGIRDGRIV	90	2.0000	17.24
40	MLMVCHHLN	321	1.9000	16.38
41	VCHHLNPRI	324	1.9000	16.38
42	MGAISMIGS	357	1.9000	16.38
43	VRRYIAKYT	409	1.9000	16.38
44	VGKLADLVL	435	1.8000	15.52
45	VLRTWQTAH	377	1.7000	14.66
46	FGGGKVLRE	48	1.6000	13.79
47	LAVADVAGV	239	1.6000	13.79
48	VADVAGVQV	241	1.6000	13.79
49	IITVAAQPN	290	1.6000	13.79
50	YIAKYTICP	412	1.5200	13.10
51	LMVCHHLNP	322	1.4000	12.07
52	FGAAAATAA	486	1.4000	12.07
53	LESLDGWPV	187	1.3000	11.21
54	LRESMGQGR	54	1.2000	10.34
55	WGIIKADIG	83	1.2000	10.34
56	VVLRTWQTA	376	1.2000	10.34
57	VEVGKLADL	433	1.0000	8.62

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	VVLKGGAIA	455	3.7000	43.02
2	IVGIGKAGN	97	3.5000	40.70
3	MKARRGALE	387	3.0000	34.88
4	VRRYIAKYT	409	3.0000	34.88
5	IRPSTIAAE	343	2.5000	29.07
6	YIAKYTICP	412	2.5000	29.07
7	LVLWEPAFF	441	2.5000	29.07
8	LDMLMVCHH	319	2.3000	26.74
9	FALLGKGNT	197	2.2000	25.58
10	WQTAHVMKA	381	2.1000	24.42
11	FGVRPHVVL	449	2.1000	24.42
12	VAGVQVALH	244	2.0000	23.26
13	YTICPAIAH	416	2.0000	23.26
14	FGGGKVLRE	48	1.9000	22.09
15	IAKYTICPA	413	1.9000	22.09
16	VVLRTWQTA	376	1.8000	20.93
17	IRLADTNLL	20	1.7000	19.77
18	VRPHVVLKG	451	1.7000	19.77
19	YWGIIKADI	82	1.6000	18.60
20	IGIRDGRIV	90	1.6000	18.60
21	LRTWQTAHV	378	1.6000	18.60
22	VRIDGQVWQ	552	1.6000	18.60
23	IAGRSIHAY	269	1.4000	16.28
24	WHLARMLES	181	1.3000	15.12
25	MLMVCHHLN	321	1.3000	15.12
26	IVTAGTVDC	131	0.8000	9.30
27	VLPRPMFGA	480	0.8000	9.30
28	WGSTPAAID	228	0.7000	8.14
29	IGSVEVGKL	430	0.7000	8.14
30	VNFALLGKG	195	0.6000	6.98

31	VMKARRGAL	386	0.6000	6.98
32	VITGAVIID	73	0.5000	5.81
33	LNPRIPEDL	328	0.5000	5.81
34	FFGVRPHVV	448	0.5000	5.81
35	WQPQPAAEL	559	0.5000	5.81
36	IHAYHTEGA	274	0.4000	4.65
37	VRAVGKTDL	526	0.4000	4.65
38	VHLICPQII	141	0.3000	3.49
39	LICPQIIVE	143	0.3000	3.49
40	WEQLRGGAS	212	0.3000	3.49
41	LAVADVAGV	239	0.3000	3.49
42	WGIIKADIG	83	0.2000	2.33
43	FVAPQSIDA	500	0.2000	2.33
44	IIVEALAAG	148	0.1000	1.16
45	LLGKGNTVN	199	0.1000	1.16
46	VHFVAPQSI	498	0.1000	1.16
47	IAAEDVLHD	348	-0.1000	0
48	LPLNDALPS	534	-0.1000	0
49	IITVAAQPN	290	-0.2000	0
50	LHDMGAISM	354	-0.2000	0
51	VWQPQPAAE	558	-0.3000	0
52	IVEALAAGT	149	-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	VVLKGGAIA	455	3.7000	46.25
2	WQTAHVMKA	381	2.1000	26.25
3	VRRYIAKYT	409	2.1000	26.25
4	YIAKYTICP	412	2.1000	26.25
5	IAKYTICPA	413	1.9000	23.75
6	VVLRTWQTA	376	1.8000	22.50
7	LVLWEPAFF	441	1.6000	20.00

8	IVGIGKAGN	97	1.5000	18.75
9	YWGIIKADI	82	1.4000	17.50
10	IGIRDGRIV	90	1.3000	16.25
11	WHLARMLES	181	1.3000	16.25
12	FALLGKGNT	197	1.3000	16.25
13	LRTWQTAHV	378	1.3000	16.25
14	FGVRPHVVL	449	1.1000	13.75
15	LDMLMVCHH	319	1.0800	13.50
16	IVTAGTVDC	131	0.8000	10.00
17	VLPRPMFGA	480	0.8000	10.00
18	VRIDGQVWQ	552	0.8000	10.00
19	VAGVQVALH	244	0.7800	9.75
20	YTICPAIAH	416	0.7800	9.75
21	IRLADTNLL	20	0.7000	8.75
22	IHAYHTEGA	274	0.4000	5.00
23	VRPHVVLKG	451	0.4000	5.00
24	WEQLRGGAS	212	0.3000	3.75
25	IAGRSIHAY	269	0.3000	3.75
26	FFGVRPHVV	448	0.2000	2.50
27	FVAPQSIDA	500	0.2000	2.50
28	VHLICPQII	141	0.1000	1.25
29	VHFVAPQSI	498	-0.1000	0
30	LPLNDALPS	534	-0.1000	0
31	FVEDTIGAI	261	-0.2000	0
32	IGSVEVGKL	430	-0.3000	0
33	IIGGGTGPA	160	-0.4000	0
34	VMKARRGAL	386	-0.4000	0
35	LRGGASGFK	215	-0.5000	0
36	LNPRIPEDL	328	-0.5000	0
37	IRPSTIAAE	343	-0.5000	0
38	WQPQPAAEL	559	-0.5000	0
39	VRAVGKTDL	526	-0.6000	0
40	IIKADIGIR	85	-0.7000	0
41	VNFALLGKG	195	-0.7000	0

42	MLMVCHHLN	321	-0.7000	0
43	IIDYWGIIK	79	-0.8000	0
44	VLHDMGAIS	353	-0.8000	0
45	FTVRIDGQV	550	-0.8000	0
46	IISGNRRIV	124	-1.0000	0
47	WAAMGDANA	464	-1.0000	0
48	FGGGKVLRE	48	-1.1000	0
49	WGIIKADIG	83	-1.1000	0
50	LMVCHHLNP	322	-1.1000	0
51	IIVEALAAG	148	-1.2000	0
52	MGAISMIGS	357	-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	VVLKGGAIA	455	4.7000	58.75
2	VRRYIAKYT	409	3.1000	38.75
3	IAKYTICPA	413	2.9000	36.25
4	VVLRTWQTA	376	2.8000	35.00
5	LVLWEPAFF	441	2.6000	32.50
6	IVGIGKAGN	97	2.5000	31.25
7	IGIRDGRIV	90	2.3000	28.75
8	LRTWQTAHV	378	2.3000	28.75
9	LDMLMVCHH	319	2.0800	26.00
10	IVTAGTVDC	131	1.8000	22.50
11	VLPRPMFGA	480	1.8000	22.50
12	VRIDGQVWQ	552	1.8000	22.50
13	VAGVQVALH	244	1.7800	22.25
14	IRLADTNLL	20	1.7000	21.25
15	IHAYHTEGA	274	1.4000	17.50
16	VRPHVVLKG	451	1.4000	17.50
17	IAGRSIHAY	269	1.3000	16.25
18	VHLICPQII	141	1.1000	13.75

19	WQTAHVMKA	381	1.1000	13.75
20	YIAKYTICP	412	1.1000	13.75
21	LAVADVAGV	239	1.0000	12.50
22	MKARRGALE	387	1.0000	12.50
23	LKGGAIAWA	457	1.0000	12.50
24	MFGAAAATA	485	1.0000	12.50
25	VHFVAPQSI	498	0.9000	11.25
26	LPLNDALPS	534	0.9000	11.25
27	IGSVEVGKL	430	0.7000	8.75
28	IIGGGTGPA	160	0.6000	7.50
29	VMKARRGAL	386	0.6000	7.50
30	LRGGASGFK	215	0.5000	6.25
31	LNPRIPEDL	328	0.5000	6.25
32	IRPSTIAAE	343	0.5000	6.25
33	YWGIIKADI	82	0.4000	5.00
34	VRAVGKTDL	526	0.4000	5.00
35	IIKADIGIR	85	0.3000	3.75
36	WHLARMLES	181	0.3000	3.75
37	VNFALLGKG	195	0.3000	3.75
38	FALLGKGNT	197	0.3000	3.75
39	MLMVCHHLN	321	0.3000	3.75
40	IIDYWGIIK	79	0.2000	2.50
41	VLHDMGAIS	353	0.2000	2.50
42	FGVRPHVVL	449	0.1000	1.25
43	LMVCHHLNP	322	-0.1000	0
44	IIVEALAAG	148	-0.2000	0
45	MGAISMIGS	357	-0.2000	0
46	YTICPAIAH	416	-0.2200	0
47	IVEALAAGT	149	-0.3000	0
48	LHDMGAISM	354	-0.3000	0
49	VNPDALWEQ	206	-0.4000	0
50	LYGPTTGDR	11	-0.6000	0
51	VIIDYWGII	78	-0.6000	0
52	IDYWGIIKA	80	-0.6000	0

53	VVGPSTEII	117	-0.6000	0
54	ISMIGSDSQ	360	-0.6000	0
55	VHRDLVVGP	112	-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	VVLKGGAIA	455	4.7000	54.65
2	IVGIGKAGN	97	4.5000	52.33
3	MKARRGALE	387	4.0000	46.51
4	VRRYIAKYT	409	4.0000	46.51
5	IRPSTIAAE	343	3.5000	40.70
6	LVLWEPAFF	441	3.5000	40.70
7	LDMLMVCHH	319	3.3000	38.37
8	VAGVQVALH	244	3.0000	34.88
9	IAKYTICPA	413	2.9000	33.72
10	VVLRTWQTA	376	2.8000	32.56
11	IRLADTNLL	20	2.7000	31.40
12	VRPHVVLKG	451	2.7000	31.40
13	IGIRDGRIV	90	2.6000	30.23
14	LRTWQTAHV	378	2.6000	30.23
15	VRIDGQVWQ	552	2.6000	30.23
16	IAGRSIHAY	269	2.4000	27.91
17	MLMVCHHLN	321	2.3000	26.74
18	IVTAGTVDC	131	1.8000	20.93
19	VLPRPMFGA	480	1.8000	20.93
20	IGSVEVGKL	430	1.7000	19.77
21	VNFALLGKG	195	1.6000	18.60
22	VMKARRGAL	386	1.6000	18.60
23	VITGAVIID	73	1.5000	17.44
24	LNPRIPEDL	328	1.5000	17.44
25	YIAKYTICP	412	1.5000	17.44
26	IHAYHTEGA	274	1.4000	16.28

27	VRAVGKTDL	526	1.4000	16.28
28	VHLICPQII	141	1.3000	15.12
29	LICPQIIVE	143	1.3000	15.12
30	LAVADVAGV	239	1.3000	15.12
31	FALLGKGNT	197	1.2000	13.95
32	IIVEALAAG	148	1.1000	12.79
33	LLGKGNTVN	199	1.1000	12.79
34	WQTAHVMKA	381	1.1000	12.79
35	FGVRPHVVL	449	1.1000	12.79
36	VHFVAPQSI	498	1.1000	12.79
37	YTICPAIAH	416	1.0000	11.63
38	LKGGAIAWA	457	1.0000	11.63
39	MFGAAAATA	485	1.0000	11.63
40	FGGGKVLRE	48	0.9000	10.47
41	IAAEDVLHD	348	0.9000	10.47
42	LPLNDALPS	534	0.9000	10.47
43	IITVAAQPN	290	0.8000	9.30
44	LHDMGAISM	354	0.8000	9.30
45	VWQPQPAAE	558	0.7000	8.14
46	YWGIIKADI	82	0.6000	6.98
47	IVEALAAGT	149	0.6000	6.98
48	IIGGGTGPA	160	0.6000	6.98
49	LARMLESLD	183	0.4000	4.65
50	VNPDALWEQ	206	0.4000	4.65
51	IIKADIGIR	85	0.3000	3.49
52	IISGNRRIV	124	0.3000	3.49
53	WHLARMLES	181	0.3000	3.49
54	LMVCHHLNP	322	0.3000	3.49
55	ITGAVIIDY	74	0.2000	2.33
56	VNTLDEHLD	312	0.2000	2.33
57	VLHDMGAIS	353	0.2000	2.33

ALLELE: DRB1_0813	Threshold for 3 % with score:	Highest Score achievable by any peptide:

	1.9	8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLKGGAIA	455	3.7000	42.53
2	WQTAHVMKA	381	3.1000	35.63
3	YIAKYTICP	412	2.9800	34.25
4	VVLRTWQTA	376	2.8000	32.18
5	IRLADTNLL	20	2.7000	31.03
6	VRAVGKTDL	526	2.2000	25.29
7	IHAYHTEGA	274	2.1000	24.14
8	FGVRPHVVL	449	2.1000	24.14
9	WHLARMLES	181	1.9000	21.84
10	IAKYTICPA	413	1.9000	21.84
11	IVTAGTVDC	131	1.8000	20.69
12	VRIDGQVWQ	552	1.8000	20.69
13	YTICPAIAH	416	1.6600	19.08
14	VLPRPMFGA	480	1.6500	18.97
15	VRRYIAKYT	409	1.6000	18.39
16	LVLWEPAFF	441	1.6000	18.39
17	IVGIGKAGN	97	1.5000	17.24
18	YWGIIKADI	82	1.4000	16.09
19	LRTWQTAHV	378	1.3000	14.94
20	LNPRIPEDL	328	1.2000	13.79
21	VHLICPQII	141	1.1000	12.64
22	LDMLMVCHH	319	1.0800	12.41
23	FVAPQSIDA	500	1.0800	12.41
24	IGIRDGRIV	90	1.0000	11.49
25	VRPHVVLKG	451	1.0000	11.49
26	LLGKGNTVN	199	0.9000	10.34
27	FGAAAATAA	486	0.9000	10.34
28	VHFVAPQSI	498	0.9000	10.34
29	IAGRSIHAY	269	0.8000	9.20
30	VAGVQVALH	244	0.7800	8.97
31	FFGVRPHVV	448	0.7000	8.05
32	LVVGPSTEI	116	0.6000	6.90

33	FALLGKGNT	197	0.6000	6.90
34	LPLNDALPS	534	0.5000	5.75
35	WGIIKADIG	83	0.1000	1.15
36	VVGPSTEII	117	0.1000	1.15
37	IIDYWGIIK	79	0.0800	0.92
38	VQVALHSDT	247	-0.1000	0
39	VLRTWQTAH	377	-0.1200	0
40	LDGWPVNFA	190	-0.2000	0
41	MLMVCHHLN	321	-0.2000	0
42	MARLSRERY	0	-0.3000	0
43	MGAISMIGS	357	-0.3200	0
44	WEQLRGGAS	212	-0.4000	0
45	VLPSSTNPT	299	-0.4000	0
46	ISMIGSDSQ	360	-0.4000	0
47	LHDMGAISM	354	-0.4200	0
48	FGGGKVLRE	48	-0.5000	0
49	LMVCHHLNP	322	-0.5000	0
50	IRPSTIAAE	343	-0.5000	0
51	WQPQPAAEL	559	-0.5000	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	YIAKYTICP	412	4.1000	40.59
2	FGGGKVLRE	48	3.7000	36.63
3	WQTAHVMKA	381	3.7000	36.63
4	VVLKGGAIA	455	3.7000	36.63
5	VRRYIAKYT	409	3.6000	35.64
6	YTICPAIAH	416	3.6000	35.64
7	IVGIGKAGN	97	3.5000	34.65
8	VRPHVVLKG	451	3.5000	34.65
9	WHLARMLES	181	3.1000	30.69
10	MKARRGALE	387	3.0000	29.70

11	FGVRPHVVL	449	2.6000	25.74
12	IRPSTIAAE	343	2.5000	24.75
13	LVLWEPAFF	441	2.5000	24.75
14	FALLGKGNT	197	2.3000	22.77
15	LDMLMVCHH	319	2.3000	22.77
16	VITGAVIID	73	2.1000	20.79
17	IAGRSIHAY	269	2.1000	20.79
18	VRIDGQVWQ	552	2.1000	20.79
19	IRLADTNLL	20	2.0000	19.80
20	VAGVQVALH	244	2.0000	19.80
21	MLMVCHHLN	321	2.0000	19.80
22	LICPQIIVE	143	1.9000	18.81
23	VVLRTWQTA	376	1.9000	18.81
24	IAKYTICPA	413	1.9000	18.81
25	IGIRDGRIV	90	1.8000	17.82
26	WPVNFALLG	193	1.8000	17.82
27	FVAPQSIDA	500	1.8000	17.82
28	IAAEDVLHD	348	1.7000	16.83
29	LPLNDALPS	534	1.7000	16.83
30	YWGIIKADI	82	1.6000	15.84
31	LNPRIPEDL	328	1.6000	15.84
32	LRTWQTAHV	378	1.6000	15.84
33	IHAYHTEGA	274	1.5000	14.85
34	VRAVGKTDL	526	1.5000	14.85
35	LHDMGAISM	354	1.4000	13.86
36	IVTAGTVDC	131	1.3000	12.87
37	VLPRPMFGA	480	1.3000	12.87
38	LLGKGNTVN	199	1.2000	11.88
39	FFGVRPHVV	448	1.2000	11.88
40	LMVCHHLNP	322	1.1000	10.89
41	ITGAVIIDY	74	0.8000	7.92
42	IGSVEVGKL	430	0.8000	7.92
43	VNFALLGKG	195	0.7000	6.93
44	WGSTPAAID	228	0.7000	6.93

45	VMKARRGAL	386	0.7000	6.93
46	WQPQPAAEL	559	0.5000	4.95
47	ISGNRRIVT	125	0.4000	3.96
48	VHLICPQII	141	0.4000	3.96
49	WEQLRGGAS	212	0.4000	3.96
50	MGAISMIGS	357	0.4000	3.96
51	LAVADVAGV	239	0.3000	2.97
52	MARLSRERY	0	0.2000	1.98
53	IKADIGIRD	86	0.2000	1.98
54	VNPDALWEQ	206	0.2000	1.98
55	VHFVAPQSI	498	0.2000	1.98
56	IIDYWGIIK	79	0.1000	0.99
57	IIVEALAAG	148	0.1000	0.99

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	WQTAHVMKA	381	3.7000	44.58
2	WHLARMLES	181	3.1000	37.35
3	VRPHVVLKG	451	2.6000	31.33
4	YTICPAIAH	416	2.3800	28.67
5	IVGIGKAGN	97	2.1000	25.30
6	YWGIIKADI	82	2.0000	24.10
7	FALLGKGNT	197	1.8000	21.69
8	LPLNDALPS	534	1.7000	20.48
9	LVLWEPAFF	441	1.5000	18.07
10	LDMLMVCHH	319	1.4800	17.83
11	IVTAGTVDC	131	1.3000	15.66
12	LRTWQTAHV	378	1.2000	14.46
13	FVAPQSIDA	500	1.1000	13.25
14	IRLADTNLL	20	1.0000	12.05
15	MGAISMIGS	357	1.0000	12.05
16	FFGVRPHVV	448	1.0000	12.05

17	YIAKYTICP	412	0.9000	10.84
18	VVLKGGAIA	455	0.9000	10.84
19	VAGVQVALH	244	0.8800	10.60
20	VHLICPQII	141	0.8000	9.64
21	WEQLRGGAS	212	0.8000	9.64
22	LMVCHHLNP	322	0.7000	8.43
23	VRAVGKTDL	526	0.6000	7.23
24	VRIDGQVWQ	552	0.6000	7.23
25	WPVNFALLG	193	0.5000	6.02
26	MLMVCHHLN	321	0.1000	1.20
27	VHFVAPQSI	498	0.1000	1.20
28	WQPQPAAEL	559	0.1000	1.20
29	IDYWGIIKA	80	-0.1000	0
30	LHDMGAISM	354	-0.1000	0
31	IGSVEVGKL	430	-0.1000	0
32	IRPSTIAAE	343	-0.2000	0
33	VRRYIAKYT	409	-0.2000	0
34	ITGAVIIDY	74	-0.3000	0
35	VMKARRGAL	386	-0.3000	0
36	MARLSRERY	0	-0.5000	0
37	ISGNRRIVT	125	-0.5000	0
38	IIKADIGIR	85	-0.6000	0
39	VNFALLGKG	195	-0.6000	0
40	FKLHEDWGS	222	-0.6000	0
41	LKGGAIAWA	457	-0.7000	0
42	WGIIKADIG	83	-0.8000	0
43	VGPSTEIIS	118	-0.8000	0
44	FVEDTIGAI	261	-0.8000	0
45	FGAAAATAA	486	-0.8000	0
46	YAQLYGPTT	8	-0.8500	0
47	FAESRIRPS	338	-0.9000	0
48	ICPQIIVEA	144	-1.0000	0
49	IIGGGTGPA	160	-1.0000	0
50	IGAIAGRSI	266	-1.0000	0

51	IAKYTICPA	413	-1.0000	0
52	LAVNRGLAP	514	-1.0000	0
53	LRGGASGFK	215	-1.1000	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	VRPHVVLKG	451	4.6000	54.76
2	LVLWEPAFF	441	3.3000	39.29
3	VVLKGGAIA	455	3.2000	38.10
4	IRLADTNLL	20	3.1000	36.90
5	LRTWQTAHV	378	3.0000	35.71
6	MVCHHLNPR	323	2.9000	34.52
7	IVTAGTVDC	131	2.8000	33.33
8	VRIDGQVWQ	552	2.4000	28.57
9	VRRYIAKYT	409	2.1000	25.00
10	IGIRDGRIV	90	2.0000	23.81
11	LDMLMVCHH	319	1.7800	21.19
12	LPLNDALPS	534	1.7000	20.24
13	IVGIGKAGN	97	1.6000	19.05
14	ICPQIIVEA	144	1.5000	17.86
15	VVLRTWQTA	376	1.5000	17.86
16	WQTAHVMKA	381	1.4000	16.67
17	IISGNRRIV	124	1.3000	15.48
18	FKLHEDWGS	222	1.3000	15.48
19	VLPRPMFGA	480	1.2000	14.29
20	IAKYTICPA	413	1.1000	13.10
21	VHLICPQII	141	1.0000	11.90
22	WHLARMLES	181	1.0000	11.90
23	LAVADVAGV	239	1.0000	11.90
24	IHAYHTEGA	274	1.0000	11.90
25	MFGAAAATA	485	1.0000	11.90
26	LDGWPVNFA	190	0.9000	10.71

27	LAFAESRIR	336	0.9000	10.71
28	IRPSTIAAE	343	0.9000	10.71
29	VNPDALWEQ	206	0.8000	9.52
30	VRAVGKTDL	526	0.7000	8.33
31	LMVCHHLNP	322	0.6000	7.14
32	VAGVQVALH	244	0.5800	6.90
33	VDCHVHLIC	137	0.5000	5.95
34	LKGGAIAWA	457	0.5000	5.95
35	VHFVAPQSI	498	0.5000	5.95
36	IDYWGIIKA	80	0.4000	4.76
37	IAGRSIHAY	269	0.4000	4.76
38	VLPSSTNPT	299	0.4000	4.76
39	VVGPSTEII	117	0.3000	3.57
40	MLMVCHHLN	321	0.3000	3.57
41	VCHHLNPRI	324	0.3000	3.57
42	ICPAIAHGM	418	0.2000	2.38
43	MARLSRERY	0	0.1000	1.19
44	IGAIAGRSI	266	0.1000	1.19
45	WQPQPAAEL	559	0.1000	1.19
46	YTICPAIAH	416	0.0800	0.95
47	VHRDLVVGP	112	-0.1000	0
48	YIAKYTICP	412	-0.1000	0
49	LVVGPSTEI	116	-0.2000	0
50	LNPRIPEDL	328	-0.2000	0
51	FAESRIRPS	338	-0.2000	0
52	VLHDMGAIS	353	-0.2000	0
53	MIGSDSQAM	362	-0.2000	0
54	VFGGGKVLR	47	-0.3000	0
55	IRDGRIVGI	92	-0.3000	0
56	IMTGVHRDL	108	-0.3000	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	VRPHVVLKG	451	3.6000	43.37
2	IVGIGKAGN	97	3.1000	37.35
3	WQTAHVMKA	381	2.7000	32.53
4	LPLNDALPS	534	2.7000	32.53
5	LVLWEPAFF	441	2.5000	30.12
6	LDMLMVCHH	319	2.4800	29.88
7	IVTAGTVDC	131	2.3000	27.71
8	LRTWQTAHV	378	2.2000	26.51
9	WHLARMLES	181	2.1000	25.30
10	IRLADTNLL	20	2.0000	24.10
11	MGAISMIGS	357	2.0000	24.10
12	VVLKGGAIA	455	1.9000	22.89
13	VAGVQVALH	244	1.8800	22.65
14	VHLICPQII	141	1.8000	21.69
15	LMVCHHLNP	322	1.7000	20.48
16	VRAVGKTDL	526	1.6000	19.28
17	VRIDGQVWQ	552	1.6000	19.28
18	YTICPAIAH	416	1.3800	16.63
19	MLMVCHHLN	321	1.1000	13.25
20	VHFVAPQSI	498	1.1000	13.25
21	YWGIIKADI	82	1.0000	12.05
22	LAVADVAGV	239	1.0000	12.05
23	MFGAAAATA	485	1.0000	12.05
24	IDYWGIIKA	80	0.9000	10.84
25	LHDMGAISM	354	0.9000	10.84
26	IGSVEVGKL	430	0.9000	10.84
27	FALLGKGNT	197	0.8000	9.64
28	IRPSTIAAE	343	0.8000	9.64
29	VRRYIAKYT	409	0.8000	9.64
30	ITGAVIIDY	74	0.7000	8.43
31	VMKARRGAL	386	0.7000	8.43
32	MARLSRERY	0	0.5000	6.02
33	ISGNRRIVT	125	0.5000	6.02

34	IIKADIGIR	85	0.4000	4.82
35	VNFALLGKG	195	0.4000	4.82
36	LKGGAIAWA	457	0.3000	3.61
37	VGPSTEIIS	118	0.2000	2.41
38	FVAPQSIDA	500	0.1000	1.20
39	LRGGASGFK	215	-0.1000	0
40	VVLRTWQTA	376	-0.1000	0
41	YIAKYTICP	412	-0.1000	0
42	LPMTQRYFL	567	-0.1000	0
43	VVGPSTEII	117	-0.2000	0
44	WEQLRGGAS	212	-0.2000	0
45	VNRGLAPVA	516	-0.2500	0
46	VITGAVIID	73	-0.3000	0
47	IVEALAAGT	149	-0.3000	0
48	VNPDALWEQ	206	-0.3000	0
49	MVCHHLNPR	323	-0.3000	0
50	ISMIGSDSQ	360	-0.3000	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	VRPHVVLKG	451	3.6000	43.37
2	IVGIGKAGN	97	3.1000	37.35
3	WQTAHVMKA	381	2.7000	32.53
4	LPLNDALPS	534	2.7000	32.53
5	LVLWEPAFF	441	2.5000	30.12
6	LDMLMVCHH	319	2.4800	29.88
7	IVTAGTVDC	131	2.3000	27.71
8	LRTWQTAHV	378	2.2000	26.51
9	WHLARMLES	181	2.1000	25.30
10	IRLADTNLL	20	2.0000	24.10
11	MGAISMIGS	357	2.0000	24.10
12	VVLKGGAIA	455	1.9000	22.89

13	VAGVQVALH	244	1.8800	22.65
14	VHLICPQII	141	1.8000	21.69
15	LMVCHHLNP	322	1.7000	20.48
16	VRAVGKTDL	526	1.6000	19.28
17	VRIDGQVWQ	552	1.6000	19.28
18	YTICPAIAH	416	1.3800	16.63
19	MLMVCHHLN	321	1.1000	13.25
20	VHFVAPQSI	498	1.1000	13.25
21	YWGIIKADI	82	1.0000	12.05
22	LAVADVAGV	239	1.0000	12.05
23	MFGAAAATA	485	1.0000	12.05
24	IDYWGIIKA	80	0.9000	10.84
25	LHDMGAISM	354	0.9000	10.84
26	IGSVEVGKL	430	0.9000	10.84
27	FALLGKGNT	197	0.8000	9.64
28	IRPSTIAAE	343	0.8000	9.64
29	VRRYIAKYT	409	0.8000	9.64
30	ITGAVIIDY	74	0.7000	8.43
31	VMKARRGAL	386	0.7000	8.43
32	MARLSRERY	0	0.5000	6.02
33	ISGNRRIVT	125	0.5000	6.02
34	IIKADIGIR	85	0.4000	4.82
35	VNFALLGKG	195	0.4000	4.82
36	LKGGAIAWA	457	0.3000	3.61
37	VGPSTEIIS	118	0.2000	2.41
38	FVAPQSIDA	500	0.1000	1.20
39	LRGGASGFK	215	-0.1000	0
40	VVLRTWQTA	376	-0.1000	0
41	YIAKYTICP	412	-0.1000	0
42	LPMTQRYFL	567	-0.1000	0
43	VVGPSTEII	117	-0.2000	0
44	WEQLRGGAS	212	-0.2000	0
45	VNRGLAPVA	516	-0.2500	0
46	VITGAVIID	73	-0.3000	0

47	IVEALAAGT	149	-0.3000	0
48	VNPDALWEQ	206	-0.3000	0
49	MVCHHLNPR	323	-0.3000	0
50	ISMIGSDSQ	360	-0.3000	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	VRIDGQVWQ	552	6.4000	70.33
2	VHRDLVVGP	112	3.9000	42.86
3	VNPDALWEQ	206	3.5000	38.46
4	VLHDMGAIS	353	3.5000	38.46
5	VIIDYWGII	78	3.3000	36.26
6	IVTAGTVDC	131	3.1000	34.07
7	LEGDPSGSQ	394	3.1000	34.07
8	IRLADTNLL	20	2.9100	31.98
9	VRPHVVLKG	451	2.9000	31.87
10	IVGIGKAGN	97	2.7000	29.67
11	IIGGGTGPA	160	2.7000	29.67
12	FVEDTIGAI	261	2.7000	29.67
13	VNRGLAPVA	516	2.7000	29.67
14	LVVGPSTEI	116	2.6000	28.57
15	LRGGASGFK	215	2.6000	28.57
16	WQTAHVMKA	381	2.5000	27.47
17	LKGGAIAWA	457	2.5000	27.47
18	VHLICPQII	141	2.4000	26.37
19	VRAVGKTDL	526	2.4000	26.37
20	LHSDTLNET	251	2.2100	24.29
21	IRPSTIAAE	343	2.2000	24.18
22	VFGGGKVLR	47	2.0000	21.98
23	IRDGRIVGI	92	2.0000	21.98
24	LAGDEAVFG	41	1.7000	18.68
25	IGSDSQAMG	363	1.7000	18.68

26	VHFVAPQSI	498	1.7000	18.68
27	VVGPSTEII	117	1.6000	17.58
28	LVLWEPAFF	441	1.6000	17.58
29	LPLNDALPS	534	1.6000	17.58
30	VLPSSTNPT	299	1.5100	16.59
31	VITGAVIID	73	1.5000	16.48
32	VAGVQVALH	244	1.4800	16.26
33	IKADIGIRD	86	1.4000	15.38
34	ISMIGSDSQ	360	1.4000	15.38
35	MIGSDSQAM	362	1.4000	15.38
36	VVLKGGAIA	455	1.4000	15.38
37	LDMLMVCHH	319	1.3800	15.16
38	VGIGKAGNP	98	1.3000	14.29
39	LRTWQTAHV	378	1.3000	14.29
40	MVCHHLNPR	323	1.2100	13.30
41	VGPSTEIIS	118	1.2000	13.19
42	IISGNRRIV	124	1.2000	13.19
43	ICPQIIVEA	144	1.2000	13.19
44	MGAISMIGS	357	1.2000	13.19
45	VMKARRGAL	386	1.2000	13.19
46	VTAGTVDCH	132	1.1800	12.97
47	MGQGRASRA	58	1.0700	11.76
48	LAVADVAGV	239	1.0000	10.99
49	IGSVEVGKL	430	1.0000	10.99
50	MFGAAAATA	485	1.0000	10.99
51	YTICPAIAH	416	0.9800	10.77
52	IIKADIGIR	85	0.9000	9.89
53	LAAGTTTII	153	0.9000	9.89
54	VNFALLGKG	195	0.9000	9.89
55	VLKGGAIAW	456	0.9000	9.89
56	WHLARMLES	181	0.8000	8.79
57	LGKGNTVNP	200	0.7000	7.69

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	VRPHVVLKG	451	3.6000	42.86
2	WQTAHVMKA	381	2.4000	28.57
3	FKLHEDWGS	222	2.3000	27.38
4	LVLWEPAFF	441	2.3000	27.38
5	VVLKGGAIA	455	2.2000	26.19
6	IRLADTNLL	20	2.1000	25.00
7	WHLARMLES	181	2.0000	23.81
8	LRTWQTAHV	378	2.0000	23.81
9	MVCHHLNPR	323	1.9000	22.62
10	IVTAGTVDC	131	1.8000	21.43
11	VRIDGQVWQ	552	1.4000	16.67
12	VRRYIAKYT	409	1.1000	13.10
13	WQPQPAAEL	559	1.1000	13.10
14	YTICPAIAH	416	1.0800	12.86
15	IGIRDGRIV	90	1.0000	11.90
16	YIAKYTICP	412	0.9000	10.71
17	FAESRIRPS	338	0.8000	9.52
18	LDMLMVCHH	319	0.7800	9.29
19	LPLNDALPS	534	0.7000	8.33
20	IVGIGKAGN	97	0.6000	7.14
21	YWGIIKADI	82	0.5000	5.95
22	ICPQIIVEA	144	0.5000	5.95
23	VVLRTWQTA	376	0.5000	5.95
24	IISGNRRIV	124	0.3000	3.57
25	FFGVRPHVV	448	0.2000	2.38
26	VLPRPMFGA	480	0.2000	2.38
27	IAKYTICPA	413	0.1000	1.19
28	LDGWPVNFA	190	-0.1000	0
29	LAFAESRIR	336	-0.1000	0
30	IRPSTIAAE	343	-0.1000	0
31	VNPDALWEQ	206	-0.2000	0

32	VRAVGKTDL	526	-0.3000	0
33	LMVCHHLNP	322	-0.4000	0
34	FGAAAATAA	486	-0.4000	0
35	VAGVQVALH	244	-0.4200	0
36	VDCHVHLIC	137	-0.5000	0
37	WPVNFALLG	193	-0.5000	0
38	LKGGAIAWA	457	-0.5000	0
39	VHFVAPQSI	498	-0.5000	0
40	IDYWGIIKA	80	-0.6000	0
41	IAGRSIHAY	269	-0.6000	0
42	VLPSSTNPT	299	-0.6000	0
43	VVGPSTEII	117	-0.7000	0
44	MLMVCHHLN	321	-0.7000	0
45	VCHHLNPRI	324	-0.7000	0
46	ICPAIAHGM	418	-0.8000	0
47	MARLSRERY	0	-0.9000	0
48	FGGGKVLRE	48	-0.9000	0
49	IGAIAGRSI	266	-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	VRPHVVLKG	451	5.0000	56.82
2	LVLWEPAFF	441	4.2000	47.73
3	MVCHHLNPR	323	3.4000	38.64
4	IRLADTNLL	20	3.0600	34.77
5	LRTWQTAHV	378	3.0000	34.09
6	FKLHEDWGS	222	2.7000	30.68
7	WHLARMLES	181	2.4000	27.27
8	WQTAHVMKA	381	2.4000	27.27
9	VVLKGGAIA	455	2.2000	25.00
10	WQPQPAAEL	559	2.0600	23.41
11	IGIRDGRIV	90	2.0000	22.73

12	YIAKYTICP	412	1.9000	21.59
13	IVTAGTVDC	131	1.8000	20.45
14	VRRYIAKYT	409	1.8000	20.45
15	YWGIIKADI	82	1.4000	15.91
16	IVGIGKAGN	97	1.4000	15.91
17	LAFAESRIR	336	1.4000	15.91
18	IISGNRRIV	124	1.3000	14.77
19	IRPSTIAAE	343	1.3000	14.77
20	FAESRIRPS	338	1.2000	13.64
21	FFGVRPHVV	448	1.2000	13.64
22	LPLNDALPS	534	1.1000	12.50
23	LAVADVAGV	239	1.0000	11.36
24	FGVRPHVVL	449	0.9600	10.91
25	VHLICPQII	141	0.9000	10.23
26	WPVNFALLG	193	0.9000	10.23
27	FALLGKGNT	197	0.7000	7.95
28	IAGRSIHAY	269	0.7000	7.95
29	ICPAIAHGM	418	0.7000	7.95
30	VRIDGQVWQ	552	0.7000	7.95
31	VRAVGKTDL	526	0.6600	7.50
32	LMVCHHLNP	322	0.6000	6.82
33	FGGGKVLRE	48	0.5000	5.68
34	ICPQIIVEA	144	0.5000	5.68
35	VVLRTWQTA	376	0.5000	5.68
36	YTICPAIAH	416	0.5000	5.68
37	MARLSRERY	0	0.4000	4.55
38	VHFVAPQSI	498	0.4000	4.55
39	WGIIKADIG	83	0.3000	3.41
40	MIGSDSQAM	362	0.3000	3.41
41	VFGGGKVLR	47	0.2000	2.27
42	VVGPSTEII	117	0.2000	2.27
43	LDMLMVCHH	319	0.2000	2.27
44	VCHHLNPRI	324	0.2000	2.27
45	VLPRPMFGA	480	0.2000	2.27

46	IIVEALAAG	148	0.1000	1.14
47	VLPSSTNPT	299	0.1000	1.14
48	MLMVCHHLN	321	0.1000	1.14
49	IAKYTICPA	413	0.1000	1.14
50	VHRDLVVGP	112	-0.1000	0
51	LDGWPVNFA	190	-0.1000	0
52	LHDMGAISM	354	-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	VRPHVVLKG	451	4.6000	54.76
2	LVLWEPAFF	441	3.3000	39.29
3	VVLKGGAIA	455	3.2000	38.10
4	IRLADTNLL	20	3.1000	36.90
5	LRTWQTAHV	378	3.0000	35.71
6	MVCHHLNPR	323	2.9000	34.52
7	IVTAGTVDC	131	2.8000	33.33
8	VRIDGQVWQ	552	2.4000	28.57
9	VRRYIAKYT	409	2.1000	25.00
10	IGIRDGRIV	90	2.0000	23.81
11	LDMLMVCHH	319	1.7800	21.19
12	LPLNDALPS	534	1.7000	20.24
13	IVGIGKAGN	97	1.6000	19.05
14	ICPQIIVEA	144	1.5000	17.86
15	VVLRTWQTA	376	1.5000	17.86
16	WQTAHVMKA	381	1.4000	16.67
17	IISGNRRIV	124	1.3000	15.48
18	FKLHEDWGS	222	1.3000	15.48
19	VLPRPMFGA	480	1.2000	14.29
20	IAKYTICPA	413	1.1000	13.10
21	VHLICPQII	141	1.0000	11.90
22	WHLARMLES	181	1.0000	11.90

23	LAVADVAGV	239	1.0000	11.90
24	IHAYHTEGA	274	1.0000	11.90
25	MFGAAAATA	485	1.0000	11.90
26	LDGWPVNFA	190	0.9000	10.71
27	LAFAESRIR	336	0.9000	10.71
28	IRPSTIAAE	343	0.9000	10.71
29	VNPDALWEQ	206	0.8000	9.52
30	VRAVGKTDL	526	0.7000	8.33
31	LMVCHHLNP	322	0.6000	7.14
32	VAGVQVALH	244	0.5800	6.90
33	VDCHVHLIC	137	0.5000	5.95
34	LKGGAIAWA	457	0.5000	5.95
35	VHFVAPQSI	498	0.5000	5.95
36	IDYWGIIKA	80	0.4000	4.76
37	IAGRSIHAY	269	0.4000	4.76
38	VLPSSTNPT	299	0.4000	4.76
39	VVGPSTEII	117	0.3000	3.57
40	MLMVCHHLN	321	0.3000	3.57
41	VCHHLNPRI	324	0.3000	3.57
42	ICPAIAHGM	418	0.2000	2.38
43	MARLSRERY	0	0.1000	1.19
44	IGAIAGRSI	266	0.1000	1.19
45	WQPQPAAEL	559	0.1000	1.19
46	YTICPAIAH	416	0.0800	0.95
47	VHRDLVVGP	112	-0.1000	0
48	YIAKYTICP	412	-0.1000	0
49	LVVGPSTEI	116	-0.2000	0
50	LNPRIPEDL	328	-0.2000	0
51	FAESRIRPS	338	-0.2000	0
52	VLHDMGAIS	353	-0.2000	0
53	MIGSDSQAM	362	-0.2000	0
54	VFGGGKVLR	47	-0.3000	0
55	IRDGRIVGI	92	-0.3000	0
56	IMTGVHRDL	108	-0.3000	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	VRPHVVLKG	451	4.0000	45.98
2	WQTAHVMKA	381	3.7000	42.53
3	WHLARMLES	181	3.5000	40.23
4	LVLWEPAFF	441	3.4000	39.08
5	YWGIIKADI	82	2.9000	33.33
6	IVGIGKAGN	97	2.9000	33.33
7	FALLGKGNT	197	2.5000	28.74
8	LRTWQTAHV	378	2.2000	25.29
9	LPLNDALPS	534	2.1000	24.14
10	FFGVRPHVV	448	2.0000	22.99
11	IRLADTNLL	20	1.9600	22.53
12	WPVNFALLG	193	1.9000	21.84
13	YIAKYTICP	412	1.9000	21.84
14	YTICPAIAH	416	1.8000	20.69
15	VHLICPQII	141	1.7000	19.54
16	LMVCHHLNP	322	1.7000	19.54
17	VRAVGKTDL	526	1.5600	17.93
18	FGGGKVLRE	48	1.4000	16.09
19	LHDMGAISM	354	1.4000	16.09
20	MGAISMIGS	357	1.4000	16.09
21	IVTAGTVDC	131	1.3000	14.94
22	WEQLRGGAS	212	1.2000	13.79
23	IRPSTIAAE	343	1.2000	13.79
24	FVAPQSIDA	500	1.1000	12.64
25	WQPQPAAEL	559	1.0600	12.18
26	ITGAVIIDY	74	1.0000	11.49
27	LAVADVAGV	239	1.0000	11.49
28	VHFVAPQSI	498	1.0000	11.49
29	IIKADIGIR	85	0.9000	10.34
30	LDMLMVCHH	319	0.9000	10.34

31	MLMVCHHLN	321	0.9000	10.34
32	VVLKGGAIA	455	0.9000	10.34
33	IGSVEVGKL	430	0.8600	9.89
34	MARLSRERY	0	0.8000	9.20
35	VNFALLGKG	195	0.8000	9.20
36	VMKARRGAL	386	0.6600	7.59
37	WGIIKADIG	83	0.6000	6.90
38	VRRYIAKYT	409	0.5000	5.75
39	VAGVQVALH	244	0.3000	3.45
40	ISGNRRIVT	125	0.2000	2.30
41	MVCHHLNPR	323	0.2000	2.30
42	ICPAIAHGM	418	0.2000	2.30
43	FVEDTIGAI	261	0.1000	1.15
44	IDYWGIIKA	80	-0.1000	0
45	IGAIAGRSI	266	-0.1000	0
46	VRIDGQVWQ	552	-0.1000	0
47	LPMTQRYFL	567	-0.1400	0
48	YAQLYGPTT	8	-0.1500	0
49	VITGAVIID	73	-0.2000	0
50	FKLHEDWGS	222	-0.2000	0
51	LAFAESRIR	336	-0.2000	0
52	VVGPSTEII	117	-0.3000	0
53	VGKLADLVL	435	-0.3400	0
54	VGPSTEIIS	118	-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	VRPHVVLKG	451	6.0000	68.18
2	LVLWEPAFF	441	5.2000	59.09
3	MVCHHLNPR	323	4.4000	50.00
4	IRLADTNLL	20	4.0600	46.14
5	LRTWQTAHV	378	4.0000	45.45

6	VVLKGGAIA	455	3.2000	36.36
7	IGIRDGRIV	90	3.0000	34.09
8	IVTAGTVDC	131	2.8000	31.82
9	VRRYIAKYT	409	2.8000	31.82
10	IVGIGKAGN	97	2.4000	27.27
11	LAFAESRIR	336	2.4000	27.27
12	IISGNRRIV	124	2.3000	26.14
13	IRPSTIAAE	343	2.3000	26.14
14	LPLNDALPS	534	2.1000	23.86
15	LAVADVAGV	239	2.0000	22.73
16	VHLICPQII	141	1.9000	21.59
17	FKLHEDWGS	222	1.7000	19.32
18	IAGRSIHAY	269	1.7000	19.32
19	ICPAIAHGM	418	1.7000	19.32
20	VRIDGQVWQ	552	1.7000	19.32
21	VRAVGKTDL	526	1.6600	18.86
22	LMVCHHLNP	322	1.6000	18.18
23	ICPQIIVEA	144	1.5000	17.05
24	VVLRTWQTA	376	1.5000	17.05
25	MARLSRERY	0	1.4000	15.91
26	WHLARMLES	181	1.4000	15.91
27	WQTAHVMKA	381	1.4000	15.91
28	VHFVAPQSI	498	1.4000	15.91
29	MIGSDSQAM	362	1.3000	14.77
30	VFGGGKVLR	47	1.2000	13.64
31	VVGPSTEII	117	1.2000	13.64
32	LDMLMVCHH	319	1.2000	13.64
33	VCHHLNPRI	324	1.2000	13.64
34	VLPRPMFGA	480	1.2000	13.64
35	IIVEALAAG	148	1.1000	12.50
36	VLPSSTNPT	299	1.1000	12.50
37	MLMVCHHLN	321	1.1000	12.50
38	IAKYTICPA	413	1.1000	12.50
39	WQPQPAAEL	559	1.0600	12.05

40	IGAIAGRSI	266	1.0000	11.36
41	IHAYHTEGA	274	1.0000	11.36
42	MFGAAAATA	485	1.0000	11.36
43	VHRDLVVGP	112	0.9000	10.23
44	LDGWPVNFA	190	0.9000	10.23
45	LHDMGAISM	354	0.9000	10.23
46	YIAKYTICP	412	0.9000	10.23
47	VLWEPAFFG	442	0.9000	10.23
48	IIKADIGIR	85	0.8000	9.09
49	LNPRIPEDL	328	0.7600	8.64
50	LLVEVTEDR	27	0.7000	7.95
51	ITGAVIIDY	74	0.7000	7.95
52	LVVGPSTEI	116	0.7000	7.95
53	LESLDGWPV	187	0.7000	7.95
54	VNFALLGKG	195	0.7000	7.95
55	IMTGVHRDL	108	0.6600	7.50
56	IRDGRIVGI	92	0.6000	6.82
57	VAPQSIDAR	501	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	VRPHVVLKG	451	5.0000	56.82
2	LVLWEPAFF	441	4.2000	47.73
3	MVCHHLNPR	323	3.4000	38.64
4	IRLADTNLL	20	3.0600	34.77
5	LRTWQTAHV	378	3.0000	34.09
6	FKLHEDWGS	222	2.7000	30.68
7	WHLARMLES	181	2.4000	27.27
8	WQTAHVMKA	381	2.4000	27.27
9	VVLKGGAIA	455	2.2000	25.00
10	WQPQPAAEL	559	2.0600	23.41
11	IGIRDGRIV	90	2.0000	22.73

12	YIAKYTICP	412	1.9000	21.59
13	IVTAGTVDC	131	1.8000	20.45
14	VRRYIAKYT	409	1.8000	20.45
15	YWGIIKADI	82	1.4000	15.91
16	IVGIGKAGN	97	1.4000	15.91
17	LAFAESRIR	336	1.4000	15.91
18	IISGNRRIV	124	1.3000	14.77
19	IRPSTIAAE	343	1.3000	14.77
20	FAESRIRPS	338	1.2000	13.64
21	FFGVRPHVV	448	1.2000	13.64
22	LPLNDALPS	534	1.1000	12.50
23	LAVADVAGV	239	1.0000	11.36
24	FGVRPHVVL	449	0.9600	10.91
25	VHLICPQII	141	0.9000	10.23
26	WPVNFALLG	193	0.9000	10.23
27	FALLGKGNT	197	0.7000	7.95
28	IAGRSIHAY	269	0.7000	7.95
29	ICPAIAHGM	418	0.7000	7.95
30	VRIDGQVWQ	552	0.7000	7.95
31	VRAVGKTDL	526	0.6600	7.50
32	LMVCHHLNP	322	0.6000	6.82
33	FGGGKVLRE	48	0.5000	5.68
34	ICPQIIVEA	144	0.5000	5.68
35	VVLRTWQTA	376	0.5000	5.68
36	YTICPAIAH	416	0.5000	5.68
37	MARLSRERY	0	0.4000	4.55
38	VHFVAPQSI	498	0.4000	4.55
39	WGIIKADIG	83	0.3000	3.41
40	MIGSDSQAM	362	0.3000	3.41
41	VFGGGKVLR	47	0.2000	2.27
42	VVGPSTEII	117	0.2000	2.27
43	LDMLMVCHH	319	0.2000	2.27
44	VCHHLNPRI	324	0.2000	2.27
45	VLPRPMFGA	480	0.2000	2.27

46	IIVEALAAG	148	0.1000	1.14
47	VLPSSTNPT	299	0.1000	1.14
48	MLMVCHHLN	321	0.1000	1.14
49	IAKYTICPA	413	0.1000	1.14
50	VHRDLVVGP	112	-0.1000	0
51	LDGWPVNFA	190	-0.1000	0
52	LHDMGAISM	354	-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	VRPHVVLKG	451	5.9000	65.56
2	LVLWEPAFF	441	4.2000	46.67
3	IRLADTNLL	20	4.1000	45.56
4	IRPSTIAAE	343	3.9000	43.33
5	IVGIGKAGN	97	3.6000	40.00
6	LRTWQTAHV	378	3.3000	36.67
7	VVLKGGAIA	455	3.2000	35.56
8	VRIDGQVWQ	552	3.2000	35.56
9	LDMLMVCHH	319	3.0000	33.33
10	VRRYIAKYT	409	3.0000	33.33
11	MVCHHLNPR	323	2.9000	32.22
12	IVTAGTVDC	131	2.8000	31.11
13	IGIRDGRIV	90	2.3000	25.56
14	MLMVCHHLN	321	2.3000	25.56
15	MKARRGALE	387	1.9000	21.11
16	VAGVQVALH	244	1.8000	20.00
17	VRAVGKTDL	526	1.7000	18.89
18	LPLNDALPS	534	1.7000	18.89
19	IISGNRRIV	124	1.6000	17.78
20	VNPDALWEQ	206	1.6000	17.78
21	ICPQIIVEA	144	1.5000	16.67
22	IAGRSIHAY	269	1.5000	16.67

23	IAAEDVLHD	348	1.5000	16.67
24	VVLRTWQTA	376	1.5000	16.67
25	WQTAHVMKA	381	1.4000	15.56
26	VITGAVIID	73	1.3000	14.44
27	FKLHEDWGS	222	1.3000	14.44
28	LAVADVAGV	239	1.3000	14.44
29	VLPSSTNPT	299	1.3000	14.44
30	YTICPAIAH	416	1.3000	14.44
31	ICPAIAHGM	418	1.3000	14.44
32	MARLSRERY	0	1.2000	13.33
33	VHLICPQII	141	1.2000	13.33
34	VLPRPMFGA	480	1.2000	13.33
35	FGGGKVLRE	48	1.1000	12.22
36	LICPQIIVE	143	1.1000	12.22
37	LLGKGNTVN	199	1.1000	12.22
38	VNTLDEHLD	312	1.1000	12.22
39	IAKYTICPA	413	1.1000	12.22
40	WQPQPAAEL	559	1.1000	12.22
41	IIVEALAAG	148	1.0000	11.11
42	WHLARMLES	181	1.0000	11.11
43	IHAYHTEGA	274	1.0000	11.11
44	LMVCHHLNP	322	1.0000	11.11
45	MFGAAAATA	485	1.0000	11.11
46	LDGWPVNFA	190	0.9000	10.00
47	LAFAESRIR	336	0.9000	10.00
48	MIGSDSQAM	362	0.9000	10.00
49	LNPRIPEDL	328	0.8000	8.89
50	VLWEPAFFG	442	0.8000	8.89
51	IMTGVHRDL	108	0.7000	7.78
52	VLRTWQTAH	377	0.7000	7.78
53	VHFVAPQSI	498	0.7000	7.78
54	IVEALAAGT	149	0.6000	6.67
55	VNFALLGKG	195	0.6000	6.67
56	VMKARRGAL	386	0.6000	6.67

57	LPMTQRYFL	567	0.6000	6.67

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	VRPHVVLKG	451	4.0000	45.98
2	WQTAHVMKA	381	3.7000	42.53
3	WHLARMLES	181	3.5000	40.23
4	LVLWEPAFF	441	3.4000	39.08
5	YWGIIKADI	82	2.9000	33.33
6	IVGIGKAGN	97	2.9000	33.33
7	FALLGKGNT	197	2.5000	28.74
8	LRTWQTAHV	378	2.2000	25.29
9	LPLNDALPS	534	2.1000	24.14
10	FFGVRPHVV	448	2.0000	22.99
11	IRLADTNLL	20	1.9600	22.53
12	WPVNFALLG	193	1.9000	21.84
13	YIAKYTICP	412	1.9000	21.84
14	YTICPAIAH	416	1.8000	20.69
15	VHLICPQII	141	1.7000	19.54
16	LMVCHHLNP	322	1.7000	19.54
17	VRAVGKTDL	526	1.5600	17.93
18	FGGGKVLRE	48	1.4000	16.09
19	LHDMGAISM	354	1.4000	16.09
20	MGAISMIGS	357	1.4000	16.09
21	IVTAGTVDC	131	1.3000	14.94
22	WEQLRGGAS	212	1.2000	13.79
23	IRPSTIAAE	343	1.2000	13.79
24	FVAPQSIDA	500	1.1000	12.64
25	WQPQPAAEL	559	1.0600	12.18
26	ITGAVIIDY	74	1.0000	11.49
27	LAVADVAGV	239	1.0000	11.49
28	VHFVAPQSI	498	1.0000	11.49

29	IIKADIGIR	85	0.9000	10.34
30	LDMLMVCHH	319	0.9000	10.34
31	MLMVCHHLN	321	0.9000	10.34
32	VVLKGGAIA	455	0.9000	10.34
33	IGSVEVGKL	430	0.8600	9.89
34	MARLSRERY	0	0.8000	9.20
35	VNFALLGKG	195	0.8000	9.20
36	VMKARRGAL	386	0.6600	7.59
37	WGIIKADIG	83	0.6000	6.90
38	VRRYIAKYT	409	0.5000	5.75
39	VAGVQVALH	244	0.3000	3.45
40	ISGNRRIVT	125	0.2000	2.30
41	MVCHHLNPR	323	0.2000	2.30
42	ICPAIAHGM	418	0.2000	2.30
43	FVEDTIGAI	261	0.1000	1.15
44	IDYWGIIKA	80	-0.1000	0
45	IGAIAGRSI	266	-0.1000	0
46	VRIDGQVWQ	552	-0.1000	0
47	LPMTQRYFL	567	-0.1400	0
48	YAQLYGPTT	8	-0.1500	0
49	VITGAVIID	73	-0.2000	0
50	FKLHEDWGS	222	-0.2000	0
51	LAFAESRIR	336	-0.2000	0
52	VVGPSTEII	117	-0.3000	0
53	VGKLADLVL	435	-0.3400	0
54	VGPSTEIIS	118	-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	IVGIGKAGN	97	2.1000	30.88
2	WQTAHVMKA	381	2.1000	30.88
3	YWGIIKADI	82	2.0000	29.41

4	FALLGKGNT	197	1.7000	25.00
5	LVLWEPAFF	441	1.5000	22.06
6	LDMLMVCHH	319	1.4800	21.76
7	WHLARMLES	181	1.3000	19.12
8	LRTWQTAHV	378	1.2000	17.65
9	VVLKGGAIA	455	0.9000	13.24
10	VAGVQVALH	244	0.8800	12.94
11	IVTAGTVDC	131	0.8000	11.76
12	VRPHVVLKG	451	0.8000	11.76
13	YTICPAIAH	416	0.7800	11.47
14	IRLADTNLL	20	0.7000	10.29
15	VHLICPQII	141	0.7000	10.29
16	WEQLRGGAS	212	0.7000	10.29
17	FFGVRPHVV	448	0.3000	4.41
18	VRIDGQVWQ	552	0.1000	1.47
19	WQPQPAAEL	559	0.1000	1.47
20	LPLNDALPS	534	-0.1000	0
21	IRPSTIAAE	343	-0.2000	0
22	IGSVEVGKL	430	-0.2000	0
23	VMKARRGAL	386	-0.4000	0
24	WGIIKADIG	83	-0.5000	0
25	FVAPQSIDA	500	-0.5000	0
26	VRAVGKTDL	526	-0.5000	0
27	MLMVCHHLN	321	-0.6000	0
28	MGAISMIGS	357	-0.6000	0
29	IIKADIGIR	85	-0.7000	0
30	VNFALLGKG	195	-0.7000	0
31	YIAKYTICP	412	-0.7000	0
32	LKGGAIAWA	457	-0.7000	0
33	VRRYIAKYT	409	-0.8000	0
34	FVEDTIGAI	261	-0.9000	0
35	ISMIGSDSQ	360	-1.0000	0
36	IAKYTICPA	413	-1.0000	0
37	IIGGGTGPA	160	-1.1000	0

38	LMVCHHLNP	322	-1.1000	0
39	FAESRIRPS	338	-1.1000	0
40	LRGGASGFK	215	-1.2000	0
41	IGAIAGRSI	266	-1.2000	0
42	VVLRTWQTA	376	-1.2000	0
43	IVEALAAGT	149	-1.3000	0
44	WPVNFALLG	193	-1.3000	0
45	FKLHEDWGS	222	-1.4000	0
46	WAAMGDANA	464	-1.4000	0
47	ICPQIIVEA	144	-1.5000	0
48	VEALAAGTT	150	-1.5000	0
49	VLHDMGAIS	353	-1.5000	0
50	MARLSRERY	0	-1.6000	0
51	WGSTPAAID	228	-1.6000	0
52	MVCHHLNPR	323	-1.6000	0
53	IDYWGIIKA	80	-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	VRPHVVLKG	451	3.6000	43.37
2	IVGIGKAGN	97	3.1000	37.35
3	WQTAHVMKA	381	2.7000	32.53
4	LPLNDALPS	534	2.7000	32.53
5	LVLWEPAFF	441	2.5000	30.12
6	LDMLMVCHH	319	2.4800	29.88
7	IVTAGTVDC	131	2.3000	27.71
8	LRTWQTAHV	378	2.2000	26.51
9	WHLARMLES	181	2.1000	25.30
10	IRLADTNLL	20	2.0000	24.10
11	MGAISMIGS	357	2.0000	24.10
12	VVLKGGAIA	455	1.9000	22.89
13	VAGVQVALH	244	1.8800	22.65

14	VHLICPQII	141	1.8000	21.69
15	LMVCHHLNP	322	1.7000	20.48
16	VRAVGKTDL	526	1.6000	19.28
17	VRIDGQVWQ	552	1.6000	19.28
18	YTICPAIAH	416	1.3800	16.63
19	MLMVCHHLN	321	1.1000	13.25
20	VHFVAPQSI	498	1.1000	13.25
21	YWGIIKADI	82	1.0000	12.05
22	LAVADVAGV	239	1.0000	12.05
23	MFGAAAATA	485	1.0000	12.05
24	IDYWGIIKA	80	0.9000	10.84
25	LHDMGAISM	354	0.9000	10.84
26	IGSVEVGKL	430	0.9000	10.84
27	FALLGKGNT	197	0.8000	9.64
28	IRPSTIAAE	343	0.8000	9.64
29	VRRYIAKYT	409	0.8000	9.64
30	ITGAVIIDY	74	0.7000	8.43
31	VMKARRGAL	386	0.7000	8.43
32	MARLSRERY	0	0.5000	6.02
33	ISGNRRIVT	125	0.5000	6.02
34	IIKADIGIR	85	0.4000	4.82
35	VNFALLGKG	195	0.4000	4.82
36	LKGGAIAWA	457	0.3000	3.61
37	VGPSTEIIS	118	0.2000	2.41
38	FVAPQSIDA	500	0.1000	1.20
39	LRGGASGFK	215	-0.1000	0
40	VVLRTWQTA	376	-0.1000	0
41	YIAKYTICP	412	-0.1000	0
42	LPMTQRYFL	567	-0.1000	0
43	VVGPSTEII	117	-0.2000	0
44	WEQLRGGAS	212	-0.2000	0
45	VNRGLAPVA	516	-0.2500	0
46	VITGAVIID	73	-0.3000	0
47	IVEALAAGT	149	-0.3000	0

48	VNPDALWEQ	206	-0.3000	0
49	MVCHHLNPR	323	-0.3000	0
50	ISMIGSDSQ	360	-0.3000	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	IVGIGKAGN	97	4.1000	46.07
2	VRPHVVLKG	451	3.9000	43.82
3	WQTAHVMKA	381	3.7000	41.57
4	YTICPAIAH	416	3.6000	40.45
5	WHLARMLES	181	3.1000	34.83
6	FGGGKVLRE	48	3.0000	33.71
7	IRPSTIAAE	343	2.8000	31.46
8	FALLGKGNT	197	2.7000	30.34
9	LDMLMVCHH	319	2.7000	30.34
10	LVLWEPAFF	441	2.4000	26.97
11	YWGIIKADI	82	2.2000	24.72
12	VAGVQVALH	244	2.1000	23.60
13	MLMVCHHLN	321	2.1000	23.60
14	IRLADTNLL	20	2.0000	22.47
15	WPVNFALLG	193	1.8000	20.22
16	LPLNDALPS	534	1.7000	19.10
17	VRAVGKTDL	526	1.6000	17.98
18	LRTWQTAHV	378	1.5000	16.85
19	VITGAVIID	73	1.4000	15.73
20	VRIDGQVWQ	552	1.4000	15.73
21	IVTAGTVDC	131	1.3000	14.61
22	YIAKYTICP	412	1.3000	14.61
23	FFGVRPHVV	448	1.3000	14.61
24	LICPQIIVE	143	1.2000	13.48
25	WGSTPAAID	228	1.1000	12.36
26	LMVCHHLNP	322	1.1000	12.36

27	FVAPQSIDA	500	1.1000	12.36
28	WQPQPAAEL	559	1.1000	12.36
29	VHLICPQII	141	1.0000	11.24
30	IAAEDVLHD	348	1.0000	11.24
31	LHDMGAISM	354	1.0000	11.24
32	MGAISMIGS	357	1.0000	11.24
33	IGSVEVGKL	430	0.9000	10.11
34	VVLKGGAIA	455	0.9000	10.11
35	ITGAVIIDY	74	0.8000	8.99
36	WEQLRGGAS	212	0.8000	8.99
37	VNFALLGKG	195	0.7000	7.87
38	VMKARRGAL	386	0.7000	7.87
39	VRRYIAKYT	409	0.7000	7.87
40	MARLSRERY	0	0.6000	6.74
41	WGIIKADIG	83	0.5000	5.62
42	ISGNRRIVT	125	0.4000	4.49
43	LAVADVAGV	239	0.3000	3.37
44	VNTLDEHLD	312	0.3000	3.37
45	VHFVAPQSI	498	0.3000	3.37
46	LADTNLLVE	22	0.1000	1.12
47	YAQLYGPTT	8	0.0500	0.56
48	IDYWGIIKA	80	-0.1000	0
49	LPMTQRYFL	567	-0.1000	0
50	VLRTWQTAH	377	-0.2000	0
51	ICPAIAHGM	418	-0.2000	0
52	VGKLADLVL	435	-0.3000	0
53	VGKTDLPLN	529	-0.3500	0

ALLELE: DRB1_1322	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VRPHVVLKG	451	4.6000	54.76
2	LVLWEPAFF	441	3.3000	39.29

3	VVLKGGAIA	455	3.2000	38.10
4	IRLADTNLL	20	3.1000	36.90
5	LRTWQTAHV	378	3.0000	35.71
6	MVCHHLNPR	323	2.9000	34.52
7	IVTAGTVDC	131	2.8000	33.33
8	VRIDGQVWQ	552	2.4000	28.57
9	VRRYIAKYT	409	2.1000	25.00
10	IGIRDGRIV	90	2.0000	23.81
11	LDMLMVCHH	319	1.7800	21.19
12	LPLNDALPS	534	1.7000	20.24
13	IVGIGKAGN	97	1.6000	19.05
14	ICPQIIVEA	144	1.5000	17.86
15	VVLRTWQTA	376	1.5000	17.86
16	WQTAHVMKA	381	1.4000	16.67
17	IISGNRRIV	124	1.3000	15.48
18	FKLHEDWGS	222	1.3000	15.48
19	VLPRPMFGA	480	1.2000	14.29
20	IAKYTICPA	413	1.1000	13.10
21	VHLICPQII	141	1.0000	11.90
22	WHLARMLES	181	1.0000	11.90
23	LAVADVAGV	239	1.0000	11.90
24	IHAYHTEGA	274	1.0000	11.90
25	MFGAAAATA	485	1.0000	11.90
26	LDGWPVNFA	190	0.9000	10.71
27	LAFAESRIR	336	0.9000	10.71
28	IRPSTIAAE	343	0.9000	10.71
29	VNPDALWEQ	206	0.8000	9.52
30	VRAVGKTDL	526	0.7000	8.33
31	LMVCHHLNP	322	0.6000	7.14
32	VAGVQVALH	244	0.5800	6.90
33	VDCHVHLIC	137	0.5000	5.95
34	LKGGAIAWA	457	0.5000	5.95
35	VHFVAPQSI	498	0.5000	5.95
36	IDYWGIIKA	80	0.4000	4.76

37	IAGRSIHAY	269	0.4000	4.76
38	VLPSSTNPT	299	0.4000	4.76
39	VVGPSTEII	117	0.3000	3.57
40	MLMVCHHLN	321	0.3000	3.57
41	VCHHLNPRI	324	0.3000	3.57
42	ICPAIAHGM	418	0.2000	2.38
43	MARLSRERY	0	0.1000	1.19
44	IGAIAGRSI	266	0.1000	1.19
45	WQPQPAAEL	559	0.1000	1.19
46	YTICPAIAH	416	0.0800	0.95
47	VHRDLVVGP	112	-0.1000	0
48	YIAKYTICP	412	-0.1000	0
49	LVVGPSTEI	116	-0.2000	0
50	LNPRIPEDL	328	-0.2000	0
51	FAESRIRPS	338	-0.2000	0
52	VLHDMGAIS	353	-0.2000	0
53	MIGSDSQAM	362	-0.2000	0
54	VFGGGKVLR	47	-0.3000	0
55	IRDGRIVGI	92	-0.3000	0
56	IMTGVHRDL	108	-0.3000	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	VRPHVVLKG	451	3.6000	42.86
2	WQTAHVMKA	381	2.4000	28.57
3	FKLHEDWGS	222	2.3000	27.38
4	LVLWEPAFF	441	2.3000	27.38
5	VVLKGGAIA	455	2.2000	26.19
6	IRLADTNLL	20	2.1000	25.00
7	WHLARMLES	181	2.0000	23.81
8	LRTWQTAHV	378	2.0000	23.81
9	MVCHHLNPR	323	1.9000	22.62

10	IVTAGTVDC	131	1.8000	21.43
11	VRIDGQVWQ	552	1.4000	16.67
12	VRRYIAKYT	409	1.1000	13.10
13	WQPQPAAEL	559	1.1000	13.10
14	YTICPAIAH	416	1.0800	12.86
15	IGIRDGRIV	90	1.0000	11.90
16	YIAKYTICP	412	0.9000	10.71
17	FAESRIRPS	338	0.8000	9.52
18	LDMLMVCHH	319	0.7800	9.29
19	LPLNDALPS	534	0.7000	8.33
20	IVGIGKAGN	97	0.6000	7.14
21	YWGIIKADI	82	0.5000	5.95
22	ICPQIIVEA	144	0.5000	5.95
23	VVLRTWQTA	376	0.5000	5.95
24	IISGNRRIV	124	0.3000	3.57
25	FFGVRPHVV	448	0.2000	2.38
26	VLPRPMFGA	480	0.2000	2.38
27	IAKYTICPA	413	0.1000	1.19
28	LDGWPVNFA	190	-0.1000	0
29	LAFAESRIR	336	-0.1000	0
30	IRPSTIAAE	343	-0.1000	0
31	VNPDALWEQ	206	-0.2000	0
32	VRAVGKTDL	526	-0.3000	0
33	LMVCHHLNP	322	-0.4000	0
34	FGAAAATAA	486	-0.4000	0
35	VAGVQVALH	244	-0.4200	0
36	VDCHVHLIC	137	-0.5000	0
37	WPVNFALLG	193	-0.5000	0
38	LKGGAIAWA	457	-0.5000	0
39	VHFVAPQSI	498	-0.5000	0
40	IDYWGIIKA	80	-0.6000	0
41	IAGRSIHAY	269	-0.6000	0
42	VLPSSTNPT	299	-0.6000	0
43	VVGPSTEII	117	-0.7000	0

44	MLMVCHHLN	321	-0.7000	0
45	VCHHLNPRI	324	-0.7000	0
46	ICPAIAHGM	418	-0.8000	0
47	MARLSRERY	0	-0.9000	0
48	FGGGKVLRE	48	-0.9000	0
49	IGAIAGRSI	266	-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	VRPHVVLKG	451	6.0000	68.18
2	LVLWEPAFF	441	5.2000	59.09
3	MVCHHLNPR	323	4.4000	50.00
4	IRLADTNLL	20	4.0600	46.14
5	LRTWQTAHV	378	4.0000	45.45
6	VVLKGGAIA	455	3.2000	36.36
7	IGIRDGRIV	90	3.0000	34.09
8	IVTAGTVDC	131	2.8000	31.82
9	VRRYIAKYT	409	2.8000	31.82
10	IVGIGKAGN	97	2.4000	27.27
11	LAFAESRIR	336	2.4000	27.27
12	IISGNRRIV	124	2.3000	26.14
13	IRPSTIAAE	343	2.3000	26.14
14	LPLNDALPS	534	2.1000	23.86
15	LAVADVAGV	239	2.0000	22.73
16	VHLICPQII	141	1.9000	21.59
17	FKLHEDWGS	222	1.7000	19.32
18	IAGRSIHAY	269	1.7000	19.32
19	ICPAIAHGM	418	1.7000	19.32
20	VRIDGQVWQ	552	1.7000	19.32
21	VRAVGKTDL	526	1.6600	18.86
22	LMVCHHLNP	322	1.6000	18.18
23	ICPQIIVEA	144	1.5000	17.05

24	VVLRTWQTA	376	1.5000	17.05
25	MARLSRERY	0	1.4000	15.91
26	WHLARMLES	181	1.4000	15.91
27	WQTAHVMKA	381	1.4000	15.91
28	VHFVAPQSI	498	1.4000	15.91
29	MIGSDSQAM	362	1.3000	14.77
30	VFGGGKVLR	47	1.2000	13.64
31	VVGPSTEII	117	1.2000	13.64
32	LDMLMVCHH	319	1.2000	13.64
33	VCHHLNPRI	324	1.2000	13.64
34	VLPRPMFGA	480	1.2000	13.64
35	IIVEALAAG	148	1.1000	12.50
36	VLPSSTNPT	299	1.1000	12.50
37	MLMVCHHLN	321	1.1000	12.50
38	IAKYTICPA	413	1.1000	12.50
39	WQPQPAAEL	559	1.0600	12.05
40	IGAIAGRSI	266	1.0000	11.36
41	IHAYHTEGA	274	1.0000	11.36
42	MFGAAAATA	485	1.0000	11.36
43	VHRDLVVGP	112	0.9000	10.23
44	LDGWPVNFA	190	0.9000	10.23
45	LHDMGAISM	354	0.9000	10.23
46	YIAKYTICP	412	0.9000	10.23
47	VLWEPAFFG	442	0.9000	10.23
48	IIKADIGIR	85	0.8000	9.09
49	LNPRIPEDL	328	0.7600	8.64
50	LLVEVTEDR	27	0.7000	7.95
51	ITGAVIIDY	74	0.7000	7.95
52	LVVGPSTEI	116	0.7000	7.95
53	LESLDGWPV	187	0.7000	7.95
54	VNFALLGKG	195	0.7000	7.95
55	IMTGVHRDL	108	0.6600	7.50
56	IRDGRIVGI	92	0.6000	6.82
57	VAPQSIDAR	501	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	VRPHVVLKG	451	6.0000	68.18
2	LVLWEPAFF	441	5.2000	59.09
3	MVCHHLNPR	323	4.4000	50.00
4	IRLADTNLL	20	4.0600	46.14
5	LRTWQTAHV	378	4.0000	45.45
6	VVLKGGAIA	455	3.2000	36.36
7	IGIRDGRIV	90	3.0000	34.09
8	IVTAGTVDC	131	2.8000	31.82
9	VRRYIAKYT	409	2.8000	31.82
10	IVGIGKAGN	97	2.4000	27.27
11	LAFAESRIR	336	2.4000	27.27
12	IISGNRRIV	124	2.3000	26.14
13	IRPSTIAAE	343	2.3000	26.14
14	LPLNDALPS	534	2.1000	23.86
15	LAVADVAGV	239	2.0000	22.73
16	VHLICPQII	141	1.9000	21.59
17	FKLHEDWGS	222	1.7000	19.32
18	IAGRSIHAY	269	1.7000	19.32
19	ICPAIAHGM	418	1.7000	19.32
20	VRIDGQVWQ	552	1.7000	19.32
21	VRAVGKTDL	526	1.6600	18.86
22	LMVCHHLNP	322	1.6000	18.18
23	ICPQIIVEA	144	1.5000	17.05
24	VVLRTWQTA	376	1.5000	17.05
25	MARLSRERY	0	1.4000	15.91
26	WHLARMLES	181	1.4000	15.91
27	WQTAHVMKA	381	1.4000	15.91
28	VHFVAPQSI	498	1.4000	15.91
29	MIGSDSQAM	362	1.3000	14.77
30	VFGGGKVLR	47	1.2000	13.64

31	VVGPSTEII	117	1.2000	13.64
32	LDMLMVCHH	319	1.2000	13.64
33	VCHHLNPRI	324	1.2000	13.64
34	VLPRPMFGA	480	1.2000	13.64
35	IIVEALAAG	148	1.1000	12.50
36	VLPSSTNPT	299	1.1000	12.50
37	MLMVCHHLN	321	1.1000	12.50
38	IAKYTICPA	413	1.1000	12.50
39	WQPQPAAEL	559	1.0600	12.05
40	IGAIAGRSI	266	1.0000	11.36
41	IHAYHTEGA	274	1.0000	11.36
42	MFGAAAATA	485	1.0000	11.36
43	VHRDLVVGP	112	0.9000	10.23
44	LDGWPVNFA	190	0.9000	10.23
45	LHDMGAISM	354	0.9000	10.23
46	YIAKYTICP	412	0.9000	10.23
47	VLWEPAFFG	442	0.9000	10.23
48	IIKADIGIR	85	0.8000	9.09
49	LNPRIPEDL	328	0.7600	8.64
50	LLVEVTEDR	27	0.7000	7.95
51	ITGAVIIDY	74	0.7000	7.95
52	LVVGPSTEI	116	0.7000	7.95
53	LESLDGWPV	187	0.7000	7.95
54	VNFALLGKG	195	0.7000	7.95
55	IMTGVHRDL	108	0.6600	7.50
56	IRDGRIVGI	92	0.6000	6.82
57	VAPQSIDAR	501	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	VRRYIAKYT	409	4.9000	50.00
2	VRPHVVLKG	451	4.4000	44.90

3	IRLADTNLL	20	4.3600	44.49
4	LVVGPSTEI	116	4.1000	41.84
5	MVCHHLNPR	323	3.1000	31.63
6	VCHHLNPRI	324	3.0000	30.61
7	VGKLADLVL	435	3.0000	30.61
8	VLPRPMFGA	480	3.0000	30.61
9	LVLWEPAFF	441	2.9000	29.59
10	VVLKGGAIA	455	2.9000	29.59
11	FVAPQSIDA	500	2.9000	29.59
12	LRTWQTAHV	378	2.8600	29.18
13	VRAVGKTDL	526	2.8000	28.57
14	LPMTQRYFL	567	2.8000	28.57
15	IIDYWGIIK	79	2.6000	26.53
16	VHLICPQII	141	2.6000	26.53
17	VVLRTWQTA	376	2.6000	26.53
18	VMKARRGAL	386	2.6000	26.53
19	IHAYHTEGA	274	2.5600	26.12
20	IAKYTICPA	413	2.5500	26.02
21	VIIDYWGII	78	2.5000	25.51
22	IGIRDGRIV	90	2.5000	25.51
23	WHLARMLES	181	2.5000	25.51
24	MGAISMIGS	357	2.4000	24.49
25	IVTAGTVDC	131	2.3600	24.08
26	IGKAGNPDI	100	2.2000	22.45
27	LESLDGWPV	187	2.2000	22.45
28	IISGNRRIV	124	2.1000	21.43
29	FKLHEDWGS	222	2.1000	21.43
30	LHDMGAISM	354	2.0800	21.22
31	ISGNRRIVT	125	2.0000	20.41
32	VHFVAPQSI	498	2.0000	20.41
33	VVGPSTEII	117	1.9600	20.00
34	IRDGRIVGI	92	1.9500	19.90
35	LMVCHHLNP	322	1.9000	19.39
36	LPLNDALPS	534	1.9000	19.39

37	IGAIAGRSI	266	1.8000	18.37
38	VNRGLAPVA	516	1.8000	18.37
39	WQTAHVMKA	381	1.6000	16.33
40	LAVNRGLAP	514	1.6000	16.33
41	MLMVCHHLN	321	1.5000	15.31
42	VLPSSTNPT	299	1.4600	14.90
43	IDYWGIIKA	80	1.4500	14.80
44	IVGIGKAGN	97	1.4000	14.29
45	MIGSDSQAM	362	1.3800	14.08
46	LKGGAIAWA	457	1.3500	13.78
47	LRGGASGFK	215	1.3000	13.27
48	VQVALHSDT	247	1.3000	13.27
49	LHSDTLNET	251	1.3000	13.27
50	VEVGKLADL	433	1.3000	13.27
51	IIGGGTGPA	160	1.2600	12.86
52	VDCHVHLIC	137	1.2000	12.24
53	MGRVGEVVL	370	1.2000	12.24
54	VRIDGQVWQ	552	1.2000	12.24
55	IAHGMDHLI	422	1.1000	11.22
56	IGSVEVGKL	430	1.1000	11.22
57	VLKGGAIAW	456	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	VRRYIAKYT	409	3.9000	39.80
2	FVAPQSIDA	500	3.9000	39.80
3	WHLARMLES	181	3.5000	35.71
4	VRPHVVLKG	451	3.4000	34.69
5	IRLADTNLL	20	3.3600	34.29
6	LVVGPSTEI	116	3.1000	31.63
7	FKLHEDWGS	222	3.1000	31.63
8	WQTAHVMKA	381	2.6000	26.53

9	MVCHHLNPR	323	2.1000	21.43
10	VCHHLNPRI	324	2.0000	20.41
11	VGKLADLVL	435	2.0000	20.41
12	VLPRPMFGA	480	2.0000	20.41
13	YTICPAIAH	416	1.9000	19.39
14	LVLWEPAFF	441	1.9000	19.39
15	FFGVRPHVV	448	1.9000	19.39
16	VVLKGGAIA	455	1.9000	19.39
17	LRTWQTAHV	378	1.8600	18.98
18	VRAVGKTDL	526	1.8000	18.37
19	LPMTQRYFL	567	1.8000	18.37
20	IIDYWGIIK	79	1.6000	16.33
21	VHLICPQII	141	1.6000	16.33
22	VVLRTWQTA	376	1.6000	16.33
23	VMKARRGAL	386	1.6000	16.33
24	IHAYHTEGA	274	1.5600	15.92
25	IAKYTICPA	413	1.5500	15.82
26	VIIDYWGII	78	1.5000	15.31
27	IGIRDGRIV	90	1.5000	15.31
28	FGVRPHVVL	449	1.5000	15.31
29	MGAISMIGS	357	1.4000	14.29
30	IVTAGTVDC	131	1.3600	13.88
31	FVEDTIGAI	261	1.2500	12.76
32	IGKAGNPDI	100	1.2000	12.24
33	LESLDGWPV	187	1.2000	12.24
34	WQPQPAAEL	559	1.2000	12.24
35	YAQLYGPTT	8	1.1000	11.22
36	YWGIIKADI	82	1.1000	11.22
37	WGIIKADIG	83	1.1000	11.22
38	IISGNRRIV	124	1.1000	11.22
39	LHDMGAISM	354	1.0800	11.02
40	YGPTTGDRI	12	1.0000	10.20
41	ISGNRRIVT	125	1.0000	10.20
42	FALLGKGNT	197	1.0000	10.20

43	VHFVAPQSI	498	1.0000	10.20
44	VVGPSTEII	117	0.9600	9.80
45	IRDGRIVGI	92	0.9500	9.69
46	WPVNFALLG	193	0.9000	9.18
47	LMVCHHLNP	322	0.9000	9.18
48	LPLNDALPS	534	0.9000	9.18
49	WEQLRGGAS	212	0.8000	8.16
50	IGAIAGRSI	266	0.8000	8.16
51	VNRGLAPVA	516	0.8000	8.16
52	YIAKYTICP	412	0.7600	7.76
53	FGAAAATAA	486	0.7000	7.14
54	WAAMGDANA	464	0.6000	6.12
55	LAVNRGLAP	514	0.6000	6.12
56	FTVRIDGQV	550	0.6000	6.12
57	MLMVCHHLN	321	0.5000	5.10

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	VRRYIAKYT	409	4.9000	50.00
2	VRPHVVLKG	451	4.4000	44.90
3	IRLADTNLL	20	4.3600	44.49
4	LVVGPSTEI	116	4.1000	41.84
5	MVCHHLNPR	323	3.1000	31.63
6	VCHHLNPRI	324	3.0000	30.61
7	VGKLADLVL	435	3.0000	30.61
8	VLPRPMFGA	480	3.0000	30.61
9	LVLWEPAFF	441	2.9000	29.59
10	VVLKGGAIA	455	2.9000	29.59
11	FVAPQSIDA	500	2.9000	29.59
12	LRTWQTAHV	378	2.8600	29.18
13	VRAVGKTDL	526	2.8000	28.57
14	LPMTQRYFL	567	2.8000	28.57

15	IIDYWGIIK	79	2.6000	26.53
16	VHLICPQII	141	2.6000	26.53
17	VVLRTWQTA	376	2.6000	26.53
18	VMKARRGAL	386	2.6000	26.53
19	IHAYHTEGA	274	2.5600	26.12
20	IAKYTICPA	413	2.5500	26.02
21	VIIDYWGII	78	2.5000	25.51
22	IGIRDGRIV	90	2.5000	25.51
23	WHLARMLES	181	2.5000	25.51
24	MGAISMIGS	357	2.4000	24.49
25	IVTAGTVDC	131	2.3600	24.08
26	IGKAGNPDI	100	2.2000	22.45
27	LESLDGWPV	187	2.2000	22.45
28	IISGNRRIV	124	2.1000	21.43
29	FKLHEDWGS	222	2.1000	21.43
30	LHDMGAISM	354	2.0800	21.22
31	ISGNRRIVT	125	2.0000	20.41
32	VHFVAPQSI	498	2.0000	20.41
33	VVGPSTEII	117	1.9600	20.00
34	IRDGRIVGI	92	1.9500	19.90
35	LMVCHHLNP	322	1.9000	19.39
36	LPLNDALPS	534	1.9000	19.39
37	IGAIAGRSI	266	1.8000	18.37
38	VNRGLAPVA	516	1.8000	18.37
39	WQTAHVMKA	381	1.6000	16.33
40	LAVNRGLAP	514	1.6000	16.33
41	MLMVCHHLN	321	1.5000	15.31
42	VLPSSTNPT	299	1.4600	14.90
43	IDYWGIIKA	80	1.4500	14.80
44	IVGIGKAGN	97	1.4000	14.29
45	MIGSDSQAM	362	1.3800	14.08
46	LKGGAIAWA	457	1.3500	13.78
47	LRGGASGFK	215	1.3000	13.27
48	VQVALHSDT	247	1.3000	13.27

49	LHSDTLNET	251	1.3000	13.27
50	VEVGKLADL	433	1.3000	13.27
51	IIGGGTGPA	160	1.2600	12.86
52	VDCHVHLIC	137	1.2000	12.24
53	MGRVGEVVL	370	1.2000	12.24
54	VRIDGQVWQ	552	1.2000	12.24
55	IAHGMDHLI	422	1.1000	11.22
56	IGSVEVGKL	430	1.1000	11.22
57	VLKGGAIAW	456	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	VHLICPQII	141	4.2000	42.86
2	VHFVAPQSI	498	3.8000	38.78
3	YTICPAIAH	416	3.7000	37.76
4	FFGVRPHVV	448	3.3000	33.67
5	IRLADTNLL	20	3.2000	32.65
6	LAFAESRIR	336	3.1000	31.63
7	IGAIAGRSI	266	3.0000	30.61
8	LRGGASGFK	215	2.6000	26.53
9	MLMVCHHLN	321	2.5000	25.51
10	LRESMGQGR	54	2.4000	24.49
11	VRAVGKTDL	526	2.4000	24.49
12	WGIIKADIG	83	2.2000	22.45
13	LVLWEPAFF	441	2.1000	21.43
14	WQPQPAAEL	559	2.1000	21.43
15	VRRYIAKYT	409	2.0000	20.41
16	IITVAAQPN	290	1.9000	19.39
17	LHDMGAISM	354	1.9000	19.39
18	IIDYWGIIK	79	1.8000	18.37
19	IIKADIGIR	85	1.8000	18.37
20	WEPAFFGVR	444	1.8000	18.37

21	WEQLRGGAS	212	1.7000	17.35
22	MVCHHLNPR	323	1.7000	17.35
23	WHLARMLES	181	1.6000	16.33
24	IGSVEVGKL	430	1.4000	14.29
25	LPMTQRYFL	567	1.4000	14.29
26	FVAPQSIDA	500	1.3000	13.27
27	MGAISMIGS	357	1.2000	12.24
28	VADVRAVGK	523	1.2000	12.24
29	YWGIIKADI	82	1.1000	11.22
30	IVGIGKAGN	97	1.1000	11.22
31	LVVGPSTEI	116	1.0000	10.20
32	ICPAIAHGM	418	1.0000	10.20
33	LYGPTTGDR	11	0.9000	9.18
34	VLRTWQTAH	377	0.9000	9.18
35	FGAAAATAA	486	0.8000	8.16
36	VMKARRGAL	386	0.7000	7.14
37	VNFALLGKG	195	0.6000	6.12
38	VLWEPAFFG	442	0.6000	6.12
39	YGPTTGDRI	12	0.5000	5.10
40	FALLGKGNT	197	0.5000	5.10
41	YHTEGAGGG	277	0.5000	5.10
42	MIGSDSQAM	362	0.5000	5.10
43	ITGAVIIDY	74	0.3000	3.06
44	MGRVGEVVL	370	0.3000	3.06
45	WQTAHVMKA	381	0.3000	3.06
46	LIGSVEVGK	429	0.2000	2.04
47	IGIRDGRIV	90	0.1000	1.02
48	VEALAAGTT	150	0.1000	1.02
49	ISMIGSDSQ	360	0.1000	1.02
50	VVLKGGAIA	455	0.1000	1.02
51	IMTGVHRDL	108	-0.1000	0

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

	2.3	9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VHLICPQII	141	4.2000	42.86
2	VHFVAPQSI	498	3.8000	38.78
3	YTICPAIAH	416	3.7000	37.76
4	FFGVRPHVV	448	3.3000	33.67
5	IRLADTNLL	20	3.2000	32.65
6	LAFAESRIR	336	3.1000	31.63
7	IGAIAGRSI	266	3.0000	30.61
8	LRGGASGFK	215	2.6000	26.53
9	MLMVCHHLN	321	2.5000	25.51
10	LRESMGQGR	54	2.4000	24.49
11	VRAVGKTDL	526	2.4000	24.49
12	WGIIKADIG	83	2.2000	22.45
13	LVLWEPAFF	441	2.1000	21.43
14	WQPQPAAEL	559	2.1000	21.43
15	VRRYIAKYT	409	2.0000	20.41
16	IITVAAQPN	290	1.9000	19.39
17	LHDMGAISM	354	1.9000	19.39
18	IIDYWGIIK	79	1.8000	18.37
19	IIKADIGIR	85	1.8000	18.37
20	WEPAFFGVR	444	1.8000	18.37
21	WEQLRGGAS	212	1.7000	17.35
22	MVCHHLNPR	323	1.7000	17.35
23	WHLARMLES	181	1.6000	16.33
24	IGSVEVGKL	430	1.4000	14.29
25	LPMTQRYFL	567	1.4000	14.29
26	FVAPQSIDA	500	1.3000	13.27
27	MGAISMIGS	357	1.2000	12.24
28	VADVRAVGK	523	1.2000	12.24
29	YWGIIKADI	82	1.1000	11.22
30	IVGIGKAGN	97	1.1000	11.22
31	LVVGPSTEI	116	1.0000	10.20
32	ICPAIAHGM	418	1.0000	10.20

33	LYGPTTGDR	11	0.9000	9.18
34	VLRTWQTAH	377	0.9000	9.18
35	FGAAAATAA	486	0.8000	8.16
36	VMKARRGAL	386	0.7000	7.14
37	VNFALLGKG	195	0.6000	6.12
38	VLWEPAFFG	442	0.6000	6.12
39	YGPTTGDRI	12	0.5000	5.10
40	FALLGKGNT	197	0.5000	5.10
41	YHTEGAGGG	277	0.5000	5.10
42	MIGSDSQAM	362	0.5000	5.10
43	ITGAVIIDY	74	0.3000	3.06
44	MGRVGEVVL	370	0.3000	3.06
45	WQTAHVMKA	381	0.3000	3.06
46	LIGSVEVGK	429	0.2000	2.04
47	IGIRDGRIV	90	0.1000	1.02
48	VEALAAGTT	150	0.1000	1.02
49	ISMIGSDSQ	360	0.1000	1.02
50	VVLKGGAIA	455	0.1000	1.02
51	IMTGVHRDL	108	-0.1000	0