MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Apr 20 00:08:07 2010
Length of input sequence	679 amino acids
Number of nanomers from input sequence	671
Number of nanomers with obligatory P1 anchor residue	182
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	67

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	IRVVSAQTA	547	1.8500	30.83
2	LMLVAATQL	97	1.6400	27.33
3	LVLMLVAAT	95	1.6000	26.67
4	FHNIAGWLM	650	1.5000	25.00
5	FFLQVSHAA	106	1.4000	23.33
6	YVQQQVQQA	320	1.3000	21.67
7	WITFAGIAT	611	1.2800	21.33
8	VLMLVAATQ	96	0.7000	11.67
9	LRAQAAGQL	116	0.7000	11.67

10	LQVSHAAGL	108	0.5000	8.33
11	VYLARAVDP	213	0.5000	8.33
12	VRQMLRAVV	558	0.5000	8.33
13	YQMAGKTGT	586	0.4900	8.17
14	FRHRTGNAV	85	0.4000	6.67
15	VNKIVAASA	386	0.3000	5.00
16	YQQGTGPTA	573	0.2700	4.50
17	LFFLQVSHA	105	0.2000	3.33
18	YVIGIMLDN	625	0.2000	3.33
19	ILVLMLVAA	94	0.1000	1.67
20	FVYLARAVD	212	0.1000	1.67
21	IVAASAVIE	389	-0.1000	0
22	VVSAQTAQT	549	-0.1000	0
23	LGLEDSLDA	265	-0.2000	0
24	YDMLRKFGL	458	-0.2000	0
25	VILVLMLVA	93	-0.4500	0
26	LFHNIAGWL	649	-0.5600	0
27	VVIPGSYRN	291	-0.6000	0
28	FEPGSVNKI	381	-0.6000	0
29	FGLGQRTGV	464	-0.6100	0
30	LPIGQGLSM	496	-0.6200	0
31	LQMTGMYQA	507	-0.7000	0
32	VSAQTAQTV	550	-0.7000	0
33	YWITFAGIA	610	-0.7000	0
34	VSRAAPRRA	0	-0.7100	0
35	MTLLQMTGM	504	-0.7300	0
36	LVAATQLFF	99	-0.8000	0
37	LRQYPGGSL	241	-0.8000	0
38	VVLTLDNDI	309	-0.8000	0
39	FGKSSNVGT	437	-0.8000	0
40	MYQAIANDG	512	-0.8000	0
41	IGIMLDNPA	627	-0.8000	0
42	MQRENVPLS	658	-0.8300	0
43	MLVAATQLF	98	-0.9000	0

44	FTIEARALT	147	-0.9000	0
45	WLMQRENVP	656	-0.9000	0
46	MGYQQGTGP	571	-0.9100	0
47	VYWITFAGI	609	-1.0000	0
48	LLQMTGMYQ	506	-1.0100	0
49	VSHAAGLRA	110	-1.1000	0
50	YQAIANDGV	513	-1.1000	0
51	LQVPGSIQM	407	-1.1200	0
52	FYVQQQVQQ	319	-1.2000	0
53	IQMGGVTVH	413	-1.2100	0
54	IGQGLSMTL	498	-1.2100	0
55	LKVTDVQPA	124	-1.3000	0
56	VHGSTVVLT	304	-1.3000	0
57	INPGCGCYF	598	-1.3000	0
58	MGGVTVHDA	415	-1.3500	0
59	VVDVGTRGA	73	-1.3600	0
60	IQFYVQQQV	317	-1.4000	0
61	VQQAKNLSG	325	-1.4000	0
62	MLDNPARNS	630	-1.4700	0
63	VDPAVASAI	219	-1.5000	0
64	LSGAHNVSA	331	-1.5000	0
65	VMPYTTTGV	428	-1.5100	0
66	IKATVAPDG	528	-1.6300	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	IRVVSAQTA	547	2.8500	47.50
2	LMLVAATQL	97	2.6400	44.00
3	LVLMLVAAT	95	2.6000	43.33
4	VLMLVAATQ	96	1.7000	28.33
5	LRAQAAGQL	116	1.7000	28.33
6	LQVSHAAGL	108	1.5000	25.00
7	VYLARAVDP	213	1.5000	25.00

8	VRQMLRAVV	558	1.5000	25.00
9	FHNIAGWLM	650	1.5000	25.00
10	FFLQVSHAA	106	1.4000	23.33
11	VNKIVAASA	386	1.3000	21.67
12	LFFLQVSHA	105	1.2000	20.00
13	ILVLMLVAA	94	1.1000	18.33
14	IVAASAVIE	389	0.9000	15.00
15	VVSAQTAQT	549	0.9000	15.00
16	LGLEDSLDA	265	0.8000	13.33
17	VILVLMLVA	93	0.5500	9.17
18	LFHNIAGWL	649	0.4400	7.33
19	FRHRTGNAV	85	0.4000	6.67
20	VVIPGSYRN	291	0.4000	6.67
21	LPIGQGLSM	496	0.3800	6.33
22	YVQQQVQQA	320	0.3000	5.00
23	LQMTGMYQA	507	0.3000	5.00
24	VSAQTAQTV	550	0.3000	5.00
25	VSRAAPRRA	0	0.2900	4.83
26	WITFAGIAT	611	0.2800	4.67
27	MTLLQMTGM	504	0.2700	4.50
28	LVAATQLFF	99	0.2000	3.33
29	LRQYPGGSL	241	0.2000	3.33
30	VVLTLDNDI	309	0.2000	3.33
31	MYQAIANDG	512	0.2000	3.33
32	IGIMLDNPA	627	0.2000	3.33
33	MQRENVPLS	658	0.1700	2.83
34	MLVAATQLF	98	0.1000	1.67
35	FVYLARAVD	212	0.1000	1.67
36	MGYQQGTGP	571	0.0900	1.50
37	LLQMTGMYQ	506	-0.0100	0
38	VSHAAGLRA	110	-0.1000	0
39	LQVPGSIQM	407	-0.1200	0
40	IQMGGVTVH	413	-0.2100	0
41	IGQGLSMTL	498	-0.2100	0

42	LKVTDVQPA	124	-0.3000	0
43	VHGSTVVLT	304	-0.3000	0
44	INPGCGCYF	598	-0.3000	0
45	MGGVTVHDA	415	-0.3500	0
46	VVDVGTRGA	73	-0.3600	0
47	IQFYVQQQV	317	-0.4000	0
48	VQQAKNLSG	325	-0.4000	0
49	MLDNPARNS	630	-0.4700	0
50	VDPAVASAI	219	-0.5000	0
51	LSGAHNVSA	331	-0.5000	0
52	VMPYTTTGV	428	-0.5100	0
53	YQMAGKTGT	586	-0.5100	0
54	FEPGSVNKI	381	-0.6000	0
55	FGLGQRTGV	464	-0.6100	0
56	IKATVAPDG	528	-0.6300	0
57	LRAVVQRDP	562	-0.6600	0
58	VQPAARGSI	129	-0.7000	0
59	VASAICAKY	223	-0.7000	0
60	LGQRTGVGL	466	-0.7000	0
61	YQQGTGPTA	573	-0.7300	0
62	LKKLQSDET	203	-0.8000	0
63	FGKSSNVGT	437	-0.8000	0
64	LMLSQRVGP	446	-0.8000	0
65	MTGMYQAIA	509	-0.8000	0

ALLELE: DRB1_0301	Threshold for 3 % with score: 2.96	Highest Score achievable by any peptide: 9.5

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDAKTGE	340	6.3000	66.32
2	LQSDETFVY	206	5.3000	55.79
3	IMLDNPARN	629	4.3000	45.26
4	MQRENVPLS	658	3.9000	41.05
5	LVLMLVAAT	95	3.8000	40.00
6	MANDNTFDP	352	3.8000	40.00

7	IQMGGVTVH	413	3.7000	38.95
8	LMLSQRVGP	446	3.7000	38.95
9	VRQMLRAVV	558	3.5000	36.84
10	VQPAARGSI	129	3.2000	33.68
11	VQRDPMGYQ	566	3.2000	33.68
12	MLVAATQLF	98	3.1000	32.63
13	VVQRDPMGY	565	3.0000	31.58
14	LVAATQLFF	99	2.9000	30.53
15	VRVPPRIIK	521	2.9000	30.53
16	LFFLQVSHA	105	2.8700	30.21
17	VTYDRGSDG	282	2.8700	30.21
18	IANDGVRVP	516	2.8000	29.47
19	VHGSTVVLT	304	2.6000	27.37
20	IRVVSAQTA	547	2.6000	27.37
21	VVSAQTAQT	549	2.6000	27.37
22	VFRHRTGNA	84	2.4000	25.26
23	LQVSHAAGL	108	2.3600	24.84
24	FVYLARAVD	212	2.3000	24.21
25	YQMAGKTGT	586	2.3000	24.21
26	LRAQAAGQL	116	2.2600	23.79
27	LSPDPGPPL	665	2.2600	23.79
28	VLMLVAATQ	96	2.2000	23.16
29	LTLDNDIQF	311	2.2000	23.16
30	YVQQQVQQA	320	2.2000	23.16
31	MLSQRVGPE	447	2.2000	23.16
32	FGLGQRTGV	464	2.2000	23.16
33	MLRAVVQRD	561	2.2000	23.16
34	LAANVVGGI	249	2.1000	22.11
35	LQVPGSIQM	407	2.1000	22.11
36	LPIGQGLSM	496	2.1000	22.11
37	LDNDIQFYV	313	2.0000	21.05
38	IVAASAVIE	389	2.0000	21.05
39	LRKFGLGQR	461	2.0000	21.05
40	LMLVAATQL	97	1.9600	20.63

41	IGQGLSMTL	498	1.9600	20.63
42	VDVGTRGAS	74	1.9000	20.00
43	ILVLMLVAA	94	1.9000	20.00
44	VAPAGRSTR	58	1.8700	19.68
45	VVIPGSYRN	291	1.8500	19.47
46	IRRQLEEAR	161	1.8000	18.95
47	VYLARAVDP	213	1.8000	18.95
48	VAASAVIEH	390	1.8000	18.95
49	INPGCGCYF	598	1.8000	18.95
50	YVIGIMLDN	625	1.8000	18.95
51	LKVTDVQPA	124	1.7000	17.89
52	LTFQPKRIR	154	1.7000	17.89
53	IIKATVAPD	527	1.7000	17.89
54	FEPGSVNKI	381	1.6100	16.95
55	VPGSIQMGG	409	1.6000	16.84
56	YRNRHKAVH	297	1.5000	15.79
57	ITFAGIATA	612	1.5000	15.79
58	VILVLMLVA	93	1.4000	14.74
59	VMPYTTTGV	428	1.4000	14.74
60	VNKIVAASA	386	1.3000	13.68
61	VAPDGSRTE	532	1.3000	13.68
62	VGTLMLSQR	443	1.2700	13.37
63	LFHNIAGWL	649	1.2600	13.26
64	MYQAIANDG	512	1.2100	12.74
65	FVFRHRTGN	83	1.2000	12.63
66	VQQAKNLSG	325	1.2000	12.63
67	LLQMTGMYQ	506	1.2000	12.63

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDAKTGE	340	3.9000	42.86
2	IQMGGVTVH	413	3.2800	36.04
3	YVQQQVQQA	320	3.2000	35.16

4	YRNRHKAVH	297	3.0800	33.85
5	LQSDETFVY	206	3.0000	32.97
6	VQRDPMGYQ	566	2.9000	31.87
7	YQMAGKTGT	586	2.6000	28.57
8	IMLDNPARN	629	2.5000	27.47
9	MQRENVPLS	658	2.5000	27.47
10	FVYLARAVD	212	2.2000	24.18
11	FGLGQRTGV	464	2.2000	24.18
12	LVLMLVAAT	95	2.1000	23.08
13	YVIGIMLDN	625	2.0000	21.98
14	VLMLVAATQ	96	1.9000	20.88
15	LFFLQVSHA	105	1.8700	20.55
16	FYVQQQVQQ	319	1.8000	19.78
17	MANDNTFDP	352	1.8000	19.78
18	VRVPPRIIK	521	1.8000	19.78
19	FEPGSVNKI	381	1.7100	18.79
20	LMLSQRVGP	446	1.7000	18.68
21	YQQGTGPTA	573	1.7000	18.68
22	IRVVSAQTA	547	1.6000	17.58
23	VRQMLRAVV	558	1.5000	16.48
24	FVFRHRTGN	83	1.4000	15.38
25	VFRHRTGNA	84	1.4000	15.38
26	VAASAVIEH	390	1.3800	15.16
27	VQPAARGSI	129	1.3000	14.29
28	ILVLMLVAA	94	0.9000	9.89
29	FFLQVSHAA	106	0.9000	9.89
30	VHGSTVVLT	304	0.9000	9.89
31	YDMLRKFGL	458	0.9000	9.89
32	LLQMTGMYQ	506	0.9000	9.89
33	VVSAQTAQT	549	0.9000	9.89
34	FQPKRIRRQ	156	0.8000	8.79
35	IANDGVRVP	516	0.8000	8.79
36	LKVTDVQPA	124	0.7000	7.69
37	VVQRDPMGY	565	0.7000	7.69

38	YLARAVDPA	214	0.6000	6.59
39	VDVGTRGAS	74	0.5000	5.49
40	YWITFAGIA	610	0.5000	5.49
41	ITFAGIATA	612	0.5000	5.49
42	VTYDRGSDG	282	0.4700	5.16
43	VILVLMLVA	93	0.4000	4.40
44	LQVSHAAGL	108	0.4000	4.40
45	YTTTGVFGK	431	0.4000	4.40
46	IPGSYRNRH	293	0.3900	4.29
47	LRAQAAGQL	116	0.3000	3.30
48	FTIEARALT	147	0.3000	3.30
49	VNKIVAASA	386	0.3000	3.30
50	FANLPIGQG	493	0.3000	3.30
51	LSPDPGPPL	665	0.3000	3.30
52	MLVAATQLF	98	0.2000	2.20
53	LAANVVGGI	249	0.2000	2.20
54	MGGVTVHDA	415	0.1000	1.10
55	MLRAVVQRD	561	0.1000	1.10
56	FAGIATADN	614	0.1000	1.10
57	FHNIAGWLM	650	0.1000	1.10
58	VVIPGSYRN	291	0.0500	0.55
59	FRHRTGNAV	85	-0.0900	0
60	VGQRKRPGK	29	-0.1000	0
61	FLQVSHAAG	107	-0.1000	0
62	LRDIAQEVA	182	-0.1000	0

ALLELE: DRB1_0306	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDAKTGE	340	4.9000	55.68
2	IQMGGVTVH	413	4.2800	48.64
3	IMLDNPARN	629	3.5000	39.77
4	LVLMLVAAT	95	3.1000	35.23
5	VLMLVAATQ	96	2.9000	32.95

6	IRVVSAQTA	547	2.7000	30.68
7	LFFLQVSHA	105	2.6000	29.55
8	LMLSQRVGP	446	2.5800	29.32
9	LQSDETFVY	206	2.5000	28.41
10	VRQMLRAVV	558	2.5000	28.41
11	VQRDPMGYQ	566	2.5000	28.41
12	VRVPPRIIK	521	2.4800	28.18
13	YVQQQVQQA	320	2.3000	26.14
14	MQRENVPLS	658	2.1000	23.86
15	IPGSYRNRH	293	2.0800	23.64
16	YRNRHKAVH	297	2.0800	23.64
17	VAASAVIEH	390	2.0600	23.41
18	VILVLMLVA	93	1.9000	21.59
19	MGGVTVHDA	415	1.9000	21.59
20	VVSAQTAQT	549	1.9000	21.59
21	LKVTDVQPA	124	1.8000	20.45
22	ILVLMLVAA	94	1.7800	20.23
23	VHGSTVVLT	304	1.7800	20.23
24	LLQMTGMYQ	506	1.6000	18.18
25	YQMAGKTGT	586	1.6000	18.18
26	LVAATQLFF	99	1.5000	17.05
27	IANDGVRVP	516	1.5000	17.05
28	ITFAGIATA	612	1.5000	17.05
29	YVIGIMLDN	625	1.5000	17.05
30	LQVSHAAGL	108	1.4000	15.91
31	FEPGSVNKI	381	1.4000	15.91
32	VVQRDPMGY	565	1.4000	15.91
33	MLVAATQLF	98	1.3000	14.77
34	LRDIAQEVA	182	1.3000	14.77
35	MANDNTFDP	352	1.3000	14.77
36	VNKIVAASA	386	1.3000	14.77
37	FVYLARAVD	212	1.2000	13.64
38	VTYDRGSDG	282	1.2000	13.64
39	MLRKFGLGQ	460	1.2000	13.64

40	FGLGQRTGV	464	1.2000	13.64
41	MLRAVVQRD	561	1.2000	13.64
42	LGLEDSLDA	265	1.1000	12.50
43	LPIGQGLSM	496	1.1000	12.50
44	VFRHRTGNA	84	1.0000	11.36
45	LMLVAATQL	97	1.0000	11.36
46	VQPAARGSI	129	0.9000	10.23
47	FFLQVSHAA	106	0.7000	7.95
48	IRRQLEEAR	161	0.7000	7.95
49	IGQGLSMTL	498	0.7000	7.95
50	VYLARAVDP	213	0.6800	7.73
51	FYVQQQVQQ	319	0.6800	7.73
52	LEEARKKTS	165	0.6000	6.82
53	VLTLDNDIQ	310	0.6000	6.82
54	VQQQVQQAK	321	0.6000	6.82
55	VLQVPGSIQ	406	0.6000	6.82
56	IIKATVAPD	527	0.6000	6.82
57	MYQAIANDG	512	0.5000	5.68
58	IVAASAVIE	389	0.4800	5.45
59	VVDVGTRGA	73	0.4000	4.55
60	FVFRHRTGN	83	0.4000	4.55
61	VMPYTTTGV	428	0.4000	4.55
62	VIGIMLDNP	626	0.4000	4.55
63	VQQAKNLSG	325	0.3000	3.41
64	LQVPGSIQM	407	0.2800	3.18
65	IGIMLDNPA	627	0.2000	2.27
66	VAPAGRSTR	58	0.1000	1.14
67	VDVGTRGAS	74	0.1000	1.14

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	VVLDAKTGE	340	4.9000	55.68
2	IQMGGVTVH	413	4.2800	48.64

3	IMLDNPARN	629	3.5000	39.77
4	LVLMLVAAT	95	3.1000	35.23
5	VLMLVAATQ	96	2.9000	32.95
6	IRVVSAQTA	547	2.7000	30.68
7	LFFLQVSHA	105	2.6000	29.55
8	LMLSQRVGP	446	2.5800	29.32
9	LQSDETFVY	206	2.5000	28.41
10	VRQMLRAVV	558	2.5000	28.41
11	VQRDPMGYQ	566	2.5000	28.41
12	VRVPPRIIK	521	2.4800	28.18
13	YVQQQVQQA	320	2.3000	26.14
14	MQRENVPLS	658	2.1000	23.86
15	IPGSYRNRH	293	2.0800	23.64
16	YRNRHKAVH	297	2.0800	23.64
17	VAASAVIEH	390	2.0600	23.41
18	VILVLMLVA	93	1.9000	21.59
19	MGGVTVHDA	415	1.9000	21.59
20	VVSAQTAQT	549	1.9000	21.59
21	LKVTDVQPA	124	1.8000	20.45
22	ILVLMLVAA	94	1.7800	20.23
23	VHGSTVVLT	304	1.7800	20.23
24	LLQMTGMYQ	506	1.6000	18.18
25	YQMAGKTGT	586	1.6000	18.18
26	LVAATQLFF	99	1.5000	17.05
27	IANDGVRVP	516	1.5000	17.05
28	ITFAGIATA	612	1.5000	17.05
29	YVIGIMLDN	625	1.5000	17.05
30	LQVSHAAGL	108	1.4000	15.91
31	FEPGSVNKI	381	1.4000	15.91
32	VVQRDPMGY	565	1.4000	15.91
33	MLVAATQLF	98	1.3000	14.77
34	LRDIAQEVA	182	1.3000	14.77
35	MANDNTFDP	352	1.3000	14.77
36	VNKIVAASA	386	1.3000	14.77

37	FVYLARAVD	212	1.2000	13.64
38	VTYDRGSDG	282	1.2000	13.64
39	MLRKFGLGQ	460	1.2000	13.64
40	FGLGQRTGV	464	1.2000	13.64
41	MLRAVVQRD	561	1.2000	13.64
42	LGLEDSLDA	265	1.1000	12.50
43	LPIGQGLSM	496	1.1000	12.50
44	VFRHRTGNA	84	1.0000	11.36
45	LMLVAATQL	97	1.0000	11.36
46	VQPAARGSI	129	0.9000	10.23
47	FFLQVSHAA	106	0.7000	7.95
48	IRRQLEEAR	161	0.7000	7.95
49	IGQGLSMTL	498	0.7000	7.95
50	VYLARAVDP	213	0.6800	7.73
51	FYVQQQVQQ	319	0.6800	7.73
52	LEEARKKTS	165	0.6000	6.82
53	VLTLDNDIQ	310	0.6000	6.82
54	VQQQVQQAK	321	0.6000	6.82
55	VLQVPGSIQ	406	0.6000	6.82
56	IIKATVAPD	527	0.6000	6.82
57	MYQAIANDG	512	0.5000	5.68
58	IVAASAVIE	389	0.4800	5.45
59	VVDVGTRGA	73	0.4000	4.55
60	FVFRHRTGN	83	0.4000	4.55
61	VMPYTTTGV	428	0.4000	4.55
62	VIGIMLDNP	626	0.4000	4.55
63	VQQAKNLSG	325	0.3000	3.41
64	LQVPGSIQM	407	0.2800	3.18
65	IGIMLDNPA	627	0.2000	2.27
66	VAPAGRSTR	58	0.1000	1.14
67	VDVGTRGAS	74	0.1000	1.14

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	VVLDAKTGE	340	4.9000	55.68
2	IQMGGVTVH	413	4.2800	48.64
3	IMLDNPARN	629	3.5000	39.77
4	LVLMLVAAT	95	3.1000	35.23
5	VLMLVAATQ	96	2.9000	32.95
6	IRVVSAQTA	547	2.7000	30.68
7	LFFLQVSHA	105	2.6000	29.55
8	LMLSQRVGP	446	2.5800	29.32
9	LQSDETFVY	206	2.5000	28.41
10	VRQMLRAVV	558	2.5000	28.41
11	VQRDPMGYQ	566	2.5000	28.41
12	VRVPPRIIK	521	2.4800	28.18
13	YVQQQVQQA	320	2.3000	26.14
14	MQRENVPLS	658	2.1000	23.86
15	IPGSYRNRH	293	2.0800	23.64
16	YRNRHKAVH	297	2.0800	23.64
17	VAASAVIEH	390	2.0600	23.41
18	VILVLMLVA	93	1.9000	21.59
19	MGGVTVHDA	415	1.9000	21.59
20	VVSAQTAQT	549	1.9000	21.59
21	LKVTDVQPA	124	1.8000	20.45
22	ILVLMLVAA	94	1.7800	20.23
23	VHGSTVVLT	304	1.7800	20.23
24	LLQMTGMYQ	506	1.6000	18.18
25	YQMAGKTGT	586	1.6000	18.18
26	LVAATQLFF	99	1.5000	17.05
27	IANDGVRVP	516	1.5000	17.05
28	ITFAGIATA	612	1.5000	17.05
29	YVIGIMLDN	625	1.5000	17.05
30	LQVSHAAGL	108	1.4000	15.91
31	FEPGSVNKI	381	1.4000	15.91
32	VVQRDPMGY	565	1.4000	15.91
33	MLVAATQLF	98	1.3000	14.77

34	LRDIAQEVA	182	1.3000	14.77
35	MANDNTFDP	352	1.3000	14.77
36	VNKIVAASA	386	1.3000	14.77
37	FVYLARAVD	212	1.2000	13.64
38	VTYDRGSDG	282	1.2000	13.64
39	MLRKFGLGQ	460	1.2000	13.64
40	FGLGQRTGV	464	1.2000	13.64
41	MLRAVVQRD	561	1.2000	13.64
42	LGLEDSLDA	265	1.1000	12.50
43	LPIGQGLSM	496	1.1000	12.50
44	VFRHRTGNA	84	1.0000	11.36
45	LMLVAATQL	97	1.0000	11.36
46	VQPAARGSI	129	0.9000	10.23
47	FFLQVSHAA	106	0.7000	7.95
48	IRRQLEEAR	161	0.7000	7.95
49	IGQGLSMTL	498	0.7000	7.95
50	VYLARAVDP	213	0.6800	7.73
51	FYVQQQVQQ	319	0.6800	7.73
52	LEEARKKTS	165	0.6000	6.82
53	VLTLDNDIQ	310	0.6000	6.82
54	VQQQVQQAK	321	0.6000	6.82
55	VLQVPGSIQ	406	0.6000	6.82
56	IIKATVAPD	527	0.6000	6.82
57	MYQAIANDG	512	0.5000	5.68
58	IVAASAVIE	389	0.4800	5.45
59	VVDVGTRGA	73	0.4000	4.55
60	FVFRHRTGN	83	0.4000	4.55
61	VMPYTTTGV	428	0.4000	4.55
62	VIGIMLDNP	626	0.4000	4.55
63	VQQAKNLSG	325	0.3000	3.41
64	LQVPGSIQM	407	0.2800	3.18
65	IGIMLDNPA	627	0.2000	2.27
66	VAPAGRSTR	58	0.1000	1.14
67	VDVGTRGAS	74	0.1000	1.14

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	VVLDAKTGE	340	5.3000	55.79
2	LQSDETFVY	206	4.3000	45.26
3	FVYLARAVD	212	3.3000	34.74
4	YQMAGKTGT	586	3.3000	34.74
5	IMLDNPARN	629	3.3000	34.74
6	YVQQQVQQA	320	3.2000	33.68
7	FGLGQRTGV	464	3.2000	33.68
8	MQRENVPLS	658	2.9000	30.53
9	LVLMLVAAT	95	2.8000	29.47
10	MANDNTFDP	352	2.8000	29.47
11	YVIGIMLDN	625	2.8000	29.47
12	IQMGGVTVH	413	2.7000	28.42
13	LMLSQRVGP	446	2.7000	28.42
14	FEPGSVNKI	381	2.6100	27.47
15	YRNRHKAVH	297	2.5000	26.32
16	VRQMLRAVV	558	2.5000	26.32
17	FVFRHRTGN	83	2.2000	23.16
18	VQPAARGSI	129	2.2000	23.16
19	VQRDPMGYQ	566	2.2000	23.16
20	MLVAATQLF	98	2.1000	22.11
21	VVQRDPMGY	565	2.0000	21.05
22	LVAATQLFF	99	1.9000	20.00
23	VRVPPRIIK	521	1.9000	20.00
24	LFFLQVSHA	105	1.8700	19.68
25	VTYDRGSDG	282	1.8700	19.68
26	YDMLRKFGL	458	1.8600	19.58
27	IANDGVRVP	516	1.8000	18.95
28	FANLPIGQG	493	1.7000	17.89
29	YQQGTGPTA	573	1.7000	17.89
30	VHGSTVVLT	304	1.6000	16.84

31	IRVVSAQTA	547	1.6000	16.84
32	VVSAQTAQT	549	1.6000	16.84
33	FHNIAGWLM	650	1.6000	16.84
34	VFRHRTGNA	84	1.4000	14.74
35	LQVSHAAGL	108	1.3600	14.32
36	FLQVSHAAG	107	1.3000	13.68
37	LRAQAAGQL	116	1.2600	13.26
38	LSPDPGPPL	665	1.2600	13.26
39	VLMLVAATQ	96	1.2000	12.63
40	LTLDNDIQF	311	1.2000	12.63
41	MLSQRVGPE	447	1.2000	12.63
42	MLRAVVQRD	561	1.2000	12.63
43	LAANVVGGI	249	1.1000	11.58
44	FYVQQQVQQ	319	1.1000	11.58
45	LQVPGSIQM	407	1.1000	11.58
46	LPIGQGLSM	496	1.1000	11.58
47	FTIEARALT	147	1.0000	10.53
48	LDNDIQFYV	313	1.0000	10.53
49	IVAASAVIE	389	1.0000	10.53
50	LRKFGLGQR	461	1.0000	10.53
51	LMLVAATQL	97	0.9600	10.11
52	IGQGLSMTL	498	0.9600	10.11
53	FRHRTGNAV	85	0.9100	9.58
54	VDVGTRGAS	74	0.9000	9.47
55	ILVLMLVAA	94	0.9000	9.47
56	FFLQVSHAA	106	0.9000	9.47
57	FAGIATADN	614	0.9000	9.47
58	VAPAGRSTR	58	0.8700	9.16
59	VVIPGSYRN	291	0.8500	8.95
60	IRRQLEEAR	161	0.8000	8.42
61	VYLARAVDP	213	0.8000	8.42
62	VAASAVIEH	390	0.8000	8.42
63	YQAIANDGV	513	0.8000	8.42
64	INPGCGCYF	598	0.8000	8.42

65	LKVTDVQPA	124	0.7000	7.37
66	LTFQPKRIR	154	0.7000	7.37
67	IIKATVAPD	527	0.7000	7.37

ALLELE: DRB1_0311	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDAKTGE	340	4.9000	55.68
2	IQMGGVTVH	413	4.2800	48.64
3	IMLDNPARN	629	3.5000	39.77
4	LVLMLVAAT	95	3.1000	35.23
5	VLMLVAATQ	96	2.9000	32.95
6	IRVVSAQTA	547	2.7000	30.68
7	LFFLQVSHA	105	2.6000	29.55
8	LMLSQRVGP	446	2.5800	29.32
9	LQSDETFVY	206	2.5000	28.41
10	VRQMLRAVV	558	2.5000	28.41
11	VQRDPMGYQ	566	2.5000	28.41
12	VRVPPRIIK	521	2.4800	28.18
13	YVQQQVQQA	320	2.3000	26.14
14	MQRENVPLS	658	2.1000	23.86
15	IPGSYRNRH	293	2.0800	23.64
16	YRNRHKAVH	297	2.0800	23.64
17	VAASAVIEH	390	2.0600	23.41
18	VILVLMLVA	93	1.9000	21.59
19	MGGVTVHDA	415	1.9000	21.59
20	VVSAQTAQT	549	1.9000	21.59
21	LKVTDVQPA	124	1.8000	20.45
22	ILVLMLVAA	94	1.7800	20.23
23	VHGSTVVLT	304	1.7800	20.23
24	LLQMTGMYQ	506	1.6000	18.18
25	YQMAGKTGT	586	1.6000	18.18
26	LVAATQLFF	99	1.5000	17.05
27	IANDGVRVP	516	1.5000	17.05

28	ITFAGIATA	612	1.5000	17.05
29	YVIGIMLDN	625	1.5000	17.05
30	LQVSHAAGL	108	1.4000	15.91
31	FEPGSVNKI	381	1.4000	15.91
32	VVQRDPMGY	565	1.4000	15.91
33	MLVAATQLF	98	1.3000	14.77
34	LRDIAQEVA	182	1.3000	14.77
35	MANDNTFDP	352	1.3000	14.77
36	VNKIVAASA	386	1.3000	14.77
37	FVYLARAVD	212	1.2000	13.64
38	VTYDRGSDG	282	1.2000	13.64
39	MLRKFGLGQ	460	1.2000	13.64
40	FGLGQRTGV	464	1.2000	13.64
41	MLRAVVQRD	561	1.2000	13.64
42	LGLEDSLDA	265	1.1000	12.50
43	LPIGQGLSM	496	1.1000	12.50
44	VFRHRTGNA	84	1.0000	11.36
45	LMLVAATQL	97	1.0000	11.36
46	VQPAARGSI	129	0.9000	10.23
47	FFLQVSHAA	106	0.7000	7.95
48	IRRQLEEAR	161	0.7000	7.95
49	IGQGLSMTL	498	0.7000	7.95
50	VYLARAVDP	213	0.6800	7.73
51	FYVQQQVQQ	319	0.6800	7.73
52	LEEARKKTS	165	0.6000	6.82
53	VLTLDNDIQ	310	0.6000	6.82
54	VQQQVQQAK	321	0.6000	6.82
55	VLQVPGSIQ	406	0.6000	6.82
56	IIKATVAPD	527	0.6000	6.82
57	MYQAIANDG	512	0.5000	5.68
58	IVAASAVIE	389	0.4800	5.45
59	VVDVGTRGA	73	0.4000	4.55
60	FVFRHRTGN	83	0.4000	4.55
61	VMPYTTTGV	428	0.4000	4.55

62	VIGIMLDNP	626	0.4000	4.55
63	VQQAKNLSG	325	0.3000	3.41
64	LQVPGSIQM	407	0.2800	3.18
65	IGIMLDNPA	627	0.2000	2.27
66	VAPAGRSTR	58	0.1000	1.14
67	VDVGTRGAS	74	0.1000	1.14

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	YVQQQVQQA	320	3.8000	44.19
2	LGLEDSLDA	265	3.7000	43.02
3	FFLQVSHAA	106	3.6000	41.86
4	MQRENVPLS	658	3.3000	38.37
5	LVLMLVAAT	95	2.7000	31.40
6	VLMLVAATQ	96	2.7000	31.40
7	VLTLDNDIQ	310	2.3000	26.74
8	YQAIANDGV	513	2.3000	26.74
9	VFRHRTGNA	84	2.2000	25.58
10	LKVTDVQPA	124	2.2000	25.58
11	LFFLQVSHA	105	2.1000	24.42
12	VVLTLDNDI	309	2.0000	23.26
13	VVSAQTAQT	549	2.0000	23.26
14	LQSDETFVY	206	1.7000	19.77
15	FAGIATADN	614	1.5000	17.44
16	FGKSSNVGT	437	1.4800	17.21
17	MLVAATQLF	98	1.4000	16.28
18	IGIMLDNPA	627	1.4000	16.28
19	FYVQQQVQQ	319	1.2800	14.88
20	VQQAKNLSG	325	1.2000	13.95
21	IMLDNPARN	629	1.1000	12.79
22	IQMGGVTVH	413	0.8800	10.23
23	VAASAVIEH	390	0.8600	10.00
24	IRVVSAQTA	547	0.8000	9.30

25	YWITFAGIA	610	0.8000	9.30
26	VLAMANDNT	349	0.7000	8.14
27	LLQMTGMYQ	506	0.7000	8.14
28	VNKIVAASA	386	0.6000	6.98
29	VHGSTVVLT	304	0.5800	6.74
30	LQVSHAAGL	108	0.5000	5.81
31	MANDNTFDP	352	0.5000	5.81
32	LKKLQSDET	203	0.4000	4.65
33	VQRDPMGYQ	566	0.4000	4.65
34	YTTTGVFGK	431	0.3000	3.49
35	ILVLMLVAA	94	0.2800	3.26
36	LSGAHNVSA	331	0.2800	3.26
37	YVIGIMLDN	625	0.2000	2.33
38	WLMQRENVP	656	0.1000	1.16
39	VMPYTTTGV	428	-0.1000	0
40	MLRAVVQRD	561	-0.1000	0
41	VILVLMLVA	93	-0.2000	0
42	LQVPGSIQM	407	-0.2200	0
43	LRAQAAGQL	116	-0.3000	0
44	YLARAVDPA	214	-0.3000	0
45	MGGVTVHDA	415	-0.3000	0
46	ITFAGIATA	612	-0.3000	0
47	VYLARAVDP	213	-0.3200	0
48	VVDVGTRGA	73	-0.4000	0
49	FVYLARAVD	212	-0.4000	0
50	MPYTTTGVF	429	-0.4000	0
51	IRRQLEEAR	161	-0.5000	0
52	MYQAIANDG	512	-0.5000	0
53	IVAASAVIE	389	-0.5200	0
54	FTIEARALT	147	-0.6000	0
55	LRDIAQEVA	182	-0.6000	0
56	VVIPGSYRN	291	-0.6000	0
57	LVPPIDQWS	481	-0.6000	0
58	LTLDNDIQF	311	-0.6200	0

59	LVAATQLFF	99	-0.7000	0
60	VVLDAKTGE	340	-0.7000	0
61	IANDGVRVP	516	-0.7000	0
62	IIKATVAPD	527	-0.7000	0
63	VYWITFAGI	609	-0.7000	0
64	VGGIDWDGH	254	-0.7200	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	VVDVGTRGA	73	3.7000	38.54
2	MLVAATQLF	98	3.5000	36.46
3	LVLMLVAAT	95	3.4000	35.42
4	VTVHDAWEH	418	3.1800	33.13
5	LKVTDVQPA	124	3.1000	32.29
6	IRVVSAQTA	547	3.1000	32.29
7	VVSAQTAQT	549	3.0000	31.25
8	IQMGGVTVH	413	2.9800	31.04
9	VVQRDPMGY	565	2.9000	30.21
10	VVIPGSYRN	291	2.8000	29.17
11	FQPKRIRRQ	156	2.7000	28.13
12	YVQQQVQQA	320	2.7000	28.13
13	LMQRENVPL	657	2.6000	27.08
14	VFRHRTGNA	84	2.5000	26.04
15	VQQAKNLSG	325	2.5000	26.04
16	VLMLVAATQ	96	2.3000	23.96
17	VMPYTTTGV	428	2.3000	23.96
18	VSRAAPRRA	0	2.1000	21.88
19	IGIMLDNPA	627	2.1000	21.88
20	MLRAVVQRD	561	2.0000	20.83
21	FFLQVSHAA	106	1.9000	19.79
22	LQMTGMYQA	507	1.9000	19.79
23	VVLTLDNDI	309	1.8000	18.75
24	MLRKFGLGQ	460	1.8000	18.75

25	LVPPIDQWS	481	1.8000	18.75
26	VFGKSSNVG	436	1.7000	17.71
27	MLDNPARNS	630	1.7000	17.71
28	LFFLQVSHA	105	1.5000	15.62
29	LQVPGSIQM	407	1.5000	15.62
30	LSGAHNVSA	331	1.4000	14.58
31	MGGVTVHDA	415	1.4000	14.58
32	LLQMTGMYQ	506	1.4000	14.58
33	VILVLMLVA	93	1.3000	13.54
34	LGLEDSLDA	265	1.2000	12.50
35	VAGKLNNKP	189	0.9000	9.38
36	VVGGIDWDG	253	0.9000	9.38
37	VNKIVAASA	386	0.8800	9.17
38	FRHRTGNAV	85	0.8000	8.33
39	VYLARAVDP	213	0.8000	8.33
40	ITFAGIATA	612	0.7000	7.29
41	LVAATQLFF	99	0.6000	6.25
42	IEARALTFQ	149	0.6000	6.25
43	IVAASAVIE	389	0.6000	6.25
44	IGQGLSMTL	498	0.6000	6.25
45	LMLVAATQL	97	0.5000	5.21
46	LQSDETFVY	206	0.5000	5.21
47	IQFYVQQQV	317	0.5000	5.21
48	MYQAIANDG	512	0.5000	5.21
49	VAASAVIEH	390	0.4800	5.00
50	VGTRGASFV	76	0.4000	4.17
51	LRAVVQRDP	562	0.4000	4.17
52	YVIGIMLDN	625	0.4000	4.17
53	YRNRHKAVH	297	0.3800	3.96
54	LNNKPDAAA	193	0.3000	3.12
55	IIKATVAPD	527	0.3000	3.12
56	MQRENVPLS	658	0.2000	2.08
57	VLTLDNDIQ	310	0.1000	1.04
58	VQQQVQQAK	321	0.1000	1.04

59	IAGWLMQRE	653	0.1000	1.04
60	VIPGSYRNR	292	-0.1000	0
61	VHGSTVVLT	304	-0.1000	0
62	LAMANDNTF	350	-0.1000	0
63	FEPGSVNKI	381	-0.1000	0
64	FHNIAGWLM	650	-0.1200	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	LVLMLVAAT	95	4.6000	52.27
2	LFFLQVSHA	105	4.0000	45.45
3	VLMLVAATQ	96	3.9000	44.32
4	IGIMLDNPA	627	3.4000	38.64
5	IRVVSAQTA	547	3.0000	34.09
6	VVSAQTAQT	549	3.0000	34.09
7	VLTLDNDIQ	310	2.6000	29.55
8	VMPYTTTGV	428	2.6000	29.55
9	LLQMTGMYQ	506	2.5000	28.41
10	VVDVGTRGA	73	2.3000	26.14
11	MLVAATQLF	98	2.2000	25.00
12	LMLVAATQL	97	2.0000	22.73
13	VNKIVAASA	386	1.9000	21.59
14	VILVLMLVA	93	1.8000	20.45
15	YVQQQVQQA	320	1.8000	20.45
16	VQQAKNLSG	325	1.8000	20.45
17	LGLEDSLDA	265	1.7000	19.32
18	VVIPGSYRN	291	1.7000	19.32
19	VLAMANDNT	349	1.7000	19.32
20	MGGVTVHDA	415	1.7000	19.32
21	IQMGGVTVH	413	1.5800	17.95
22	VVLTLDNDI	309	1.5000	17.05
23	FFLQVSHAA	106	1.4000	15.91
24	LKVTDVQPA	124	1.4000	15.91

25	MQRENVPLS	658	1.4000	15.91
26	ILVLMLVAA	94	1.3000	14.77
27	VFRHRTGNA	84	1.2000	13.64
28	LQSDETFVY	206	1.1500	13.07
29	LSGAHNVSA	331	1.1000	12.50
30	LQVPGSIQM	407	1.0800	12.27
31	VLQVPGSIQ	406	1.0000	11.36
32	MTLLQMTGM	504	0.9000	10.23
33	VRQMLRAVV	558	0.9000	10.23
34	FAGIATADN	614	0.8000	9.09
35	LKKLQSDET	203	0.7000	7.95
36	YQAIANDGV	513	0.7000	7.95
37	MLRAVVQRD	561	0.7000	7.95
38	ITFAGIATA	612	0.7000	7.95
39	MYQAIANDG	512	0.6000	6.82
40	VYWITFAGI	609	0.6000	6.82
41	VYLARAVDP	213	0.5000	5.68
42	LVPPIDQWS	481	0.5000	5.68
43	MTGMYQAIA	509	0.5000	5.68
44	LQMTGMYQA	507	0.4000	4.55
45	VAASAVIEH	390	0.3600	4.09
46	IVAASAVIE	389	0.3000	3.41
47	IIKATVAPD	527	0.3000	3.41
48	VFGKSSNVG	436	0.2000	2.27
49	MANDNTFDP	352	-0.0500	0
50	LVAATQLFF	99	-0.1000	0
51	LLGLEDSLD	264	-0.1000	0
52	VHGSTVVLT	304	-0.1000	0
53	VGTLMLSQR	443	-0.1000	0
54	LRKFGLGQR	461	-0.1000	0
55	LRDIAQEVA	182	-0.2000	0
56	LGNPAVSSP	372	-0.2000	0
57	VLDAKTGEV	341	-0.3000	0
58	VGGIDWDGH	254	-0.3200	0

59	IMLDNPARN	629	-0.4000	0
60	VSRAAPRRA	0	-0.5000	0
61	MLRKFGLGQ	460	-0.5000	0
62	VAGKLNNKP	189	-0.6000	0
63	VVQRDPMGY	565	-0.6000	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	LVLMLVAAT	95	4.5000	47.87
2	FAGIATADN	614	3.8000	40.43
3	VLMLVAATQ	96	3.7000	39.36
4	LFFLQVSHA	105	3.0000	31.91
5	VVSAQTAQT	549	2.9000	30.85
6	YVQQQVQQA	320	2.8000	29.79
7	VVIPGSYRN	291	2.7000	28.72
8	FVYLARAVD	212	2.5000	26.60
9	FFLQVSHAA	106	2.4000	25.53
10	VLTLDNDIQ	310	2.4000	25.53
11	MLRAVVQRD	561	2.4000	25.53
12	IGIMLDNPA	627	2.4000	25.53
13	IVAASAVIE	389	2.3000	24.47
14	LLQMTGMYQ	506	2.3000	24.47
15	MLVAATQLF	98	2.1000	22.34
16	VQQAKNLSG	325	2.1000	22.34
17	LMLVAATQL	97	2.0000	21.28
18	YQAIANDGV	513	2.0000	21.28
19	IIKATVAPD	527	2.0000	21.28
20	IRVVSAQTA	547	2.0000	21.28
21	VMPYTTTGV	428	1.9000	20.21
22	IQMGGVTVH	413	1.8000	19.15
23	LLGLEDSLD	264	1.6000	17.02
24	VLAMANDNT	349	1.6000	17.02
25	VVDVGTRGA	73	1.3000	13.83

26	LQSDETFVY	206	1.2500	13.30
27	MLSQRVGPE	447	1.2000	12.77
28	LQVPGSIQM	407	1.1800	12.55
29	FYVQQQVQQ	319	1.1000	11.70
30	MTLLQMTGM	504	1.0000	10.64
31	YVIGIMLDN	625	1.0000	10.64
32	VNKIVAASA	386	0.9000	9.57
33	MYQAIANDG	512	0.9000	9.57
34	FHNIAGWLM	650	0.9000	9.57
35	VILVLMLVA	93	0.8000	8.51
36	VLQVPGSIQ	406	0.8000	8.51
37	LGLEDSLDA	265	0.7000	7.45
38	VVLTLDNDI	309	0.7000	7.45
39	MGGVTVHDA	415	0.7000	7.45
40	FGKSSNVGT	437	0.7000	7.45
41	LKKLQSDET	203	0.6000	6.38
42	IMLDNPARN	629	0.6000	6.38
43	VAASAVIEH	390	0.5800	6.17
44	VFGKSSNVG	436	0.5000	5.32
45	FANLPIGQG	493	0.5000	5.32
46	LRRPPGAQE	20	0.4000	4.26
47	FLQVSHAAG	107	0.4000	4.26
48	LKVTDVQPA	124	0.4000	4.26
49	MQRENVPLS	658	0.4000	4.26
50	WITFAGIAT	611	0.3800	4.04
51	ILVLMLVAA	94	0.3000	3.19
52	FQPKRIRRQ	156	0.3000	3.19
53	VVLDAKTGE	340	0.3000	3.19
54	YQMAGKTGT	586	0.3000	3.19
55	VFRHRTGNA	84	0.2000	2.13
56	VRQMLRAVV	558	0.2000	2.13
57	LSGAHNVSA	331	0.1000	1.06
58	VYLARAVDP	213	-0.1000	0
59	VGGIDWDGH	254	-0.1000	0

60	LAMANDNTF	350	-0.1000	0
61	LVAATQLFF	99	-0.2000	0
62	VHGSTVVLT	304	-0.2000	0
63	VYWITFAGI	609	-0.2000	0
64	WLMQRENVP	656	-0.2000	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	LVLMLVAAT	95	3.6000	40.91
2	LFFLQVSHA	105	3.0000	34.09
3	VLMLVAATQ	96	2.9000	32.95
4	YVQQQVQQA	320	2.8000	31.82
5	FFLQVSHAA	106	2.4000	27.27
6	IGIMLDNPA	627	2.4000	27.27
7	IRVVSAQTA	547	2.0000	22.73
8	VVSAQTAQT	549	2.0000	22.73
9	FAGIATADN	614	1.8000	20.45
10	YQAIANDGV	513	1.7000	19.32
11	VLTLDNDIQ	310	1.6000	18.18
12	VMPYTTTGV	428	1.6000	18.18
13	LLQMTGMYQ	506	1.5000	17.05
14	VVDVGTRGA	73	1.3000	14.77
15	MLVAATQLF	98	1.2000	13.64
16	LMLVAATQL	97	1.0000	11.36
17	VNKIVAASA	386	0.9000	10.23
18	VILVLMLVA	93	0.8000	9.09
19	VQQAKNLSG	325	0.8000	9.09
20	LGLEDSLDA	265	0.7000	7.95
21	VVIPGSYRN	291	0.7000	7.95
22	VLAMANDNT	349	0.7000	7.95
23	MGGVTVHDA	415	0.7000	7.95
24	IQMGGVTVH	413	0.5800	6.59
25	VVLTLDNDI	309	0.5000	5.68

26	LKVTDVQPA	124	0.4000	4.55
27	MQRENVPLS	658	0.4000	4.55
28	ILVLMLVAA	94	0.3000	3.41
29	FYVQQQVQQ	319	0.3000	3.41
30	VFRHRTGNA	84	0.2000	2.27
31	LQSDETFVY	206	0.1500	1.70
32	LSGAHNVSA	331	0.1000	1.14
33	LQVPGSIQM	407	0.0800	0.91
34	MTLLQMTGM	504	-0.1000	0
35	VRQMLRAVV	558	-0.1000	0
36	FVYLARAVD	212	-0.2000	0
37	FGKSSNVGT	437	-0.2000	0
38	FHNIAGWLM	650	-0.2000	0
39	LKKLQSDET	203	-0.3000	0
40	MLRAVVQRD	561	-0.3000	0
41	ITFAGIATA	612	-0.3000	0
42	YTTTGVFGK	431	-0.3500	0
43	MYQAIANDG	512	-0.4000	0
44	VYWITFAGI	609	-0.4000	0
45	FQPKRIRRQ	156	-0.5000	0
46	VYLARAVDP	213	-0.5000	0
47	LVPPIDQWS	481	-0.5000	0
48	MTGMYQAIA	509	-0.5000	0
49	WITFAGIAT	611	-0.5200	0
50	LQMTGMYQA	507	-0.6000	0
51	YQMAGKTGT	586	-0.6000	0
52	WLMQRENVP	656	-0.6000	0
53	VAASAVIEH	390	-0.6400	0
54	FEPGSVNKI	381	-0.7000	0
55	IVAASAVIE	389	-0.7000	0
56	IIKATVAPD	527	-0.7000	0
57	YWITFAGIA	610	-0.7000	0
58	VFGKSSNVG	436	-0.8000	0
59	FANLPIGQG	493	-0.8000	0

60	FLQVSHAAG	107	-0.9000	0
61	LQVSHAAGL	108	-1.0000	0
62	LRAQAAGQL	116	-1.0000	0
63	LAMANDNTF	350	-1.0000	0
64	YVIGIMLDN	625	-1.0000	0
65	MANDNTFDP	352	-1.0500	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	LVLMLVAAT	95	5.5000	58.51
2	VLMLVAATQ	96	4.7000	50.00
3	LFFLQVSHA	105	4.0000	42.55
4	VVSAQTAQT	549	3.9000	41.49
5	VVIPGSYRN	291	3.7000	39.36
6	VLTLDNDIQ	310	3.4000	36.17
7	MLRAVVQRD	561	3.4000	36.17
8	IGIMLDNPA	627	3.4000	36.17
9	IVAASAVIE	389	3.3000	35.11
10	LLQMTGMYQ	506	3.3000	35.11
11	MLVAATQLF	98	3.1000	32.98
12	VQQAKNLSG	325	3.1000	32.98
13	LMLVAATQL	97	3.0000	31.91
14	IIKATVAPD	527	3.0000	31.91
15	IRVVSAQTA	547	3.0000	31.91
16	VMPYTTTGV	428	2.9000	30.85
17	IQMGGVTVH	413	2.8000	29.79
18	FAGIATADN	614	2.8000	29.79
19	LLGLEDSLD	264	2.6000	27.66
20	VLAMANDNT	349	2.6000	27.66
21	VVDVGTRGA	73	2.3000	24.47
22	LQSDETFVY	206	2.2500	23.94
23	MLSQRVGPE	447	2.2000	23.40
24	LQVPGSIQM	407	2.1800	23.19

25	MTLLQMTGM	504	2.0000	21.28
26	VNKIVAASA	386	1.9000	20.21
27	MYQAIANDG	512	1.9000	20.21
28	VILVLMLVA	93	1.8000	19.15
29	YVQQQVQQA	320	1.8000	19.15
30	VLQVPGSIQ	406	1.8000	19.15
31	LGLEDSLDA	265	1.7000	18.09
32	VVLTLDNDI	309	1.7000	18.09
33	MGGVTVHDA	415	1.7000	18.09
34	LKKLQSDET	203	1.6000	17.02
35	IMLDNPARN	629	1.6000	17.02
36	VAASAVIEH	390	1.5800	16.81
37	FVYLARAVD	212	1.5000	15.96
38	VFGKSSNVG	436	1.5000	15.96
39	LRRPPGAQE	20	1.4000	14.89
40	FFLQVSHAA	106	1.4000	14.89
41	LKVTDVQPA	124	1.4000	14.89
42	MQRENVPLS	658	1.4000	14.89
43	ILVLMLVAA	94	1.3000	13.83
44	VVLDAKTGE	340	1.3000	13.83
45	VFRHRTGNA	84	1.2000	12.77
46	VRQMLRAVV	558	1.2000	12.77
47	LSGAHNVSA	331	1.1000	11.70
48	LQVSHAAGL	108	1.0000	10.64
49	LRAQAAGQL	116	1.0000	10.64
50	YQAIANDGV	513	1.0000	10.64
51	VYLARAVDP	213	0.9000	9.57
52	VGGIDWDGH	254	0.9000	9.57
53	LAMANDNTF	350	0.9000	9.57
54	LVAATQLFF	99	0.8000	8.51
55	VHGSTVVLT	304	0.8000	8.51
56	VYWITFAGI	609	0.8000	8.51
57	ITFAGIATA	612	0.7000	7.45
58	VAPDGSRTE	532	0.6000	6.38

59	LVPPIDQWS	481	0.5000	5.32
60	MTGMYQAIA	509	0.5000	5.32
61	VVQRDPMGY	565	0.5000	5.32
62	IEHGLSSPD	396	0.4000	4.26
63	LQMTGMYQA	507	0.4000	4.26
64	IATADNPRY	617	0.4000	4.26
65	MANDNTFDP	352	0.3500	3.72
66	VASAICAKY	223	0.3000	3.19
67	MLRKFGLGQ	460	0.3000	3.19

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YVQQQVQQA	320	3.8000	42.22
2	LGLEDSLDA	265	3.7000	41.11
3	MQRENVPLS	658	3.7000	41.11
4	FFLQVSHAA	106	3.6000	40.00
5	LVLMLVAAT	95	3.4000	37.78
6	MLVAATQLF	98	3.3000	36.67
7	YQAIANDGV	513	3.3000	36.67
8	LQSDETFVY	206	3.0000	33.33
9	VVLTLDNDI	309	2.9000	32.22
10	VVSAQTAQT	549	2.7000	30.00
11	VQQAKNLSG	325	2.6000	28.89
12	FAGIATADN	614	2.3000	25.56
13	VFRHRTGNA	84	2.2000	24.44
14	LKVTDVQPA	124	2.2000	24.44
15	FGKSSNVGT	437	2.1800	24.22
16	LFFLQVSHA	105	2.1000	23.33
17	VLMLVAATQ	96	2.0000	22.22
18	IMLDNPARN	629	1.9000	21.11
19	VLTLDNDIQ	310	1.6000	17.78
20	MANDNTFDP	352	1.5000	16.67
21	MPYTTTGVF	429	1.5000	16.67

22	LQVSHAAGL	108	1.4600	16.22
23	VLAMANDNT	349	1.4000	15.56
24	IGIMLDNPA	627	1.4000	15.56
25	VHGSTVVLT	304	1.2800	14.22
26	LTLDNDIQF	311	1.2800	14.22
27	LQVPGSIQM	407	1.2800	14.22
28	LVAATQLFF	99	1.2000	13.33
29	LKKLQSDET	203	1.1000	12.22
30	WLMQRENVP	656	1.1000	12.22
31	IRRQLEEAR	161	1.0000	11.11
32	MLRAVVQRD	561	1.0000	11.11
33	YVIGIMLDN	625	1.0000	11.11
34	FEPGSVNKI	381	0.9000	10.00
35	VMPYTTTGV	428	0.9000	10.00
36	MYQAIANDG	512	0.9000	10.00
37	IVAASAVIE	389	0.8800	9.78
38	LAMANDNTF	350	0.8000	8.89
39	IRVVSAQTA	547	0.8000	8.89
40	YWITFAGIA	610	0.8000	8.89
41	FVYLARAVD	212	0.7000	7.78
42	VVLDAKTGE	340	0.7000	7.78
43	MTLLQMTGM	504	0.7000	7.78
44	VYLARAVDP	213	0.6800	7.56
45	LRAQAAGQL	116	0.6600	7.33
46	VNKIVAASA	386	0.6000	6.67
47	FYVQQQVQQ	319	0.5800	6.44
48	IKATVAPDG	528	0.5000	5.56
49	YTTTGVFGK	431	0.4000	4.44
50	IIKATVAPD	527	0.4000	4.44
51	IQMGGVTVH	413	0.3000	3.33
52	VFGKSSNVG	436	0.3000	3.33
53	MLSQRVGPE	447	0.3000	3.33
54	FANLPIGQG	493	0.3000	3.33
55	IANDGVRVP	516	0.3000	3.33

56	VVQRDPMGY	565	0.3000	3.33
57	FHNIAGWLM	650	0.3000	3.33
58	ILVLMLVAA	94	0.2800	3.11
59	LSGAHNVSA	331	0.2800	3.11
60	VAASAVIEH	390	0.2800	3.11
61	VVIPGSYRN	291	0.2000	2.22
62	VAPDGSRTE	532	0.2000	2.22
63	VYWITFAGI	609	0.2000	2.22
64	FTIEARALT	147	0.1000	1.11
65	LAANVVGGI	249	0.1000	1.11
66	LMLVAATQL	97	0.0600	0.67

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	LVLMLVAAT	95	4.6000	52.27
2	LFFLQVSHA	105	4.0000	45.45
3	VLMLVAATQ	96	3.9000	44.32
4	IGIMLDNPA	627	3.4000	38.64
5	IRVVSAQTA	547	3.0000	34.09
6	VVSAQTAQT	549	3.0000	34.09
7	VLTLDNDIQ	310	2.6000	29.55
8	VMPYTTTGV	428	2.6000	29.55
9	LLQMTGMYQ	506	2.5000	28.41
10	VVDVGTRGA	73	2.3000	26.14
11	MLVAATQLF	98	2.2000	25.00
12	LMLVAATQL	97	2.0000	22.73
13	VNKIVAASA	386	1.9000	21.59
14	VILVLMLVA	93	1.8000	20.45
15	YVQQQVQQA	320	1.8000	20.45
16	VQQAKNLSG	325	1.8000	20.45
17	LGLEDSLDA	265	1.7000	19.32
18	VVIPGSYRN	291	1.7000	19.32
19	VLAMANDNT	349	1.7000	19.32

20	MGGVTVHDA	415	1.7000	19.32
21	IQMGGVTVH	413	1.5800	17.95
22	VVLTLDNDI	309	1.5000	17.05
23	FFLQVSHAA	106	1.4000	15.91
24	LKVTDVQPA	124	1.4000	15.91
25	MQRENVPLS	658	1.4000	15.91
26	ILVLMLVAA	94	1.3000	14.77
27	VFRHRTGNA	84	1.2000	13.64
28	LQSDETFVY	206	1.1500	13.07
29	LSGAHNVSA	331	1.1000	12.50
30	LQVPGSIQM	407	1.0800	12.27
31	VLQVPGSIQ	406	1.0000	11.36
32	MTLLQMTGM	504	0.9000	10.23
33	VRQMLRAVV	558	0.9000	10.23
34	FAGIATADN	614	0.8000	9.09
35	LKKLQSDET	203	0.7000	7.95
36	YQAIANDGV	513	0.7000	7.95
37	MLRAVVQRD	561	0.7000	7.95
38	ITFAGIATA	612	0.7000	7.95
39	MYQAIANDG	512	0.6000	6.82
40	VYWITFAGI	609	0.6000	6.82
41	VYLARAVDP	213	0.5000	5.68
42	LVPPIDQWS	481	0.5000	5.68
43	MTGMYQAIA	509	0.5000	5.68
44	LQMTGMYQA	507	0.4000	4.55
45	VAASAVIEH	390	0.3600	4.09
46	IVAASAVIE	389	0.3000	3.41
47	IIKATVAPD	527	0.3000	3.41
48	VFGKSSNVG	436	0.2000	2.27
49	MANDNTFDP	352	-0.0500	0
50	LVAATQLFF	99	-0.1000	0
51	LLGLEDSLD	264	-0.1000	0
52	VHGSTVVLT	304	-0.1000	0
53	VGTLMLSQR	443	-0.1000	0

54	LRKFGLGQR	461	-0.1000	0
55	LRDIAQEVA	182	-0.2000	0
56	LGNPAVSSP	372	-0.2000	0
57	VLDAKTGEV	341	-0.3000	0
58	VGGIDWDGH	254	-0.3200	0
59	IMLDNPARN	629	-0.4000	0
60	VSRAAPRRA	0	-0.5000	0
61	MLRKFGLGQ	460	-0.5000	0
62	VAGKLNNKP	189	-0.6000	0
63	VVQRDPMGY	565	-0.6000	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	YVQQQVQQA	320	3.8000	44.19
2	LGLEDSLDA	265	3.7000	43.02
3	FFLQVSHAA	106	3.6000	41.86
4	MQRENVPLS	658	3.3000	38.37
5	LVLMLVAAT	95	2.7000	31.40
6	VLMLVAATQ	96	2.7000	31.40
7	VLTLDNDIQ	310	2.3000	26.74
8	YQAIANDGV	513	2.3000	26.74
9	VFRHRTGNA	84	2.2000	25.58
10	LKVTDVQPA	124	2.2000	25.58
11	LFFLQVSHA	105	2.1000	24.42
12	VVLTLDNDI	309	2.0000	23.26
13	VVSAQTAQT	549	2.0000	23.26
14	LQSDETFVY	206	1.7000	19.77
15	FAGIATADN	614	1.5000	17.44
16	FGKSSNVGT	437	1.4800	17.21
17	MLVAATQLF	98	1.4000	16.28
18	IGIMLDNPA	627	1.4000	16.28
19	FYVQQQVQQ	319	1.2800	14.88
20	VQQAKNLSG	325	1.2000	13.95

21	IMLDNPARN	629	1.1000	12.79
22	IQMGGVTVH	413	0.8800	10.23
23	VAASAVIEH	390	0.8600	10.00
24	IRVVSAQTA	547	0.8000	9.30
25	YWITFAGIA	610	0.8000	9.30
26	VLAMANDNT	349	0.7000	8.14
27	LLQMTGMYQ	506	0.7000	8.14
28	VNKIVAASA	386	0.6000	6.98
29	VHGSTVVLT	304	0.5800	6.74
30	LQVSHAAGL	108	0.5000	5.81
31	MANDNTFDP	352	0.5000	5.81
32	LKKLQSDET	203	0.4000	4.65
33	VQRDPMGYQ	566	0.4000	4.65
34	YTTTGVFGK	431	0.3000	3.49
35	ILVLMLVAA	94	0.2800	3.26
36	LSGAHNVSA	331	0.2800	3.26
37	YVIGIMLDN	625	0.2000	2.33
38	WLMQRENVP	656	0.1000	1.16
39	VMPYTTTGV	428	-0.1000	0
40	MLRAVVQRD	561	-0.1000	0
41	VILVLMLVA	93	-0.2000	0
42	LQVPGSIQM	407	-0.2200	0
43	LRAQAAGQL	116	-0.3000	0
44	YLARAVDPA	214	-0.3000	0
45	MGGVTVHDA	415	-0.3000	0
46	ITFAGIATA	612	-0.3000	0
47	VYLARAVDP	213	-0.3200	0
48	VVDVGTRGA	73	-0.4000	0
49	FVYLARAVD	212	-0.4000	0
50	MPYTTTGVF	429	-0.4000	0
51	IRRQLEEAR	161	-0.5000	0
52	MYQAIANDG	512	-0.5000	0
53	IVAASAVIE	389	-0.5200	0
54	FTIEARALT	147	-0.6000	0

55	LRDIAQEVA	182	-0.6000	0
56	VVIPGSYRN	291	-0.6000	0
57	LVPPIDQWS	481	-0.6000	0
58	LTLDNDIQF	311	-0.6200	0
59	LVAATQLFF	99	-0.7000	0
60	VVLDAKTGE	340	-0.7000	0
61	IANDGVRVP	516	-0.7000	0
62	IIKATVAPD	527	-0.7000	0
63	VYWITFAGI	609	-0.7000	0
64	VGGIDWDGH	254	-0.7200	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	LMLVAATQL	97	6.3000	54.31
2	VVLTLDNDI	309	5.8000	50.00
3	LQVSHAAGL	108	5.6000	48.28
4	FHNIAGWLM	650	5.2000	44.83
5	VAATQLFFL	100	5.0000	43.10
6	LQVPGSIQM	407	4.5000	38.79
7	LVAATQLFF	99	4.3000	37.07
8	FEPGSVNKI	381	4.2000	36.21
9	IGQGLSMTL	498	4.2000	36.21
10	FRHRTGNAV	85	4.1000	35.34
11	WSGSTFANL	488	4.0000	34.48
12	LQMTGMYQA	507	3.9000	33.62
13	WDGHGLLGL	259	3.7000	31.90
14	YDMLRKFGL	458	3.7000	31.90
15	IRVVSAQTA	547	3.7000	31.90
16	MLVAATQLF	98	3.6200	31.21
17	VHGSTVVLT	304	3.6000	31.03
18	VYWITFAGI	609	3.6000	31.03
19	WITFAGIAT	611	3.5000	30.17
20	VILVLMLVA	93	3.4000	29.31

21	FGKSSNVGT	437	3.4000	29.31
22	YVIGIMLDN	625	3.4000	29.31
23	LMQRENVPL	657	3.4000	29.31
24	LKVTDVQPA	124	3.2000	27.59
25	VVIPGSYRN	291	3.2000	27.59
26	LRAQAAGQL	116	3.1000	26.72
27	LRQYPGGSL	241	3.1000	26.72
28	VQPAARGSI	129	2.8000	24.14
29	VAASAVIEH	390	2.8000	24.14
30	LGQRTGVGL	466	2.8000	24.14
31	YQMAGKTGT	586	2.8000	24.14
32	YWITFAGIA	610	2.8000	24.14
33	MPYTTTGVF	429	2.7200	23.45
34	YTTTGVFGK	431	2.5000	21.55
35	LMLSQRVGP	446	2.5000	21.55
36	LPIGQGLSM	496	2.5000	21.55
37	IVAASAVIE	389	2.4000	20.69
38	YQAIANDGV	513	2.4000	20.69
39	VVQRDPMGY	565	2.4000	20.69
40	VMPYTTTGV	428	2.3200	20.00
41	LFHNIAGWL	649	2.3000	19.83
42	LVLMLVAAT	95	2.2000	18.97
43	FGLGQRTGV	464	2.2000	18.97
44	IQFYVQQQV	317	2.1000	18.10
45	LSMTLLQMT	502	2.1000	18.10
46	LQSDETFVY	206	1.9200	16.55
47	VYLARAVDP	213	1.9000	16.38
48	LGLEDSLDA	265	1.9000	16.38
49	FDDVYWITF	606	1.9000	16.38
50	FFLQVSHAA	106	1.8000	15.52
51	VDPAVASAI	219	1.8000	15.52
52	YVQQQVQQA	320	1.8000	15.52
53	VRQMLRAVV	558	1.7000	14.66
54	VVSAQTAQT	549	1.6200	13.97

55	MGGVTVHDA	415	1.6000	13.79
56	LAANVVGGI	249	1.4000	12.07
57	LAMANDNTF	350	1.4000	12.07
58	VVDVGTRGA	73	1.3200	11.38
59	IQMGGVTVH	413	1.3000	11.21
60	MTLLQMTGM	504	1.3000	11.21
61	VQQAKNLSG	325	1.2000	10.34
62	FVFRHRTGN	83	1.1000	9.48
63	VGPERYYDM	452	1.1000	9.48
64	LRAVVQRDP	562	1.1000	9.48
65	IAQEVAGKL	185	1.0000	8.62
66	VNKIVAASA	386	0.9000	7.76
67	VGTRGASFV	76	0.8000	6.90

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	LMLVAATQL	97	6.3000	54.31
2	VVLTLDNDI	309	5.8000	50.00
3	LQVSHAAGL	108	5.6000	48.28
4	FHNIAGWLM	650	5.2000	44.83
5	VAATQLFFL	100	5.0000	43.10
6	LQVPGSIQM	407	4.5000	38.79
7	LVAATQLFF	99	4.3000	37.07
8	FEPGSVNKI	381	4.2000	36.21
9	IGQGLSMTL	498	4.2000	36.21
10	FRHRTGNAV	85	4.1000	35.34
11	WSGSTFANL	488	4.0000	34.48
12	LQMTGMYQA	507	3.9000	33.62
13	WDGHGLLGL	259	3.7000	31.90
14	YDMLRKFGL	458	3.7000	31.90
15	IRVVSAQTA	547	3.7000	31.90
16	MLVAATQLF	98	3.6200	31.21
17	VHGSTVVLT	304	3.6000	31.03

18	VYWITFAGI	609	3.6000	31.03
19	WITFAGIAT	611	3.5000	30.17
20	VILVLMLVA	93	3.4000	29.31
21	FGKSSNVGT	437	3.4000	29.31
22	YVIGIMLDN	625	3.4000	29.31
23	LMQRENVPL	657	3.4000	29.31
24	LKVTDVQPA	124	3.2000	27.59
25	VVIPGSYRN	291	3.2000	27.59
26	LRAQAAGQL	116	3.1000	26.72
27	LRQYPGGSL	241	3.1000	26.72
28	VQPAARGSI	129	2.8000	24.14
29	VAASAVIEH	390	2.8000	24.14
30	LGQRTGVGL	466	2.8000	24.14
31	YQMAGKTGT	586	2.8000	24.14
32	YWITFAGIA	610	2.8000	24.14
33	MPYTTTGVF	429	2.7200	23.45
34	YTTTGVFGK	431	2.5000	21.55
35	LMLSQRVGP	446	2.5000	21.55
36	LPIGQGLSM	496	2.5000	21.55
37	IVAASAVIE	389	2.4000	20.69
38	YQAIANDGV	513	2.4000	20.69
39	VVQRDPMGY	565	2.4000	20.69
40	VMPYTTTGV	428	2.3200	20.00
41	LFHNIAGWL	649	2.3000	19.83
42	LVLMLVAAT	95	2.2000	18.97
43	FGLGQRTGV	464	2.2000	18.97
44	IQFYVQQQV	317	2.1000	18.10
45	LSMTLLQMT	502	2.1000	18.10
46	LQSDETFVY	206	1.9200	16.55
47	VYLARAVDP	213	1.9000	16.38
48	LGLEDSLDA	265	1.9000	16.38
49	FDDVYWITF	606	1.9000	16.38
50	FFLQVSHAA	106	1.8000	15.52
51	VDPAVASAI	219	1.8000	15.52

52	YVQQQVQQA	320	1.8000	15.52
53	VRQMLRAVV	558	1.7000	14.66
54	VVSAQTAQT	549	1.6200	13.97
55	MGGVTVHDA	415	1.6000	13.79
56	LAANVVGGI	249	1.4000	12.07
57	LAMANDNTF	350	1.4000	12.07
58	VVDVGTRGA	73	1.3200	11.38
59	IQMGGVTVH	413	1.3000	11.21
60	MTLLQMTGM	504	1.3000	11.21
61	VQQAKNLSG	325	1.2000	10.34
62	FVFRHRTGN	83	1.1000	9.48
63	VGPERYYDM	452	1.1000	9.48
64	LRAVVQRDP	562	1.1000	9.48
65	IAQEVAGKL	185	1.0000	8.62
66	VNKIVAASA	386	0.9000	7.76
67	VGTRGASFV	76	0.8000	6.90

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	YRNRHKAVH	297	7.6000	88.37
2	FVYLARAVD	212	5.6000	65.12
3	FQPKRIRRQ	156	5.2000	60.47
4	FVFRHRTGN	83	4.4000	51.16
5	LVLMLVAAT	95	4.4000	51.16
6	VVQRDPMGY	565	3.7000	43.02
7	VLMLVAATQ	96	3.4000	39.53
8	MLRKFGLGQ	460	3.3000	38.37
9	VRQMLRAVV	558	3.2000	37.21
10	FRHRTGNAV	85	2.3000	26.74
11	IIKATVAPD	527	2.3000	26.74
12	LRQYPGGSL	241	2.2000	25.58
13	YLARAVDPA	214	2.1000	24.42
14	VLKKLQSDE	202	2.0000	23.26

15	YVIGIMLDN	625	2.0000	23.26
16	FAGIATADN	614	1.9000	22.09
17	VVSAQTAQT	549	1.8000	20.93
18	FANLPIGQG	493	1.7000	19.77
19	LLQMTGMYQ	506	1.7000	19.77
20	MLRAVVQRD	561	1.7000	19.77
21	LRRPPGAQE	20	1.5000	17.44
22	FLQVSHAAG	107	1.5000	17.44
23	YYDMLRKFG	457	1.5000	17.44
24	IQFYVQQQV	317	1.3000	15.12
25	VVLDAKTGE	340	1.3000	15.12
26	IVAASAVIE	389	1.3000	15.12
27	LFFLQVSHA	105	1.2000	13.95
28	FTIEARALT	147	1.2000	13.95
29	VFGKSSNVG	436	1.2000	13.95
30	MLSQRVGPE	447	1.2000	13.95
31	YDMLRKFGL	458	1.2000	13.95
32	YQMAGKTGT	586	1.2000	13.95
33	IMLDNPARN	629	1.2000	13.95
34	YVQQQVQQA	320	1.1000	12.79
35	VVIPGSYRN	291	1.0000	11.63
36	VQPAARGSI	129	0.9000	10.47
37	IRVVSAQTA	547	0.8000	9.30
38	IQMGGVTVH	413	0.7000	8.14
39	VPPRIIKAT	523	0.7000	8.14
40	LMQRENVPL	657	0.7000	8.14
41	VGQRKRPGK	29	0.6000	6.98
42	VMPYTTTGV	428	0.6000	6.98
43	MQRENVPLS	658	0.6000	6.98
44	IEARALTFQ	149	0.5000	5.81
45	ITFAGIATA	612	0.5000	5.81
46	LVAATQLFF	99	0.4000	4.65
47	LRKFGLGQR	461	0.4000	4.65
48	FHNIAGWLM	650	0.4000	4.65

49	VVDVGTRGA	73	0.3000	3.49
50	ILVLMLVAA	94	0.3000	3.49
51	FYVQQQVQQ	319	0.3000	3.49
52	MGGVTVHDA	415	0.3000	3.49
53	MTGMYQAIA	509	0.3000	3.49
54	VILVLMLVA	93	0.2000	2.33
55	LNNKPDAAA	193	0.2000	2.33
56	VGTRGASFV	76	0.1000	1.16
57	VNKIVAASA	386	0.1000	1.16
58	VRVPPRIIK	521	-0.1000	0
59	YWITFAGIA	610	-0.1000	0
60	VFRHRTGNA	84	-0.2000	0
61	FFLQVSHAA	106	-0.2000	0
62	VQRDPMGYQ	566	-0.2000	0
63	WITFAGIAT	611	-0.2000	0
64	LQVSHAAGL	108	-0.3000	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	YRNRHKAVH	297	6.3800	79.75
2	FQPKRIRRQ	156	4.4000	55.00
3	LVLMLVAAT	95	3.5000	43.75
4	FVYLARAVD	212	2.9000	36.25
5	VRQMLRAVV	558	2.9000	36.25
6	VLMLVAATQ	96	2.6000	32.50
7	VVQRDPMGY	565	2.6000	32.50
8	MLRKFGLGQ	460	2.5000	31.25
9	FVFRHRTGN	83	2.4000	30.00
10	YLARAVDPA	214	2.1000	26.25
11	FRHRTGNAV	85	2.0000	25.00
12	VGQRKRPGK	29	1.3000	16.25
13	LFFLQVSHA	105	1.2000	15.00
14	LRQYPGGSL	241	1.2000	15.00

15	YVQQQVQQA	320	1.1000	13.75
16	IQFYVQQQV	317	1.0000	12.50
17	LLQMTGMYQ	506	0.9000	11.25
18	VVSAQTAQT	549	0.9000	11.25
19	IRVVSAQTA	547	0.8000	10.00
20	VQPAARGSI	129	0.7000	8.75
21	VRVPPRIIK	521	0.6000	7.50
22	MQRENVPLS	658	0.6000	7.50
23	ITFAGIATA	612	0.5000	6.25
24	LRKFGLGQR	461	0.4000	5.00
25	FANLPIGQG	493	0.4000	5.00
26	VVDVGTRGA	73	0.3000	3.75
27	ILVLMLVAA	94	0.3000	3.75
28	FTIEARALT	147	0.3000	3.75
29	MGGVTVHDA	415	0.3000	3.75
30	VMPYTTTGV	428	0.3000	3.75
31	MTGMYQAIA	509	0.3000	3.75
32	YQMAGKTGT	586	0.3000	3.75
33	VILVLMLVA	93	0.2000	2.50
34	FLQVSHAAG	107	0.2000	2.50
35	LNNKPDAAA	193	0.2000	2.50
36	YYDMLRKFG	457	0.2000	2.50
37	YDMLRKFGL	458	0.2000	2.50
38	VNKIVAASA	386	0.1000	1.25
39	VFGKSSNVG	436	-0.1000	0
40	YWITFAGIA	610	-0.1000	0
41	FAGIATADN	614	-0.1000	0
42	VGTRGASFV	76	-0.2000	0
43	VFRHRTGNA	84	-0.2000	0
44	FFLQVSHAA	106	-0.2000	0
45	VPPRIIKAT	523	-0.2000	0
46	IEARALTFQ	149	-0.3000	0
47	VPGYQMAGK	583	-0.3000	0
48	LMQRENVPL	657	-0.3000	0

49	LKVTDVQPA	124	-0.4000	0
50	IIKATVAPD	527	-0.4000	0
51	LVAATQLFF	99	-0.5000	0
52	FYVQQQVQQ	319	-0.5000	0
53	IQMGGVTVH	413	-0.5200	0
54	LAANVVGGI	249	-0.6000	0
55	VSRAAPRRA	0	-0.7000	0
56	LRAVVQRDP	562	-0.7000	0
57	FHNIAGWLM	650	-0.7000	0
58	IMLDNPARN	629	-0.8000	0
59	MLVAATQLF	98	-0.9000	0
60	LEEARKKTS	165	-0.9000	0
61	LGLEDSLDA	265	-0.9000	0
62	VLKKLQSDE	202	-1.0000	0
63	VVIPGSYRN	291	-1.0000	0
64	FEPGSVNKI	381	-1.0000	0
65	YTTTGVFGK	431	-1.0000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8

Rank	Sequence	At Position	Score	% of Highest Score
1	YRNRHKAVH	297	5.3800	67.25
2	LVLMLVAAT	95	4.5000	56.25
3	VRQMLRAVV	558	3.9000	48.75
4	VLMLVAATQ	96	3.6000	45.00
5	VVQRDPMGY	565	3.6000	45.00
6	MLRKFGLGQ	460	3.5000	43.75
7	FQPKRIRRQ	156	3.4000	42.50
8	VGQRKRPGK	29	2.3000	28.75
9	LFFLQVSHA	105	2.2000	27.50
10	LRQYPGGSL	241	2.2000	27.50
11	IQFYVQQQV	317	2.0000	25.00
12	FVYLARAVD	212	1.9000	23.75
13	LLQMTGMYQ	506	1.9000	23.75

14	VVSAQTAQT	549	1.9000	23.75
15	IRVVSAQTA	547	1.8000	22.50
16	VQPAARGSI	129	1.7000	21.25
17	VRVPPRIIK	521	1.6000	20.00
18	MQRENVPLS	658	1.6000	20.00
19	ITFAGIATA	612	1.5000	18.75
20	FVFRHRTGN	83	1.4000	17.50
21	LRKFGLGQR	461	1.4000	17.50
22	VVDVGTRGA	73	1.3000	16.25
23	ILVLMLVAA	94	1.3000	16.25
24	MGGVTVHDA	415	1.3000	16.25
25	VMPYTTTGV	428	1.3000	16.25
26	MTGMYQAIA	509	1.3000	16.25
27	VILVLMLVA	93	1.2000	15.00
28	LNNKPDAAA	193	1.2000	15.00
29	YLARAVDPA	214	1.1000	13.75
30	VNKIVAASA	386	1.1000	13.75
31	FRHRTGNAV	85	1.0000	12.50
32	VFGKSSNVG	436	0.9000	11.25
33	VGTRGASFV	76	0.8000	10.00
34	VFRHRTGNA	84	0.8000	10.00
35	VPPRIIKAT	523	0.8000	10.00
36	IEARALTFQ	149	0.7000	8.75
37	VPGYQMAGK	583	0.7000	8.75
38	LMQRENVPL	657	0.7000	8.75
39	LKVTDVQPA	124	0.6000	7.50
40	IIKATVAPD	527	0.6000	7.50
41	LVAATQLFF	99	0.5000	6.25
42	IQMGGVTVH	413	0.4800	6.00
43	LAANVVGGI	249	0.4000	5.00
44	VSRAAPRRA	0	0.3000	3.75
45	LRAVVQRDP	562	0.3000	3.75
46	IMLDNPARN	629	0.2000	2.50
47	MLVAATQLF	98	0.1000	1.25

48	LEEARKKTS	165	0.1000	1.25
49	LGLEDSLDA	265	0.1000	1.25
50	YVQQQVQQA	320	0.1000	1.25
51	MAGKTGTAQ	588	-0.1000	0
52	VLQVPGSIQ	406	-0.2000	0
53	MLDNPARNS	630	-0.2000	0
54	LQVSHAAGL	108	-0.3000	0
55	LRAQAAGQL	116	-0.3000	0
56	LMLSQRVGP	446	-0.3000	0
57	IGIMLDNPA	627	-0.3000	0
58	LQMTGMYQA	507	-0.4000	0
59	LRRPPGAQE	20	-0.5000	0
60	LTFQPKRIR	154	-0.5000	0
61	VYLARAVDP	213	-0.5000	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	YRNRHKAVH	297	6.6000	76.74
2	LVLMLVAAT	95	5.4000	62.79
3	VVQRDPMGY	565	4.7000	54.65
4	FVYLARAVD	212	4.6000	53.49
5	VLMLVAATQ	96	4.4000	51.16
6	MLRKFGLGQ	460	4.3000	50.00
7	FQPKRIRRQ	156	4.2000	48.84
8	VRQMLRAVV	558	4.2000	48.84
9	FVFRHRTGN	83	3.4000	39.53
10	IIKATVAPD	527	3.3000	38.37
11	LRQYPGGSL	241	3.2000	37.21
12	VLKKLQSDE	202	3.0000	34.88
13	VVSAQTAQT	549	2.8000	32.56
14	LLQMTGMYQ	506	2.7000	31.40
15	MLRAVVQRD	561	2.7000	31.40
16	LRRPPGAQE	20	2.5000	29.07

17	IQFYVQQQV	317	2.3000	26.74
18	VVLDAKTGE	340	2.3000	26.74
19	IVAASAVIE	389	2.3000	26.74
20	LFFLQVSHA	105	2.2000	25.58
21	VFGKSSNVG	436	2.2000	25.58
22	MLSQRVGPE	447	2.2000	25.58
23	IMLDNPARN	629	2.2000	25.58
24	VVIPGSYRN	291	2.0000	23.26
25	VQPAARGSI	129	1.9000	22.09
26	IRVVSAQTA	547	1.8000	20.93
27	IQMGGVTVH	413	1.7000	19.77
28	VPPRIIKAT	523	1.7000	19.77
29	LMQRENVPL	657	1.7000	19.77
30	VGQRKRPGK	29	1.6000	18.60
31	VMPYTTTGV	428	1.6000	18.60
32	MQRENVPLS	658	1.6000	18.60
33	IEARALTFQ	149	1.5000	17.44
34	ITFAGIATA	612	1.5000	17.44
35	LVAATQLFF	99	1.4000	16.28
36	LRKFGLGQR	461	1.4000	16.28
37	VVDVGTRGA	73	1.3000	15.12
38	FRHRTGNAV	85	1.3000	15.12
39	ILVLMLVAA	94	1.3000	15.12
40	MGGVTVHDA	415	1.3000	15.12
41	MTGMYQAIA	509	1.3000	15.12
42	VILVLMLVA	93	1.2000	13.95
43	LNNKPDAAA	193	1.2000	13.95
44	VGTRGASFV	76	1.1000	12.79
45	YLARAVDPA	214	1.1000	12.79
46	VNKIVAASA	386	1.1000	12.79
47	MLVAATQLF	98	1.0000	11.63
48	LGQRTGVGL	466	1.0000	11.63
49	YVIGIMLDN	625	1.0000	11.63
50	VRVPPRIIK	521	0.9000	10.47

51	FAGIATADN	614	0.9000	10.47
52	VFRHRTGNA	84	0.8000	9.30
53	VQRDPMGYQ	566	0.8000	9.30
54	LQVSHAAGL	108	0.7000	8.14
55	LRAQAAGQL	116	0.7000	8.14
56	ICAKYPEVG	227	0.7000	8.14
57	VAASAVIEH	390	0.7000	8.14
58	FANLPIGQG	493	0.7000	8.14
59	LRAVVQRDP	562	0.7000	8.14
60	MAGKTGTAQ	588	0.7000	8.14
61	LKVTDVQPA	124	0.6000	6.98
62	LAANVVGGI	249	0.6000	6.98
63	VQQAKNLSG	325	0.6000	6.98
64	VLQVPGSIQ	406	0.6000	6.98
65	FLQVSHAAG	107	0.5000	5.81
66	LQVPGSIQM	407	0.5000	5.81
67	YYDMLRKFG	457	0.5000	5.81

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	YRNRHKAVH	297	6.3800	73.33
2	FVFRHRTGN	83	5.2000	59.77
3	FQPKRIRRQ	156	4.1000	47.13
4	FRHRTGNAV	85	4.0000	45.98
5	VVQRDPMGY	565	3.6000	41.38
6	LVLMLVAAT	95	3.5000	40.23
7	YLARAVDPA	214	3.3000	37.93
8	VMPYTTTGV	428	3.1000	35.63
9	MLRKFGLGQ	460	3.1000	35.63
10	YQMAGKTGT	586	3.1000	35.63
11	LFFLQVSHA	105	3.0000	34.48
12	FVYLARAVD	212	2.9000	33.33
13	VRQMLRAVV	558	2.9000	33.33

14	VLMLVAATQ	96	2.6000	29.89
15	IEARALTFQ	149	2.5000	28.74
16	IQMGGVTVH	413	2.2800	26.21
17	YVQQQVQQA	320	2.1000	24.14
18	IQFYVQQQV	317	2.0000	22.99
19	VFGKSSNVG	436	1.9000	21.84
20	LLQMTGMYQ	506	1.9000	21.84
21	IRVVSAQTA	547	1.8000	20.69
22	MAGKTGTAQ	588	1.7000	19.54
23	VGTRGASFV	76	1.6000	18.39
24	VGQRKRPGK	29	1.5000	17.24
25	VRVPPRIIK	521	1.4800	17.01
26	ILVLMLVAA	94	1.3000	14.94
27	FGLGQRTGV	464	1.2000	13.79
28	VVLDAKTGE	340	1.1000	12.64
29	YDMLRKFGL	458	1.0500	12.07
30	FEPGSVNKI	381	1.0000	11.49
31	VVSAQTAQT	549	0.9000	10.34
32	VILVLMLVA	93	0.8000	9.20
33	LMLVAATQL	97	0.8000	9.20
34	VLKKLQSDE	202	0.8000	9.20
35	MGGVTVHDA	415	0.8000	9.20
36	MQRENVPLS	658	0.8000	9.20
37	IGIMLDNPA	627	0.7000	8.05
38	LMQRENVPL	657	0.7000	8.05
39	LKVTDVQPA	124	0.6000	6.90
40	VLQVPGSIQ	406	0.6000	6.90
41	YVIGIMLDN	625	0.6000	6.90
42	LRQYPGGSL	241	0.5000	5.75
43	FYVQQQVQQ	319	0.5000	5.75
44	ITFAGIATA	612	0.5000	5.75
45	FFLQVSHAA	106	0.3000	3.45
46	FTIEARALT	147	0.3000	3.45
47	VAGKLNNKP	189	0.3000	3.45

48	MTGMYQAIA	509	0.3000	3.45
49	FLQVSHAAG	107	0.2000	2.30
50	LNNKPDAAA	193	0.2000	2.30
51	MLVAATQLF	98	0.1000	1.15
52	LVAATQLFF	99	0.1000	1.15
53	ICAKYPEVG	227	0.1000	1.15
54	VNKIVAASA	386	0.1000	1.15
55	VVIPGSYRN	291	-0.1000	0
56	VGTLMLSQR	443	-0.1000	0
57	FAGIATADN	614	-0.1000	0
58	YTTTGVFGK	431	-0.1500	0
59	VAPAGRSTR	58	-0.2000	0
60	MTLLQMTGM	504	-0.2000	0
61	FHNIAGWLM	650	-0.2000	0
62	WITFAGIAT	611	-0.2200	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	YRNRHKAVH	297	7.6000	75.25
2	FVYLARAVD	212	5.6000	55.45
3	FVFRHRTGN	83	5.5000	54.46
4	FQPKRIRRQ	156	5.4000	53.47
5	VVQRDPMGY	565	5.3000	52.48
6	MLRKFGLGQ	460	5.1000	50.50
7	LVLMLVAAT	95	4.4000	43.56
8	YVIGIMLDN	625	3.8000	37.62
9	VLMLVAATQ	96	3.4000	33.66
10	LLQMTGMYQ	506	3.3000	32.67
11	VRQMLRAVV	558	3.2000	31.68
12	FRHRTGNAV	85	2.6000	25.74
13	VVLDAKTGE	340	2.4000	23.76
14	LRQYPGGSL	241	2.3000	22.77
15	IIKATVAPD	527	2.3000	22.77

16	YQMAGKTGT	586	2.3000	22.77
17	LVAATQLFF	99	2.2000	21.78
18	YYDMLRKFG	457	2.1000	20.79
19	VILVLMLVA	93	2.0000	19.80
20	VLKKLQSDE	202	2.0000	19.80
21	FAGIATADN	614	1.9000	18.81
22	YLARAVDPA	214	1.8000	17.82
23	IVAASAVIE	389	1.8000	17.82
24	IQMGGVTVH	413	1.8000	17.82
25	FANLPIGQG	493	1.8000	17.82
26	VVSAQTAQT	549	1.8000	17.82
27	MLRAVVQRD	561	1.8000	17.82
28	VGQRKRPGK	29	1.7500	17.33
29	MQRENVPLS	658	1.7500	17.33
30	VVIPGSYRN	291	1.7000	16.83
31	VMPYTTTGV	428	1.7000	16.83
32	YDMLRKFGL	458	1.7000	16.83
33	IEARALTFQ	149	1.6000	15.84
34	LRRPPGAQE	20	1.5000	14.85
35	FLQVSHAAG	107	1.5000	14.85
36	VFGKSSNVG	436	1.5000	14.85
37	VRVPPRIIK	521	1.5000	14.85
38	IQFYVQQQV	317	1.4000	13.86
39	VQQAKNLSG	325	1.4000	13.86
40	WITFAGIAT	611	1.4000	13.86
41	VAASAVIEH	390	1.3000	12.87
42	MLSQRVGPE	447	1.3000	12.87
43	VPPRIIKAT	523	1.3000	12.87
44	LFFLQVSHA	105	1.2000	11.88
45	FTIEARALT	147	1.2000	11.88
46	YVQQQVQQA	320	1.2000	11.88
47	IMLDNPARN	629	1.2000	11.88
48	FHNIAGWLM	650	1.2000	11.88
49	LMQRENVPL	657	1.2000	11.88

50	LQVPGSIQM	407	1.1000	10.89
51	VQPAARGSI	129	1.0000	9.90
52	MGGVTVHDA	415	1.0000	9.90
53	LGLEDSLDA	265	0.9000	8.91
54	IRVVSAQTA	547	0.9000	8.91
55	ILVLMLVAA	94	0.8000	7.92
56	ICAKYPEVG	227	0.8000	7.92
57	FYVQQQVQQ	319	0.8000	7.92
58	MAGKTGTAQ	588	0.8000	7.92
59	VVDVGTRGA	73	0.5000	4.95
60	FFLQVSHAA	106	0.5000	4.95
61	LRKFGLGQR	461	0.5000	4.95
62	LGQRTGVGL	466	0.5000	4.95
63	LPIGQGLSM	496	0.5000	4.95
64	ITFAGIATA	612	0.5000	4.95
65	MTGMYQAIA	509	0.3000	2.97
66	LNNKPDAAA	193	0.2000	1.98
67	VGTRGASFV	76	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	YRNRHKAVH	297	3.3800	40.72
2	FVYLARAVD	212	3.3000	39.76
3	LVLMLVAAT	95	3.1000	37.35
4	VLMLVAATQ	96	3.0000	36.14
5	VRQMLRAVV	558	2.5000	30.12
6	VILVLMLVA	93	2.1000	25.30
7	LLQMTGMYQ	506	2.1000	25.30
8	FQPKRIRRQ	156	1.8000	21.69
9	YVQQQVQQA	320	1.8000	21.69
10	LFFLQVSHA	105	1.6000	19.28
11	MLRKFGLGQ	460	1.5000	18.07
12	VRVPPRIIK	521	1.5000	18.07

13	YQMAGKTGT	586	1.4000	16.87
14	LVAATQLFF	99	1.3000	15.66
15	ILVLMLVAA	94	1.2000	14.46
16	VVQRDPMGY	565	1.2000	14.46
17	FFLQVSHAA	106	1.1000	13.25
18	MGGVTVHDA	415	1.1000	13.25
19	YDMLRKFGL	458	1.1000	13.25
20	YVIGIMLDN	625	1.1000	13.25
21	MQRENVPLS	658	1.0500	12.65
22	IRVVSAQTA	547	1.0000	12.05
23	FANLPIGQG	493	0.9000	10.84
24	VVSAQTAQT	549	0.9000	10.84
25	VQPAARGSI	129	0.8000	9.64
26	VNKIVAASA	386	0.7000	8.43
27	FHNIAGWLM	650	0.7000	8.43
28	VVDVGTRGA	73	0.6000	7.23
29	FYVQQQVQQ	319	0.6000	7.23
30	FVFRHRTGN	83	0.5000	6.02
31	ITFAGIATA	612	0.5000	6.02
32	FAGIATADN	614	0.5000	6.02
33	YYDMLRKFG	457	0.4000	4.82
34	LRKFGLGQR	461	0.4000	4.82
35	YWITFAGIA	610	0.4000	4.82
36	WITFAGIAT	611	0.4000	4.82
37	VAASAVIEH	390	0.3800	4.58
38	VFRHRTGNA	84	0.3000	3.61
39	FLQVSHAAG	107	0.3000	3.61
40	LGLEDSLDA	265	0.2000	2.41
41	LKVTDVQPA	124	0.1000	1.20
42	VQQAKNLSG	325	0.1000	1.20
43	YTTTGVFGK	431	-0.1000	0
44	MTGMYQAIA	509	-0.1000	0
45	IQMGGVTVH	413	-0.1200	0
46	VSHAAGLRA	110	-0.3000	0

47	LEEARKKTS	165	-0.3000	0
48	LQMTGMYQA	507	-0.3000	0
49	FTIEARALT	147	-0.4000	0
50	IIKATVAPD	527	-0.4000	0
51	LRAVVQRDP	562	-0.4000	0
52	VSRAAPRRA	0	-0.5000	0
53	LAANVVGGI	249	-0.5000	0
54	LMLSQRVGP	446	-0.5000	0
55	VGQRKRPGK	29	-0.5500	0
56	LRAQAAGQL	116	-0.6000	0
57	FRHRTGNAV	85	-0.7000	0
58	LTFQPKRIR	154	-0.7000	0
59	LQVPGSIQM	407	-0.7000	0
60	LMLVAATQL	97	-0.8000	0
61	MLVAATQLF	98	-0.8000	0
62	LRDIAQEVA	182	-0.8000	0
63	MLRAVVQRD	561	-0.9000	0
64	VYWITFAGI	609	-0.9000	0
65	LQVSHAAGL	108	-1.0000	0
66	VYLARAVDP	213	-1.0000	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	LVLMLVAAT	95	3.9000	46.43
2	FQPKRIRRQ	156	3.7000	44.05
3	VLMLVAATQ	96	3.3000	39.29
4	VRQMLRAVV	558	3.3000	39.29
5	YRNRHKAVH	297	3.2800	39.05
6	LTFQPKRIR	154	2.9000	34.52
7	MLRKFGLGQ	460	2.7000	32.14
8	YVQQQVQQA	320	2.5000	29.76
9	VTVHDAWEH	418	2.4800	29.52
10	VFRHRTGNA	84	2.3000	27.38

11	LFFLQVSHA	105	2.3000	27.38
12	MQRENVPLS	658	2.2000	26.19
13	VSRAAPRRA	0	2.1000	25.00
14	ILVLMLVAA	94	2.0000	23.81
15	VVDVGTRGA	73	1.9000	22.62
16	VVSAQTAQT	549	1.9000	22.62
17	VVQRDPMGY	565	1.8000	21.43
18	MLDNPARNS	630	1.7000	20.24
19	FFLQVSHAA	106	1.6000	19.05
20	FVYLARAVD	212	1.6000	19.05
21	LLQMTGMYQ	506	1.6000	19.05
22	ITFAGIATA	612	1.5000	17.86
23	IQMGGVTVH	413	1.4800	17.62
24	VRVPPRIIK	521	1.4000	16.67
25	IRVVSAQTA	547	1.4000	16.67
26	LKVTDVQPA	124	1.3000	15.48
27	MGGVTVHDA	415	1.3000	15.48
28	LVAATQLFF	99	1.2000	14.29
29	FYVQQQVQQ	319	1.1000	13.10
30	LMLSQRVGP	446	1.1000	13.10
31	IQFYVQQQV	317	1.0000	11.90
32	VMPYTTTGV	428	1.0000	11.90
33	VGQRKRPGK	29	0.9000	10.71
34	MLVAATQLF	98	0.9000	10.71
35	LEEARKKTS	165	0.9000	10.71
36	LRAVVQRDP	562	0.9000	10.71
37	FVFRHRTGN	83	0.8000	9.52
38	VQQQVQQAK	321	0.8000	9.52
39	VFGKSSNVG	436	0.8000	9.52
40	MLRAVVQRD	561	0.8000	9.52
41	YQMAGKTGT	586	0.8000	9.52
42	VILVLMLVA	93	0.7000	8.33
43	VQPAARGSI	129	0.7000	8.33
44	LGLEDSLDA	265	0.7000	8.33

45	LRKFGLGQR	461	0.7000	8.33
46	MTGMYQAIA	509	0.7000	8.33
47	IIKATVAPD	527	0.6000	7.14
48	VYLARAVDP	213	0.5000	5.95
49	IGIMLDNPA	627	0.5000	5.95
50	LQSDETFVY	206	0.4000	4.76
51	VVIPGSYRN	291	0.4000	4.76
52	VVLDAKTGE	340	0.4000	4.76
53	YDMLRKFGL	458	0.4000	4.76
54	LQMTGMYQA	507	0.4000	4.76
55	FRHRTGNAV	85	0.3000	3.57
56	LRAQAAGQL	116	0.3000	3.57
57	VHGSTVVLT	304	0.3000	3.57
58	IVAASAVIE	389	0.3000	3.57
59	IPGSYRNRH	293	0.2800	3.33
60	VNKIVAASA	386	0.2000	2.38
61	IANDGVRVP	516	0.2000	2.38
62	VAASAVIEH	390	0.1800	2.14
63	LQVSHAAGL	108	0.1000	1.19
64	IEARALTFQ	149	0.1000	1.19
65	IRRQLEEAR	161	0.1000	1.19

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	LVLMLVAAT	95	4.1000	49.40
2	VLMLVAATQ	96	4.0000	48.19
3	VRQMLRAVV	558	3.5000	42.17
4	VILVLMLVA	93	3.1000	37.35
5	LLQMTGMYQ	506	3.1000	37.35
6	LFFLQVSHA	105	2.6000	31.33
7	MLRKFGLGQ	460	2.5000	30.12
8	VRVPPRIIK	521	2.5000	30.12
9	YRNRHKAVH	297	2.3800	28.67

10	LVAATQLFF	99	2.3000	27.71
11	FVYLARAVD	212	2.3000	27.71
12	ILVLMLVAA	94	2.2000	26.51
13	VVQRDPMGY	565	2.2000	26.51
14	MGGVTVHDA	415	2.1000	25.30
15	MQRENVPLS	658	2.0500	24.70
16	IRVVSAQTA	547	2.0000	24.10
17	VVSAQTAQT	549	1.9000	22.89
18	VQPAARGSI	129	1.8000	21.69
19	VNKIVAASA	386	1.7000	20.48
20	VVDVGTRGA	73	1.6000	19.28
21	ITFAGIATA	612	1.5000	18.07
22	LRKFGLGQR	461	1.4000	16.87
23	VAASAVIEH	390	1.3800	16.63
24	VFRHRTGNA	84	1.3000	15.66
25	LGLEDSLDA	265	1.2000	14.46
26	LKVTDVQPA	124	1.1000	13.25
27	VQQAKNLSG	325	1.1000	13.25
28	MTGMYQAIA	509	0.9000	10.84
29	IQMGGVTVH	413	0.8800	10.60
30	FQPKRIRRQ	156	0.8000	9.64
31	YVQQQVQQA	320	0.8000	9.64
32	VSHAAGLRA	110	0.7000	8.43
33	LEEARKKTS	165	0.7000	8.43
34	LQMTGMYQA	507	0.7000	8.43
35	IIKATVAPD	527	0.6000	7.23
36	LRAVVQRDP	562	0.6000	7.23
37	VSRAAPRRA	0	0.5000	6.02
38	LAANVVGGI	249	0.5000	6.02
39	LMLSQRVGP	446	0.5000	6.02
40	VGQRKRPGK	29	0.4500	5.42
41	LRAQAAGQL	116	0.4000	4.82
42	YQMAGKTGT	586	0.4000	4.82
43	LTFQPKRIR	154	0.3000	3.61

44	LQVPGSIQM	407	0.3000	3.61
45	LMLVAATQL	97	0.2000	2.41
46	MLVAATQLF	98	0.2000	2.41
47	LRDIAQEVA	182	0.2000	2.41
48	FFLQVSHAA	106	0.1000	1.20
49	YDMLRKFGL	458	0.1000	1.20
50	MLRAVVQRD	561	0.1000	1.20
51	VYWITFAGI	609	0.1000	1.20
52	YVIGIMLDN	625	0.1000	1.20
53	VLQVPGSIQ	406	-0.1000	0
54	MLSQRVGPE	447	-0.1000	0
55	FANLPIGQG	493	-0.1000	0
56	IVAASAVIE	389	-0.2000	0
57	VHGSTVVLT	304	-0.3000	0
58	VVLDAKTGE	340	-0.3000	0
59	LPIGQGLSM	496	-0.3000	0
60	FHNIAGWLM	650	-0.3000	0
61	FYVQQQVQQ	319	-0.4000	0
62	IGIMLDNPA	627	-0.4000	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	LVLMLVAAT	95	4.1000	49.40
2	VLMLVAATQ	96	4.0000	48.19
3	VRQMLRAVV	558	3.5000	42.17
4	VILVLMLVA	93	3.1000	37.35
5	LLQMTGMYQ	506	3.1000	37.35
6	LFFLQVSHA	105	2.6000	31.33
7	MLRKFGLGQ	460	2.5000	30.12
8	VRVPPRIIK	521	2.5000	30.12
9	YRNRHKAVH	297	2.3800	28.67
10	LVAATQLFF	99	2.3000	27.71
11	FVYLARAVD	212	2.3000	27.71

12	ILVLMLVAA	94	2.2000	26.51
13	VVQRDPMGY	565	2.2000	26.51
14	MGGVTVHDA	415	2.1000	25.30
15	MQRENVPLS	658	2.0500	24.70
16	IRVVSAQTA	547	2.0000	24.10
17	VVSAQTAQT	549	1.9000	22.89
18	VQPAARGSI	129	1.8000	21.69
19	VNKIVAASA	386	1.7000	20.48
20	VVDVGTRGA	73	1.6000	19.28
21	ITFAGIATA	612	1.5000	18.07
22	LRKFGLGQR	461	1.4000	16.87
23	VAASAVIEH	390	1.3800	16.63
24	VFRHRTGNA	84	1.3000	15.66
25	LGLEDSLDA	265	1.2000	14.46
26	LKVTDVQPA	124	1.1000	13.25
27	VQQAKNLSG	325	1.1000	13.25
28	MTGMYQAIA	509	0.9000	10.84
29	IQMGGVTVH	413	0.8800	10.60
30	FQPKRIRRQ	156	0.8000	9.64
31	YVQQQVQQA	320	0.8000	9.64
32	VSHAAGLRA	110	0.7000	8.43
33	LEEARKKTS	165	0.7000	8.43
34	LQMTGMYQA	507	0.7000	8.43
35	IIKATVAPD	527	0.6000	7.23
36	LRAVVQRDP	562	0.6000	7.23
37	VSRAAPRRA	0	0.5000	6.02
38	LAANVVGGI	249	0.5000	6.02
39	LMLSQRVGP	446	0.5000	6.02
40	VGQRKRPGK	29	0.4500	5.42
41	LRAQAAGQL	116	0.4000	4.82
42	YQMAGKTGT	586	0.4000	4.82
43	LTFQPKRIR	154	0.3000	3.61
44	LQVPGSIQM	407	0.3000	3.61
45	LMLVAATQL	97	0.2000	2.41

46	MLVAATQLF	98	0.2000	2.41
47	LRDIAQEVA	182	0.2000	2.41
48	FFLQVSHAA	106	0.1000	1.20
49	YDMLRKFGL	458	0.1000	1.20
50	MLRAVVQRD	561	0.1000	1.20
51	VYWITFAGI	609	0.1000	1.20
52	YVIGIMLDN	625	0.1000	1.20
53	VLQVPGSIQ	406	-0.1000	0
54	MLSQRVGPE	447	-0.1000	0
55	FANLPIGQG	493	-0.1000	0
56	IVAASAVIE	389	-0.2000	0
57	VHGSTVVLT	304	-0.3000	0
58	VVLDAKTGE	340	-0.3000	0
59	LPIGQGLSM	496	-0.3000	0
60	FHNIAGWLM	650	-0.3000	0
61	FYVQQQVQQ	319	-0.4000	0
62	IGIMLDNPA	627	-0.4000	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	VVLDAKTGE	340	4.9000	53.85
2	IQMGGVTVH	413	4.2800	47.03
3	LQSDETFVY	206	4.0000	43.96
4	VQRDPMGYQ	566	3.9000	42.86
5	IMLDNPARN	629	3.5000	38.46
6	MQRENVPLS	658	3.5000	38.46
7	LVLMLVAAT	95	3.1000	34.07
8	VLMLVAATQ	96	2.9000	31.87
9	LFFLQVSHA	105	2.8700	31.54
10	MANDNTFDP	352	2.8000	30.77
11	VRVPPRIIK	521	2.8000	30.77
12	LMLSQRVGP	446	2.7000	29.67
13	IRVVSAQTA	547	2.6000	28.57

14	VRQMLRAVV	558	2.5000	27.47
15	VFRHRTGNA	84	2.4000	26.37
16	VAASAVIEH	390	2.3800	26.15
17	VQPAARGSI	129	2.3000	25.27
18	YVQQQVQQA	320	2.2000	24.18
19	YRNRHKAVH	297	2.0800	22.86
20	ILVLMLVAA	94	1.9000	20.88
21	VHGSTVVLT	304	1.9000	20.88
22	LLQMTGMYQ	506	1.9000	20.88
23	VVSAQTAQT	549	1.9000	20.88
24	IANDGVRVP	516	1.8000	19.78
25	LKVTDVQPA	124	1.7000	18.68
26	VVQRDPMGY	565	1.7000	18.68
27	YQMAGKTGT	586	1.6000	17.58
28	VDVGTRGAS	74	1.5000	16.48
29	ITFAGIATA	612	1.5000	16.48
30	VTYDRGSDG	282	1.4700	16.15
31	VILVLMLVA	93	1.4000	15.38
32	LQVSHAAGL	108	1.4000	15.38
33	IPGSYRNRH	293	1.3900	15.27
34	LRAQAAGQL	116	1.3000	14.29
35	VNKIVAASA	386	1.3000	14.29
36	LSPDPGPPL	665	1.3000	14.29
37	MLVAATQLF	98	1.2000	13.19
38	FVYLARAVD	212	1.2000	13.19
39	LAANVVGGI	249	1.2000	13.19
40	FGLGQRTGV	464	1.2000	13.19
41	MGGVTVHDA	415	1.1000	12.09
42	MLRAVVQRD	561	1.1000	12.09
43	VVIPGSYRN	291	1.0500	11.54
44	LMLVAATQL	97	1.0000	10.99
45	LVAATQLFF	99	1.0000	10.99
46	LDNDIQFYV	313	1.0000	10.99
47	IGQGLSMTL	498	1.0000	10.99

48	YVIGIMLDN	625	1.0000	10.99
49	VGQRKRPGK	29	0.9000	9.89
50	LRDIAQEVA	182	0.9000	9.89
51	VLQVPGSIQ	406	0.8700	9.56
52	VYLARAVDP	213	0.8000	8.79
53	FYVQQQVQQ	319	0.8000	8.79
54	MLSQRVGPE	447	0.8000	8.79
55	FEPGSVNKI	381	0.7100	7.80
56	VVDVGTRGA	73	0.7000	7.69
57	MLRKFGLGQ	460	0.7000	7.69
58	YQQGTGPTA	573	0.7000	7.69
59	LQMTGMYQA	507	0.6500	7.14
60	LGLEDSLDA	265	0.6000	6.59
61	IVAASAVIE	389	0.6000	6.59
62	LQVPGSIQM	407	0.6000	6.59
63	LPIGQGLSM	496	0.6000	6.59
64	IIKATVAPD	527	0.6000	6.59
65	VQQQVQQAK	321	0.5000	5.49
66	LRKFGLGQR	461	0.5000	5.49
67	FVFRHRTGN	83	0.4000	4.40

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	FQPKRIRRQ	156	4.7000	55.95
2	YRNRHKAVH	297	4.2800	50.95
3	YVQQQVQQA	320	3.5000	41.67
4	LVLMLVAAT	95	2.9000	34.52
5	FFLQVSHAA	106	2.6000	30.95
6	FVYLARAVD	212	2.6000	30.95
7	VLMLVAATQ	96	2.3000	27.38
8	VRQMLRAVV	558	2.3000	27.38
9	FYVQQQVQQ	319	2.1000	25.00
10	LTFQPKRIR	154	1.9000	22.62

11	FVFRHRTGN	83	1.8000	21.43
12	YQMAGKTGT	586	1.8000	21.43
13	MLRKFGLGQ	460	1.7000	20.24
14	VTVHDAWEH	418	1.4800	17.62
15	YDMLRKFGL	458	1.4000	16.67
16	VFRHRTGNA	84	1.3000	15.48
17	FRHRTGNAV	85	1.3000	15.48
18	LFFLQVSHA	105	1.3000	15.48
19	MQRENVPLS	658	1.2000	14.29
20	VSRAAPRRA	0	1.1000	13.10
21	ILVLMLVAA	94	1.0000	11.90
22	VVDVGTRGA	73	0.9000	10.71
23	YLARAVDPA	214	0.9000	10.71
24	VVSAQTAQT	549	0.9000	10.71
25	VVQRDPMGY	565	0.8000	9.52
26	MLDNPARNS	630	0.7000	8.33
27	LLQMTGMYQ	506	0.6000	7.14
28	ITFAGIATA	612	0.5000	5.95
29	IQMGGVTVH	413	0.4800	5.71
30	YTTTGVFGK	431	0.4000	4.76
31	YYDMLRKFG	457	0.4000	4.76
32	VRVPPRIIK	521	0.4000	4.76
33	IRVVSAQTA	547	0.4000	4.76
34	WLMQRENVP	656	0.4000	4.76
35	LKVTDVQPA	124	0.3000	3.57
36	MGGVTVHDA	415	0.3000	3.57
37	LVAATQLFF	99	0.2000	2.38
38	FTIEARALT	147	0.2000	2.38
39	YVIGIMLDN	625	0.2000	2.38
40	LMLSQRVGP	446	0.1000	1.19
41	VGQRKRPGK	29	-0.1000	0
42	MLVAATQLF	98	-0.1000	0
43	LEEARKKTS	165	-0.1000	0
44	FEPGSVNKI	381	-0.1000	0

45	LRAVVQRDP	562	-0.1000	0
46	VQQQVQQAK	321	-0.2000	0
47	VFGKSSNVG	436	-0.2000	0
48	MLRAVVQRD	561	-0.2000	0
49	VILVLMLVA	93	-0.3000	0
50	VQPAARGSI	129	-0.3000	0
51	LGLEDSLDA	265	-0.3000	0
52	LRKFGLGQR	461	-0.3000	0
53	MTGMYQAIA	509	-0.3000	0
54	IIKATVAPD	527	-0.4000	0
55	VYLARAVDP	213	-0.5000	0
56	WITFAGIAT	611	-0.5000	0
57	IGIMLDNPA	627	-0.5000	0
58	LQSDETFVY	206	-0.6000	0
59	VVIPGSYRN	291	-0.6000	0
60	VVLDAKTGE	340	-0.6000	0
61	FGLGQRTGV	464	-0.6000	0
62	LQMTGMYQA	507	-0.6000	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	FQPKRIRRQ	156	4.0000	45.45
2	FVYLARAVD	212	3.7000	42.05
3	YRNRHKAVH	297	3.7000	42.05
4	LVLMLVAAT	95	3.6000	40.91
5	YVQQQVQQA	320	3.5000	39.77
6	LTFQPKRIR	154	3.4000	38.64
7	VRQMLRAVV	558	3.3000	37.50
8	FVFRHRTGN	83	2.6000	29.55
9	FFLQVSHAA	106	2.6000	29.55
10	YQMAGKTGT	586	2.5000	28.41
11	YDMLRKFGL	458	2.3600	26.82
12	FRHRTGNAV	85	2.3000	26.14

13	LVAATQLFF	99	2.1000	23.86
14	VVQRDPMGY	565	2.1000	23.86
15	MLVAATQLF	98	1.8000	20.45
16	YYDMLRKFG	457	1.8000	20.45
17	VLMLVAATQ	96	1.6000	18.18
18	VVSAQTAQT	549	1.6000	18.18
19	MQRENVPLS	658	1.6000	18.18
20	FHNIAGWLM	650	1.5000	17.05
21	FYVQQQVQQ	319	1.4000	15.91
22	WLMQRENVP	656	1.4000	15.91
23	VFRHRTGNA	84	1.3000	14.77
24	LFFLQVSHA	105	1.3000	14.77
25	VFGKSSNVG	436	1.2000	13.64
26	LRKFGLGQR	461	1.2000	13.64
27	VSRAAPRRA	0	1.1000	12.50
28	LMLSQRVGP	446	1.1000	12.50
29	MLDNPARNS	630	1.1000	12.50
30	ILVLMLVAA	94	1.0000	11.36
31	IQFYVQQQV	317	1.0000	11.36
32	VMPYTTTGV	428	1.0000	11.36
33	MLRKFGLGQ	460	1.0000	11.36
34	YVIGIMLDN	625	1.0000	11.36
35	WDGHGLLGL	259	0.9600	10.91
36	VVDVGTRGA	73	0.9000	10.23
37	FTIEARALT	147	0.9000	10.23
38	YLARAVDPA	214	0.9000	10.23
39	VTVHDAWEH	418	0.9000	10.23
40	MLRAVVQRD	561	0.9000	10.23
41	LRAVVQRDP	562	0.9000	10.23
42	VVLDAKTGE	340	0.8000	9.09
43	FEPGSVNKI	381	0.8000	9.09
44	LQSDETFVY	206	0.7000	7.95
45	IVAASAVIE	389	0.7000	7.95
46	IIKATVAPD	527	0.7000	7.95

47	VQPAARGSI	129	0.6000	6.82
48	IRRQLEEAR	161	0.6000	6.82
49	VYLARAVDP	213	0.5000	5.68
50	YTTTGVFGK	431	0.5000	5.68
51	FANLPIGQG	493	0.5000	5.68
52	VRVPPRIIK	521	0.5000	5.68
53	ITFAGIATA	612	0.5000	5.68
54	FLQVSHAAG	107	0.4000	4.55
55	VQQAKNLSG	325	0.4000	4.55
56	FGLGQRTGV	464	0.4000	4.55
57	MYQAIANDG	512	0.4000	4.55
58	IRVVSAQTA	547	0.4000	4.55
59	LKVTDVQPA	124	0.3000	3.41
60	LEEARKKTS	165	0.3000	3.41
61	MGGVTVHDA	415	0.3000	3.41
62	LRAQAAGQL	116	0.2600	2.95
63	VVIPGSYRN	291	0.2000	2.27
64	MLSQRVGPE	447	0.2000	2.27
65	IANDGVRVP	516	0.2000	2.27
66	WITFAGIAT	611	0.2000	2.27
67	LQVSHAAGL	108	0.0600	0.68

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	LVLMLVAAT	95	3.9000	46.43
2	FQPKRIRRQ	156	3.7000	44.05
3	VLMLVAATQ	96	3.3000	39.29
4	VRQMLRAVV	558	3.3000	39.29
5	YRNRHKAVH	297	3.2800	39.05
6	LTFQPKRIR	154	2.9000	34.52
7	MLRKFGLGQ	460	2.7000	32.14
8	YVQQQVQQA	320	2.5000	29.76
9	VTVHDAWEH	418	2.4800	29.52

10	VFRHRTGNA	84	2.3000	27.38
11	LFFLQVSHA	105	2.3000	27.38
12	MQRENVPLS	658	2.2000	26.19
13	VSRAAPRRA	0	2.1000	25.00
14	ILVLMLVAA	94	2.0000	23.81
15	VVDVGTRGA	73	1.9000	22.62
16	VVSAQTAQT	549	1.9000	22.62
17	VVQRDPMGY	565	1.8000	21.43
18	MLDNPARNS	630	1.7000	20.24
19	FFLQVSHAA	106	1.6000	19.05
20	FVYLARAVD	212	1.6000	19.05
21	LLQMTGMYQ	506	1.6000	19.05
22	ITFAGIATA	612	1.5000	17.86
23	IQMGGVTVH	413	1.4800	17.62
24	VRVPPRIIK	521	1.4000	16.67
25	IRVVSAQTA	547	1.4000	16.67
26	LKVTDVQPA	124	1.3000	15.48
27	MGGVTVHDA	415	1.3000	15.48
28	LVAATQLFF	99	1.2000	14.29
29	FYVQQQVQQ	319	1.1000	13.10
30	LMLSQRVGP	446	1.1000	13.10
31	IQFYVQQQV	317	1.0000	11.90
32	VMPYTTTGV	428	1.0000	11.90
33	VGQRKRPGK	29	0.9000	10.71
34	MLVAATQLF	98	0.9000	10.71
35	LEEARKKTS	165	0.9000	10.71
36	LRAVVQRDP	562	0.9000	10.71
37	FVFRHRTGN	83	0.8000	9.52
38	VQQQVQQAK	321	0.8000	9.52
39	VFGKSSNVG	436	0.8000	9.52
40	MLRAVVQRD	561	0.8000	9.52
41	YQMAGKTGT	586	0.8000	9.52
42	VILVLMLVA	93	0.7000	8.33
43	VQPAARGSI	129	0.7000	8.33

44	LGLEDSLDA	265	0.7000	8.33
45	LRKFGLGQR	461	0.7000	8.33
46	MTGMYQAIA	509	0.7000	8.33
47	IIKATVAPD	527	0.6000	7.14
48	VYLARAVDP	213	0.5000	5.95
49	IGIMLDNPA	627	0.5000	5.95
50	LQSDETFVY	206	0.4000	4.76
51	VVIPGSYRN	291	0.4000	4.76
52	VVLDAKTGE	340	0.4000	4.76
53	YDMLRKFGL	458	0.4000	4.76
54	LQMTGMYQA	507	0.4000	4.76
55	FRHRTGNAV	85	0.3000	3.57
56	LRAQAAGQL	116	0.3000	3.57
57	VHGSTVVLT	304	0.3000	3.57
58	IVAASAVIE	389	0.3000	3.57
59	IPGSYRNRH	293	0.2800	3.33
60	VNKIVAASA	386	0.2000	2.38
61	IANDGVRVP	516	0.2000	2.38
62	VAASAVIEH	390	0.1800	2.14
63	LQVSHAAGL	108	0.1000	1.19
64	IEARALTFQ	149	0.1000	1.19
65	IRRQLEEAR	161	0.1000	1.19

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	FVYLARAVD	212	4.4000	50.57
2	LVLMLVAAT	95	3.8000	43.68
3	VRQMLRAVV	558	3.5000	40.23
4	LVAATQLFF	99	3.2000	36.78
5	YRNRHKAVH	297	2.8000	32.18
6	VVQRDPMGY	565	2.5000	28.74
7	VLMLVAATQ	96	2.3000	26.44
8	FANLPIGQG	493	2.3000	26.44

9	FHNIAGWLM	650	2.2000	25.29
10	VILVLMLVA	93	2.1000	24.14
11	YQMAGKTGT	586	2.1000	24.14
12	YDMLRKFGL	458	2.0600	23.68
13	LRKFGLGQR	461	1.9000	21.84
14	YVIGIMLDN	625	1.9000	21.84
15	YVQQQVQQA	320	1.8000	20.69
16	YYDMLRKFG	457	1.8000	20.69
17	FLQVSHAAG	107	1.7000	19.54
18	VQPAARGSI	129	1.7000	19.54
19	LFFLQVSHA	105	1.6000	18.39
20	VRVPPRIIK	521	1.6000	18.39
21	VVSAQTAQT	549	1.6000	18.39
22	VQQAKNLSG	325	1.5000	17.24
23	MQRENVPLS	658	1.4500	16.67
24	LLQMTGMYQ	506	1.4000	16.09
25	FVFRHRTGN	83	1.3000	14.94
26	FAGIATADN	614	1.3000	14.94
27	ILVLMLVAA	94	1.2000	13.79
28	MLVAATQLF	98	1.1000	12.64
29	FFLQVSHAA	106	1.1000	12.64
30	FQPKRIRRQ	156	1.1000	12.64
31	MGGVTVHDA	415	1.1000	12.64
32	WITFAGIAT	611	1.1000	12.64
33	IRVVSAQTA	547	1.0000	11.49
34	LTFQPKRIR	154	0.8000	9.20
35	LQVPGSIQM	407	0.8000	9.20
36	MLRKFGLGQ	460	0.8000	9.20
37	VNKIVAASA	386	0.7000	8.05
38	IIKATVAPD	527	0.7000	8.05
39	VVDVGTRGA	73	0.6000	6.90
40	LRAVVQRDP	562	0.6000	6.90
41	LMLSQRVGP	446	0.5000	5.75
42	ITFAGIATA	612	0.5000	5.75

43	LAANVVGGI	249	0.4000	4.60
44	YWITFAGIA	610	0.4000	4.60
45	LRAQAAGQL	116	0.3600	4.14
46	VFRHRTGNA	84	0.3000	3.45
47	FRHRTGNAV	85	0.3000	3.45
48	FTIEARALT	147	0.3000	3.45
49	MLSQRVGPE	447	0.3000	3.45
50	LGLEDSLDA	265	0.2000	2.30
51	IVAASAVIE	389	0.2000	2.30
52	LPIGQGLSM	496	0.2000	2.30
53	MLRAVVQRD	561	0.2000	2.30
54	LMLVAATQL	97	0.1600	1.84
55	LKVTDVQPA	124	0.1000	1.15
56	LEEARKKTS	165	0.1000	1.15
57	VVLDAKTGE	340	0.1000	1.15
58	LQVSHAAGL	108	-0.0400	0
59	WDGHGLLGL	259	-0.0400	0
60	FYVQQQVQQ	319	-0.1000	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	LVLMLVAAT	95	4.6000	52.27
2	LTFQPKRIR	154	4.4000	50.00
3	VRQMLRAVV	558	4.3000	48.86
4	LVAATQLFF	99	3.1000	35.23
5	VVQRDPMGY	565	3.1000	35.23
6	FQPKRIRRQ	156	3.0000	34.09
7	MLVAATQLF	98	2.8000	31.82
8	FVYLARAVD	212	2.7000	30.68
9	YRNRHKAVH	297	2.7000	30.68
10	VLMLVAATQ	96	2.6000	29.55
11	VVSAQTAQT	549	2.6000	29.55
12	MQRENVPLS	658	2.6000	29.55

13	YVQQQVQQA	320	2.5000	28.41
14	VFRHRTGNA	84	2.3000	26.14
15	LFFLQVSHA	105	2.3000	26.14
16	VFGKSSNVG	436	2.2000	25.00
17	LRKFGLGQR	461	2.2000	25.00
18	VSRAAPRRA	0	2.1000	23.86
19	LMLSQRVGP	446	2.1000	23.86
20	MLDNPARNS	630	2.1000	23.86
21	ILVLMLVAA	94	2.0000	22.73
22	IQFYVQQQV	317	2.0000	22.73
23	VMPYTTTGV	428	2.0000	22.73
24	MLRKFGLGQ	460	2.0000	22.73
25	VVDVGTRGA	73	1.9000	21.59
26	VTVHDAWEH	418	1.9000	21.59
27	MLRAVVQRD	561	1.9000	21.59
28	LRAVVQRDP	562	1.9000	21.59
29	VVLDAKTGE	340	1.8000	20.45
30	LQSDETFVY	206	1.7000	19.32
31	IVAASAVIE	389	1.7000	19.32
32	IIKATVAPD	527	1.7000	19.32
33	FVFRHRTGN	83	1.6000	18.18
34	FFLQVSHAA	106	1.6000	18.18
35	VQPAARGSI	129	1.6000	18.18
36	IRRQLEEAR	161	1.6000	18.18
37	VYLARAVDP	213	1.5000	17.05
38	VRVPPRIIK	521	1.5000	17.05
39	YQMAGKTGT	586	1.5000	17.05
40	ITFAGIATA	612	1.5000	17.05
41	VQQAKNLSG	325	1.4000	15.91
42	MYQAIANDG	512	1.4000	15.91
43	IRVVSAQTA	547	1.4000	15.91
44	YDMLRKFGL	458	1.3600	15.45
45	FRHRTGNAV	85	1.3000	14.77
46	LKVTDVQPA	124	1.3000	14.77

47	LEEARKKTS	165	1.3000	14.77
48	MGGVTVHDA	415	1.3000	14.77
49	LRAQAAGQL	116	1.2600	14.32
50	VVIPGSYRN	291	1.2000	13.64
51	MLSQRVGPE	447	1.2000	13.64
52	IANDGVRVP	516	1.2000	13.64
53	LQVSHAAGL	108	1.0600	12.05
54	VGQRKRPGK	29	1.0000	11.36
55	VHGSTVVLT	304	1.0000	11.36
56	VAPAGRSTR	58	0.9000	10.23
57	VQQQVQQAK	321	0.9000	10.23
58	IQMGGVTVH	413	0.9000	10.23
59	LLQMTGMYQ	506	0.9000	10.23
60	YYDMLRKFG	457	0.8000	9.09
61	VILVLMLVA	93	0.7000	7.95
62	ICAKYPEVG	227	0.7000	7.95
63	LGLEDSLDA	265	0.7000	7.95
64	LQVPGSIQM	407	0.7000	7.95
65	VGTLMLSQR	443	0.7000	7.95
66	MTLLQMTGM	504	0.7000	7.95
67	MTGMYQAIA	509	0.7000	7.95

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FQPKRIRRQ	156	4.0000	45.45
2	FVYLARAVD	212	3.7000	42.05
3	YRNRHKAVH	297	3.7000	42.05
4	LVLMLVAAT	95	3.6000	40.91
5	YVQQQVQQA	320	3.5000	39.77
6	LTFQPKRIR	154	3.4000	38.64
7	VRQMLRAVV	558	3.3000	37.50
8	FVFRHRTGN	83	2.6000	29.55
9	FFLQVSHAA	106	2.6000	29.55

10	YQMAGKTGT	586	2.5000	28.41
11	YDMLRKFGL	458	2.3600	26.82
12	FRHRTGNAV	85	2.3000	26.14
13	LVAATQLFF	99	2.1000	23.86
14	VVQRDPMGY	565	2.1000	23.86
15	MLVAATQLF	98	1.8000	20.45
16	YYDMLRKFG	457	1.8000	20.45
17	VLMLVAATQ	96	1.6000	18.18
18	VVSAQTAQT	549	1.6000	18.18
19	MQRENVPLS	658	1.6000	18.18
20	FHNIAGWLM	650	1.5000	17.05
21	FYVQQQVQQ	319	1.4000	15.91
22	WLMQRENVP	656	1.4000	15.91
23	VFRHRTGNA	84	1.3000	14.77
24	LFFLQVSHA	105	1.3000	14.77
25	VFGKSSNVG	436	1.2000	13.64
26	LRKFGLGQR	461	1.2000	13.64
27	VSRAAPRRA	0	1.1000	12.50
28	LMLSQRVGP	446	1.1000	12.50
29	MLDNPARNS	630	1.1000	12.50
30	ILVLMLVAA	94	1.0000	11.36
31	IQFYVQQQV	317	1.0000	11.36
32	VMPYTTTGV	428	1.0000	11.36
33	MLRKFGLGQ	460	1.0000	11.36
34	YVIGIMLDN	625	1.0000	11.36
35	WDGHGLLGL	259	0.9600	10.91
36	VVDVGTRGA	73	0.9000	10.23
37	FTIEARALT	147	0.9000	10.23
38	YLARAVDPA	214	0.9000	10.23
39	VTVHDAWEH	418	0.9000	10.23
40	MLRAVVQRD	561	0.9000	10.23
41	LRAVVQRDP	562	0.9000	10.23
42	VVLDAKTGE	340	0.8000	9.09
43	FEPGSVNKI	381	0.8000	9.09

44	LQSDETFVY	206	0.7000	7.95
45	IVAASAVIE	389	0.7000	7.95
46	IIKATVAPD	527	0.7000	7.95
47	VQPAARGSI	129	0.6000	6.82
48	IRRQLEEAR	161	0.6000	6.82
49	VYLARAVDP	213	0.5000	5.68
50	YTTTGVFGK	431	0.5000	5.68
51	FANLPIGQG	493	0.5000	5.68
52	VRVPPRIIK	521	0.5000	5.68
53	ITFAGIATA	612	0.5000	5.68
54	FLQVSHAAG	107	0.4000	4.55
55	VQQAKNLSG	325	0.4000	4.55
56	FGLGQRTGV	464	0.4000	4.55
57	MYQAIANDG	512	0.4000	4.55
58	IRVVSAQTA	547	0.4000	4.55
59	LKVTDVQPA	124	0.3000	3.41
60	LEEARKKTS	165	0.3000	3.41
61	MGGVTVHDA	415	0.3000	3.41
62	LRAQAAGQL	116	0.2600	2.95
63	VVIPGSYRN	291	0.2000	2.27
64	MLSQRVGPE	447	0.2000	2.27
65	IANDGVRVP	516	0.2000	2.27
66	WITFAGIAT	611	0.2000	2.27
67	LQVSHAAGL	108	0.0600	0.68

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	LVLMLVAAT	95	4.8000	53.33
2	FQPKRIRRQ	156	4.5000	50.00
3	YRNRHKAVH	297	4.5000	50.00
4	FVYLARAVD	212	4.3000	47.78
5	VLMLVAATQ	96	4.1000	45.56
6	VTVHDAWEH	418	3.7000	41.11

7	VRQMLRAVV	558	3.6000	40.00
8	MLRKFGLGQ	460	3.5000	38.89
9	MLRAVVQRD	561	3.5000	38.89
10	VVLDAKTGE	340	3.4000	37.78
11	IVAASAVIE	389	3.3000	36.67
12	IIKATVAPD	527	3.3000	36.67
13	LTFQPKRIR	154	2.9000	32.22
14	VVQRDPMGY	565	2.9000	32.22
15	FVFRHRTGN	83	2.8000	31.11
16	MLSQRVGPE	447	2.8000	31.11
17	VVSAQTAQT	549	2.8000	31.11
18	IQMGGVTVH	413	2.7000	30.00
19	YVQQQVQQA	320	2.5000	27.78
20	VVIPGSYRN	291	2.4000	26.67
21	LLQMTGMYQ	506	2.4000	26.67
22	VFRHRTGNA	84	2.3000	25.56
23	LFFLQVSHA	105	2.3000	25.56
24	MQRENVPLS	658	2.2000	24.44
25	VSRAAPRRA	0	2.1000	23.33
26	LVAATQLFF	99	2.1000	23.33
27	VFGKSSNVG	436	2.1000	23.33
28	LRRPPGAQE	20	2.0000	22.22
29	ILVLMLVAA	94	2.0000	22.22
30	VVDVGTRGA	73	1.9000	21.11
31	VLKKLQSDE	202	1.9000	21.11
32	FYVQQQVQQ	319	1.9000	21.11
33	MLVAATQLF	98	1.8000	20.00
34	IMLDNPARN	629	1.8000	20.00
35	YQMAGKTGT	586	1.7000	18.89
36	MLDNPARNS	630	1.7000	18.89
37	FFLQVSHAA	106	1.6000	17.78
38	LQSDETFVY	206	1.5000	16.67
39	IPGSYRNRH	293	1.5000	16.67
40	LMLSQRVGP	446	1.5000	16.67

41	ITFAGIATA	612	1.5000	16.67
42	VAASAVIEH	390	1.4000	15.56
43	YDMLRKFGL	458	1.4000	15.56
44	IRVVSAQTA	547	1.4000	15.56
45	LRAQAAGQL	116	1.3000	14.44
46	LKVTDVQPA	124	1.3000	14.44
47	IQFYVQQQV	317	1.3000	14.44
48	VQQAKNLSG	325	1.3000	14.44
49	MGGVTVHDA	415	1.3000	14.44
50	VMPYTTTGV	428	1.3000	14.44
51	MYQAIANDG	512	1.3000	14.44
52	VAPDGSRTE	532	1.3000	14.44
53	LRAVVQRDP	562	1.3000	14.44
54	VHGSTVVLT	304	1.2000	13.33
55	YVIGIMLDN	625	1.2000	13.33
56	LQVSHAAGL	108	1.1000	12.22
57	VQPAARGSI	129	0.9000	10.00
58	IEARALTFQ	149	0.9000	10.00
59	LEEARKKTS	165	0.9000	10.00
60	VYLARAVDP	213	0.9000	10.00
61	IAGWLMQRE	653	0.9000	10.00
62	VILVLMLVA	93	0.7000	7.78
63	LGLEDSLDA	265	0.7000	7.78
64	YYDMLRKFG	457	0.7000	7.78
65	LRKFGLGQR	461	0.7000	7.78
66	MTGMYQAIA	509	0.7000	7.78
67	VRVPPRIIK	521	0.7000	7.78

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	FVYLARAVD	212	4.4000	50.57
2	LVLMLVAAT	95	3.8000	43.68
3	VRQMLRAVV	558	3.5000	40.23

4	LVAATQLFF	99	3.2000	36.78
5	YRNRHKAVH	297	2.8000	32.18
6	VVQRDPMGY	565	2.5000	28.74
7	VLMLVAATQ	96	2.3000	26.44
8	FANLPIGQG	493	2.3000	26.44
9	FHNIAGWLM	650	2.2000	25.29
10	VILVLMLVA	93	2.1000	24.14
11	YQMAGKTGT	586	2.1000	24.14
12	YDMLRKFGL	458	2.0600	23.68
13	LRKFGLGQR	461	1.9000	21.84
14	YVIGIMLDN	625	1.9000	21.84
15	YVQQQVQQA	320	1.8000	20.69
16	YYDMLRKFG	457	1.8000	20.69
17	FLQVSHAAG	107	1.7000	19.54
18	VQPAARGSI	129	1.7000	19.54
19	LFFLQVSHA	105	1.6000	18.39
20	VRVPPRIIK	521	1.6000	18.39
21	VVSAQTAQT	549	1.6000	18.39
22	VQQAKNLSG	325	1.5000	17.24
23	MQRENVPLS	658	1.4500	16.67
24	LLQMTGMYQ	506	1.4000	16.09
25	FVFRHRTGN	83	1.3000	14.94
26	FAGIATADN	614	1.3000	14.94
27	ILVLMLVAA	94	1.2000	13.79
28	MLVAATQLF	98	1.1000	12.64
29	FFLQVSHAA	106	1.1000	12.64
30	FQPKRIRRQ	156	1.1000	12.64
31	MGGVTVHDA	415	1.1000	12.64
32	WITFAGIAT	611	1.1000	12.64
33	IRVVSAQTA	547	1.0000	11.49
34	LTFQPKRIR	154	0.8000	9.20
35	LQVPGSIQM	407	0.8000	9.20
36	MLRKFGLGQ	460	0.8000	9.20
37	VNKIVAASA	386	0.7000	8.05

38	IIKATVAPD	527	0.7000	8.05
39	VVDVGTRGA	73	0.6000	6.90
40	LRAVVQRDP	562	0.6000	6.90
41	LMLSQRVGP	446	0.5000	5.75
42	ITFAGIATA	612	0.5000	5.75
43	LAANVVGGI	249	0.4000	4.60
44	YWITFAGIA	610	0.4000	4.60
45	LRAQAAGQL	116	0.3600	4.14
46	VFRHRTGNA	84	0.3000	3.45
47	FRHRTGNAV	85	0.3000	3.45
48	FTIEARALT	147	0.3000	3.45
49	MLSQRVGPE	447	0.3000	3.45
50	LGLEDSLDA	265	0.2000	2.30
51	IVAASAVIE	389	0.2000	2.30
52	LPIGQGLSM	496	0.2000	2.30
53	MLRAVVQRD	561	0.2000	2.30
54	LMLVAATQL	97	0.1600	1.84
55	LKVTDVQPA	124	0.1000	1.15
56	LEEARKKTS	165	0.1000	1.15
57	VVLDAKTGE	340	0.1000	1.15
58	LQVSHAAGL	108	-0.0400	0
59	WDGHGLLGL	259	-0.0400	0
60	FYVQQQVQQ	319	-0.1000	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	YRNRHKAVH	297	3.3800	49.71
2	FVYLARAVD	212	3.3000	48.53
3	LVLMLVAAT	95	3.1000	45.59
4	VLMLVAATQ	96	3.0000	44.12
5	VRQMLRAVV	558	2.5000	36.76
6	YVQQQVQQA	320	1.7000	25.00
7	LFFLQVSHA	105	1.6000	23.53

8	FQPKRIRRQ	156	1.6000	23.53
9	IRVVSAQTA	547	0.9000	13.24
10	VVSAQTAQT	549	0.9000	13.24
11	FANLPIGQG	493	0.8000	11.76
12	ILVLMLVAA	94	0.7000	10.29
13	VQPAARGSI	129	0.7000	10.29
14	VNKIVAASA	386	0.7000	10.29
15	YDMLRKFGL	458	0.6000	8.82
16	LLQMTGMYQ	506	0.5000	7.35
17	ITFAGIATA	612	0.5000	7.35
18	FAGIATADN	614	0.5000	7.35
19	VVDVGTRGA	73	0.4000	5.88
20	FFLQVSHAA	106	0.4000	5.88
21	MGGVTVHDA	415	0.4000	5.88
22	VILVLMLVA	93	0.3000	4.41
23	FLQVSHAAG	107	0.3000	4.41
24	LRKFGLGQR	461	0.3000	4.41
25	YQMAGKTGT	586	0.3000	4.41
26	YWITFAGIA	610	0.3000	4.41
27	VFRHRTGNA	84	0.2000	2.94
28	FYVQQQVQQ	319	0.1000	1.47
29	MTGMYQAIA	509	-0.1000	0
30	VRVPPRIIK	521	-0.1000	0
31	FHNIAGWLM	650	-0.1000	0
32	MQRENVPLS	658	-0.1000	0
33	YYDMLRKFG	457	-0.2000	0
34	MLRKFGLGQ	460	-0.3000	0
35	FTIEARALT	147	-0.4000	0
36	IIKATVAPD	527	-0.4000	0
37	VVQRDPMGY	565	-0.4000	0
38	LVAATQLFF	99	-0.5000	0
39	FVFRHRTGN	83	-0.6000	0
40	LAANVVGGI	249	-0.6000	0
41	YTTTGVFGK	431	-0.6000	0

42	LRAVVQRDP	562	-0.6000	0
43	VSRAAPRRA	0	-0.7000	0
44	LRAQAAGQL	116	-0.7000	0
45	YVIGIMLDN	625	-0.7000	0
46	MLVAATQLF	98	-0.9000	0
47	LTFQPKRIR	154	-0.9000	0
48	LEEARKKTS	165	-0.9000	0
49	YLARAVDPA	214	-0.9000	0
50	VYWITFAGI	609	-0.9000	0
51	FRHRTGNAV	85	-1.0000	0
52	LQVSHAAGL	108	-1.0000	0
53	LMLSQRVGP	446	-1.0000	0
54	LQMTGMYQA	507	-1.0000	0
55	MLRAVVQRD	561	-1.0000	0
56	VLQVPGSIQ	406	-1.1000	0
57	MLSQRVGPE	447	-1.2000	0
58	WITFAGIAT	611	-1.2000	0
59	MLDNPARNS	630	-1.2000	0
60	VAASAVIEH	390	-1.2200	0
61	IQMGGVTVH	413	-1.2200	0
62	VLTLDNDIQ	310	-1.4000	0
63	VYLARAVDP	213	-1.5000	0
64	VGTLMLSQR	443	-1.5000	0
65	IMLDNPARN	629	-1.5000	0

ALLELE: DRB1_1311	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LVLMLVAAT	95	4.1000	49.40
2	VLMLVAATQ	96	4.0000	48.19
3	VRQMLRAVV	558	3.5000	42.17
4	VILVLMLVA	93	3.1000	37.35
5	LLQMTGMYQ	506	3.1000	37.35
6	LFFLQVSHA	105	2.6000	31.33

7	MLRKFGLGQ	460	2.5000	30.12
8	VRVPPRIIK	521	2.5000	30.12
9	YRNRHKAVH	297	2.3800	28.67
10	LVAATQLFF	99	2.3000	27.71
11	FVYLARAVD	212	2.3000	27.71
12	ILVLMLVAA	94	2.2000	26.51
13	VVQRDPMGY	565	2.2000	26.51
14	MGGVTVHDA	415	2.1000	25.30
15	MQRENVPLS	658	2.0500	24.70
16	IRVVSAQTA	547	2.0000	24.10
17	VVSAQTAQT	549	1.9000	22.89
18	VQPAARGSI	129	1.8000	21.69
19	VNKIVAASA	386	1.7000	20.48
20	VVDVGTRGA	73	1.6000	19.28
21	ITFAGIATA	612	1.5000	18.07
22	LRKFGLGQR	461	1.4000	16.87
23	VAASAVIEH	390	1.3800	16.63
24	VFRHRTGNA	84	1.3000	15.66
25	LGLEDSLDA	265	1.2000	14.46
26	LKVTDVQPA	124	1.1000	13.25
27	VQQAKNLSG	325	1.1000	13.25
28	MTGMYQAIA	509	0.9000	10.84
29	IQMGGVTVH	413	0.8800	10.60
30	FQPKRIRRQ	156	0.8000	9.64
31	YVQQQVQQA	320	0.8000	9.64
32	VSHAAGLRA	110	0.7000	8.43
33	LEEARKKTS	165	0.7000	8.43
34	LQMTGMYQA	507	0.7000	8.43
35	IIKATVAPD	527	0.6000	7.23
36	LRAVVQRDP	562	0.6000	7.23
37	VSRAAPRRA	0	0.5000	6.02
38	LAANVVGGI	249	0.5000	6.02
39	LMLSQRVGP	446	0.5000	6.02
40	VGQRKRPGK	29	0.4500	5.42

41	LRAQAAGQL	116	0.4000	4.82
42	YQMAGKTGT	586	0.4000	4.82
43	LTFQPKRIR	154	0.3000	3.61
44	LQVPGSIQM	407	0.3000	3.61
45	LMLVAATQL	97	0.2000	2.41
46	MLVAATQLF	98	0.2000	2.41
47	LRDIAQEVA	182	0.2000	2.41
48	FFLQVSHAA	106	0.1000	1.20
49	YDMLRKFGL	458	0.1000	1.20
50	MLRAVVQRD	561	0.1000	1.20
51	VYWITFAGI	609	0.1000	1.20
52	YVIGIMLDN	625	0.1000	1.20
53	VLQVPGSIQ	406	-0.1000	0
54	MLSQRVGPE	447	-0.1000	0
55	FANLPIGQG	493	-0.1000	0
56	IVAASAVIE	389	-0.2000	0
57	VHGSTVVLT	304	-0.3000	0
58	VVLDAKTGE	340	-0.3000	0
59	LPIGQGLSM	496	-0.3000	0
60	FHNIAGWLM	650	-0.3000	0
61	FYVQQQVQQ	319	-0.4000	0
62	IGIMLDNPA	627	-0.4000	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	FVYLARAVD	212	6.0000	67.42
2	YRNRHKAVH	297	4.6000	51.69
3	LVLMLVAAT	95	4.0000	44.94
4	VLMLVAATQ	96	3.8000	42.70
5	YVIGIMLDN	625	3.1000	34.83
6	LLQMTGMYQ	506	2.9000	32.58
7	VRQMLRAVV	558	2.8000	31.46
8	FQPKRIRRQ	156	2.6000	29.21

9	FVFRHRTGN	83	2.5000	28.09
10	FAGIATADN	614	2.5000	28.09
11	MLRKFGLGQ	460	2.3000	25.84
12	IIKATVAPD	527	2.3000	25.84
13	VVQRDPMGY	565	2.3000	25.84
14	YQMAGKTGT	586	2.3000	25.84
15	LVAATQLFF	99	2.2000	24.72
16	FANLPIGQG	493	2.2000	24.72
17	VILVLMLVA	93	2.1000	23.60
18	YDMLRKFGL	458	2.1000	23.60
19	MLSQRVGPE	447	1.9000	21.35
20	YVQQQVQQA	320	1.8000	20.22
21	IVAASAVIE	389	1.8000	20.22
22	VVSAQTAQT	549	1.8000	20.22
23	MLRAVVQRD	561	1.8000	20.22
24	FHNIAGWLM	650	1.8000	20.22
25	VVLDAKTGE	340	1.7000	19.10
26	YYDMLRKFG	457	1.7000	19.10
27	LFFLQVSHA	105	1.6000	17.98
28	FLQVSHAAG	107	1.6000	17.98
29	VAASAVIEH	390	1.6000	17.98
30	FYVQQQVQQ	319	1.4000	15.73
31	VQQAKNLSG	325	1.4000	15.73
32	WITFAGIAT	611	1.3000	14.61
33	ILVLMLVAA	94	1.2000	13.48
34	FFLQVSHAA	106	1.1000	12.36
35	IQMGGVTVH	413	1.1000	12.36
36	MGGVTVHDA	415	1.1000	12.36
37	MQRENVPLS	658	1.0500	11.80
38	VQPAARGSI	129	1.0000	11.24
39	VVIPGSYRN	291	1.0000	11.24
40	IRVVSAQTA	547	1.0000	11.24
41	LRRPPGAQE	20	0.8000	8.99
42	VRVPPRIIK	521	0.8000	8.99

43	VNKIVAASA	386	0.7000	7.87
44	VVDVGTRGA	73	0.6000	6.74
45	FTIEARALT	147	0.5000	5.62
46	ITFAGIATA	612	0.5000	5.62
47	IMLDNPARN	629	0.5000	5.62
48	LRAQAAGQL	116	0.4000	4.49
49	LQVPGSIQM	407	0.4000	4.49
50	LRKFGLGQR	461	0.4000	4.49
51	YWITFAGIA	610	0.4000	4.49
52	VFRHRTGNA	84	0.3000	3.37
53	LMLVAATQL	97	0.2000	2.25
54	LGLEDSLDA	265	0.2000	2.25
55	MLVAATQLF	98	0.1000	1.12
56	LKVTDVQPA	124	0.1000	1.12
57	LMLSQRVGP	446	-0.1000	0
58	MTGMYQAIA	509	-0.1000	0
59	VTVHDAWEH	418	-0.2000	0
60	LPIGQGLSM	496	-0.2000	0
61	IKATVAPDG	528	-0.2500	0
62	VSHAAGLRA	110	-0.3000	0
63	LEEARKKTS	165	-0.3000	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	LVLMLVAAT	95	3.9000	46.43
2	FQPKRIRRQ	156	3.7000	44.05
3	VLMLVAATQ	96	3.3000	39.29
4	VRQMLRAVV	558	3.3000	39.29
5	YRNRHKAVH	297	3.2800	39.05
6	LTFQPKRIR	154	2.9000	34.52
7	MLRKFGLGQ	460	2.7000	32.14
8	YVQQQVQQA	320	2.5000	29.76
9	VTVHDAWEH	418	2.4800	29.52

10	VFRHRTGNA	84	2.3000	27.38
11	LFFLQVSHA	105	2.3000	27.38
12	MQRENVPLS	658	2.2000	26.19
13	VSRAAPRRA	0	2.1000	25.00
14	ILVLMLVAA	94	2.0000	23.81
15	VVDVGTRGA	73	1.9000	22.62
16	VVSAQTAQT	549	1.9000	22.62
17	VVQRDPMGY	565	1.8000	21.43
18	MLDNPARNS	630	1.7000	20.24
19	FFLQVSHAA	106	1.6000	19.05
20	FVYLARAVD	212	1.6000	19.05
21	LLQMTGMYQ	506	1.6000	19.05
22	ITFAGIATA	612	1.5000	17.86
23	IQMGGVTVH	413	1.4800	17.62
24	VRVPPRIIK	521	1.4000	16.67
25	IRVVSAQTA	547	1.4000	16.67
26	LKVTDVQPA	124	1.3000	15.48
27	MGGVTVHDA	415	1.3000	15.48
28	LVAATQLFF	99	1.2000	14.29
29	FYVQQQVQQ	319	1.1000	13.10
30	LMLSQRVGP	446	1.1000	13.10
31	IQFYVQQQV	317	1.0000	11.90
32	VMPYTTTGV	428	1.0000	11.90
33	VGQRKRPGK	29	0.9000	10.71
34	MLVAATQLF	98	0.9000	10.71
35	LEEARKKTS	165	0.9000	10.71
36	LRAVVQRDP	562	0.9000	10.71
37	FVFRHRTGN	83	0.8000	9.52
38	VQQQVQQAK	321	0.8000	9.52
39	VFGKSSNVG	436	0.8000	9.52
40	MLRAVVQRD	561	0.8000	9.52
41	YQMAGKTGT	586	0.8000	9.52
42	VILVLMLVA	93	0.7000	8.33
43	VQPAARGSI	129	0.7000	8.33

44	LGLEDSLDA	265	0.7000	8.33
45	LRKFGLGQR	461	0.7000	8.33
46	MTGMYQAIA	509	0.7000	8.33
47	IIKATVAPD	527	0.6000	7.14
48	VYLARAVDP	213	0.5000	5.95
49	IGIMLDNPA	627	0.5000	5.95
50	LQSDETFVY	206	0.4000	4.76
51	VVIPGSYRN	291	0.4000	4.76
52	VVLDAKTGE	340	0.4000	4.76
53	YDMLRKFGL	458	0.4000	4.76
54	LQMTGMYQA	507	0.4000	4.76
55	FRHRTGNAV	85	0.3000	3.57
56	LRAQAAGQL	116	0.3000	3.57
57	VHGSTVVLT	304	0.3000	3.57
58	IVAASAVIE	389	0.3000	3.57
59	IPGSYRNRH	293	0.2800	3.33
60	VNKIVAASA	386	0.2000	2.38
61	IANDGVRVP	516	0.2000	2.38
62	VAASAVIEH	390	0.1800	2.14
63	LQVSHAAGL	108	0.1000	1.19
64	IEARALTFQ	149	0.1000	1.19
65	IRRQLEEAR	161	0.1000	1.19

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	FQPKRIRRQ	156	4.7000	55.95
2	YRNRHKAVH	297	4.2800	50.95
3	YVQQQVQQA	320	3.5000	41.67
4	LVLMLVAAT	95	2.9000	34.52
5	FFLQVSHAA	106	2.6000	30.95
6	FVYLARAVD	212	2.6000	30.95
7	VLMLVAATQ	96	2.3000	27.38
8	VRQMLRAVV	558	2.3000	27.38

9	FYVQQQVQQ	319	2.1000	25.00
10	LTFQPKRIR	154	1.9000	22.62
11	FVFRHRTGN	83	1.8000	21.43
12	YQMAGKTGT	586	1.8000	21.43
13	MLRKFGLGQ	460	1.7000	20.24
14	VTVHDAWEH	418	1.4800	17.62
15	YDMLRKFGL	458	1.4000	16.67
16	VFRHRTGNA	84	1.3000	15.48
17	FRHRTGNAV	85	1.3000	15.48
18	LFFLQVSHA	105	1.3000	15.48
19	MQRENVPLS	658	1.2000	14.29
20	VSRAAPRRA	0	1.1000	13.10
21	ILVLMLVAA	94	1.0000	11.90
22	VVDVGTRGA	73	0.9000	10.71
23	YLARAVDPA	214	0.9000	10.71
24	VVSAQTAQT	549	0.9000	10.71
25	VVQRDPMGY	565	0.8000	9.52
26	MLDNPARNS	630	0.7000	8.33
27	LLQMTGMYQ	506	0.6000	7.14
28	ITFAGIATA	612	0.5000	5.95
29	IQMGGVTVH	413	0.4800	5.71
30	YTTTGVFGK	431	0.4000	4.76
31	YYDMLRKFG	457	0.4000	4.76
32	VRVPPRIIK	521	0.4000	4.76
33	IRVVSAQTA	547	0.4000	4.76
34	WLMQRENVP	656	0.4000	4.76
35	LKVTDVQPA	124	0.3000	3.57
36	MGGVTVHDA	415	0.3000	3.57
37	LVAATQLFF	99	0.2000	2.38
38	FTIEARALT	147	0.2000	2.38
39	YVIGIMLDN	625	0.2000	2.38
40	LMLSQRVGP	446	0.1000	1.19
41	VGQRKRPGK	29	-0.1000	0
42	MLVAATQLF	98	-0.1000	0

43	LEEARKKTS	165	-0.1000	0
44	FEPGSVNKI	381	-0.1000	0
45	LRAVVQRDP	562	-0.1000	0
46	VQQQVQQAK	321	-0.2000	0
47	VFGKSSNVG	436	-0.2000	0
48	MLRAVVQRD	561	-0.2000	0
49	VILVLMLVA	93	-0.3000	0
50	VQPAARGSI	129	-0.3000	0
51	LGLEDSLDA	265	-0.3000	0
52	LRKFGLGQR	461	-0.3000	0
53	MTGMYQAIA	509	-0.3000	0
54	IIKATVAPD	527	-0.4000	0
55	VYLARAVDP	213	-0.5000	0
56	WITFAGIAT	611	-0.5000	0
57	IGIMLDNPA	627	-0.5000	0
58	LQSDETFVY	206	-0.6000	0
59	VVIPGSYRN	291	-0.6000	0
60	VVLDAKTGE	340	-0.6000	0
61	FGLGQRTGV	464	-0.6000	0
62	LQMTGMYQA	507	-0.6000	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	LVLMLVAAT	95	4.6000	52.27
2	LTFQPKRIR	154	4.4000	50.00
3	VRQMLRAVV	558	4.3000	48.86
4	LVAATQLFF	99	3.1000	35.23
5	VVQRDPMGY	565	3.1000	35.23
6	FQPKRIRRQ	156	3.0000	34.09
7	MLVAATQLF	98	2.8000	31.82
8	FVYLARAVD	212	2.7000	30.68
9	YRNRHKAVH	297	2.7000	30.68
10	VLMLVAATQ	96	2.6000	29.55

11	VVSAQTAQT	549	2.6000	29.55
12	MQRENVPLS	658	2.6000	29.55
13	YVQQQVQQA	320	2.5000	28.41
14	VFRHRTGNA	84	2.3000	26.14
15	LFFLQVSHA	105	2.3000	26.14
16	VFGKSSNVG	436	2.2000	25.00
17	LRKFGLGQR	461	2.2000	25.00
18	VSRAAPRRA	0	2.1000	23.86
19	LMLSQRVGP	446	2.1000	23.86
20	MLDNPARNS	630	2.1000	23.86
21	ILVLMLVAA	94	2.0000	22.73
22	IQFYVQQQV	317	2.0000	22.73
23	VMPYTTTGV	428	2.0000	22.73
24	MLRKFGLGQ	460	2.0000	22.73
25	VVDVGTRGA	73	1.9000	21.59
26	VTVHDAWEH	418	1.9000	21.59
27	MLRAVVQRD	561	1.9000	21.59
28	LRAVVQRDP	562	1.9000	21.59
29	VVLDAKTGE	340	1.8000	20.45
30	LQSDETFVY	206	1.7000	19.32
31	IVAASAVIE	389	1.7000	19.32
32	IIKATVAPD	527	1.7000	19.32
33	FVFRHRTGN	83	1.6000	18.18
34	FFLQVSHAA	106	1.6000	18.18
35	VQPAARGSI	129	1.6000	18.18
36	IRRQLEEAR	161	1.6000	18.18
37	VYLARAVDP	213	1.5000	17.05
38	VRVPPRIIK	521	1.5000	17.05
39	YQMAGKTGT	586	1.5000	17.05
40	ITFAGIATA	612	1.5000	17.05
41	VQQAKNLSG	325	1.4000	15.91
42	MYQAIANDG	512	1.4000	15.91
43	IRVVSAQTA	547	1.4000	15.91
44	YDMLRKFGL	458	1.3600	15.45

45	FRHRTGNAV	85	1.3000	14.77
46	LKVTDVQPA	124	1.3000	14.77
47	LEEARKKTS	165	1.3000	14.77
48	MGGVTVHDA	415	1.3000	14.77
49	LRAQAAGQL	116	1.2600	14.32
50	VVIPGSYRN	291	1.2000	13.64
51	MLSQRVGPE	447	1.2000	13.64
52	IANDGVRVP	516	1.2000	13.64
53	LQVSHAAGL	108	1.0600	12.05
54	VGQRKRPGK	29	1.0000	11.36
55	VHGSTVVLT	304	1.0000	11.36
56	VAPAGRSTR	58	0.9000	10.23
57	VQQQVQQAK	321	0.9000	10.23
58	IQMGGVTVH	413	0.9000	10.23
59	LLQMTGMYQ	506	0.9000	10.23
60	YYDMLRKFG	457	0.8000	9.09
61	VILVLMLVA	93	0.7000	7.95
62	ICAKYPEVG	227	0.7000	7.95
63	LGLEDSLDA	265	0.7000	7.95
64	LQVPGSIQM	407	0.7000	7.95
65	VGTLMLSQR	443	0.7000	7.95
66	MTLLQMTGM	504	0.7000	7.95
67	MTGMYQAIA	509	0.7000	7.95

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVLMLVAAT	95	4.6000	52.27
2	LTFQPKRIR	154	4.4000	50.00
3	VRQMLRAVV	558	4.3000	48.86
4	LVAATQLFF	99	3.1000	35.23
5	VVQRDPMGY	565	3.1000	35.23
6	FQPKRIRRQ	156	3.0000	34.09
7	MLVAATQLF	98	2.8000	31.82

8	FVYLARAVD	212	2.7000	30.68
9	YRNRHKAVH	297	2.7000	30.68
10	VLMLVAATQ	96	2.6000	29.55
11	VVSAQTAQT	549	2.6000	29.55
12	MQRENVPLS	658	2.6000	29.55
13	YVQQQVQQA	320	2.5000	28.41
14	VFRHRTGNA	84	2.3000	26.14
15	LFFLQVSHA	105	2.3000	26.14
16	VFGKSSNVG	436	2.2000	25.00
17	LRKFGLGQR	461	2.2000	25.00
18	VSRAAPRRA	0	2.1000	23.86
19	LMLSQRVGP	446	2.1000	23.86
20	MLDNPARNS	630	2.1000	23.86
21	ILVLMLVAA	94	2.0000	22.73
22	IQFYVQQQV	317	2.0000	22.73
23	VMPYTTTGV	428	2.0000	22.73
24	MLRKFGLGQ	460	2.0000	22.73
25	VVDVGTRGA	73	1.9000	21.59
26	VTVHDAWEH	418	1.9000	21.59
27	MLRAVVQRD	561	1.9000	21.59
28	LRAVVQRDP	562	1.9000	21.59
29	VVLDAKTGE	340	1.8000	20.45
30	LQSDETFVY	206	1.7000	19.32
31	IVAASAVIE	389	1.7000	19.32
32	IIKATVAPD	527	1.7000	19.32
33	FVFRHRTGN	83	1.6000	18.18
34	FFLQVSHAA	106	1.6000	18.18
35	VQPAARGSI	129	1.6000	18.18
36	IRRQLEEAR	161	1.6000	18.18
37	VYLARAVDP	213	1.5000	17.05
38	VRVPPRIIK	521	1.5000	17.05
39	YQMAGKTGT	586	1.5000	17.05
40	ITFAGIATA	612	1.5000	17.05
41	VQQAKNLSG	325	1.4000	15.91

42	MYQAIANDG	512	1.4000	15.91
43	IRVVSAQTA	547	1.4000	15.91
44	YDMLRKFGL	458	1.3600	15.45
45	FRHRTGNAV	85	1.3000	14.77
46	LKVTDVQPA	124	1.3000	14.77
47	LEEARKKTS	165	1.3000	14.77
48	MGGVTVHDA	415	1.3000	14.77
49	LRAQAAGQL	116	1.2600	14.32
50	VVIPGSYRN	291	1.2000	13.64
51	MLSQRVGPE	447	1.2000	13.64
52	IANDGVRVP	516	1.2000	13.64
53	LQVSHAAGL	108	1.0600	12.05
54	VGQRKRPGK	29	1.0000	11.36
55	VHGSTVVLT	304	1.0000	11.36
56	VAPAGRSTR	58	0.9000	10.23
57	VQQQVQQAK	321	0.9000	10.23
58	IQMGGVTVH	413	0.9000	10.23
59	LLQMTGMYQ	506	0.9000	10.23
60	YYDMLRKFG	457	0.8000	9.09
61	VILVLMLVA	93	0.7000	7.95
62	ICAKYPEVG	227	0.7000	7.95
63	LGLEDSLDA	265	0.7000	7.95
64	LQVPGSIQM	407	0.7000	7.95
65	VGTLMLSQR	443	0.7000	7.95
66	MTLLQMTGM	504	0.7000	7.95
67	MTGMYQAIA	509	0.7000	7.95

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRQYPGGSL	241	5.7000	58.16
2	VRQMLRAVV	558	4.5000	45.92
3	VMPYTTTGV	428	4.3600	44.49
4	VILVLMLVA	93	4.3000	43.88

5	WITFAGIAT	611	4.3000	43.88
6	VVLTLDNDI	309	3.8000	38.78
7	LRKFGLGQR	461	3.8000	38.78
8	IQFYVQQQV	317	3.7000	37.76
9	LVLMLVAAT	95	3.6000	36.73
10	LQVPGSIQM	407	3.5800	36.53
11	LPIGQGLSM	496	3.4800	35.51
12	LGLEDSLDA	265	3.4000	34.69
13	VVIPGSYRN	291	3.4000	34.69
14	YVIGIMLDN	625	3.4000	34.69
15	IGQGLSMTL	498	3.3000	33.67
16	IGIMLDNPA	627	3.3000	33.67
17	VQPAARGSI	129	3.2000	32.65
18	VRVPPRIIK	521	3.2000	32.65
19	FRHRTGNAV	85	3.1000	31.63
20	LQMTGMYQA	507	3.1000	31.63
21	LMLVAATQL	97	3.0000	30.61
22	VQQAKNLSG	325	3.0000	30.61
23	VVQRDPMGY	565	2.9000	29.59
24	LVAATQLFF	99	2.8000	28.57
25	LMQRENVPL	657	2.8000	28.57
26	LLQMTGMYQ	506	2.6000	26.53
27	IRVVSAQTA	547	2.6000	26.53
28	VFRHRTGNA	84	2.5600	26.12
29	ILVLMLVAA	94	2.5000	25.51
30	VSHAAGLRA	110	2.3000	23.47
31	FVFRHRTGN	83	2.1000	21.43
32	LFFLQVSHA	105	2.1000	21.43
33	FHNIAGWLM	650	2.0800	21.22
34	VVSAQTAQT	549	2.0600	21.02
35	LMLSQRVGP	446	2.0000	20.41
36	FGLGQRTGV	464	2.0000	20.41
37	LGQRTGVGL	466	2.0000	20.41
38	LQVSHAAGL	108	1.9000	19.39

39	LRAQAAGQL	116	1.9000	19.39
40	VYWITFAGI	609	1.9000	19.39
41	MTLLQMTGM	504	1.8800	19.18
42	VAATQLFFL	100	1.8000	18.37
43	VLAMANDNT	349	1.8000	18.37
44	MLRKFGLGQ	460	1.8000	18.37
45	VVGGIDWDG	253	1.7000	17.35
46	WDGHGLLGL	259	1.6000	16.33
47	IVDRNNDRL	137	1.5000	15.31
48	FVYLARAVD	212	1.5000	15.31
49	LQSDETFVY	206	1.4600	14.90
50	VNKIVAASA	386	1.4000	14.29
51	IQMGGVTVH	413	1.4000	14.29
52	VGPERYYDM	452	1.3800	14.08
53	VGTRGASFV	76	1.3000	13.27
54	VLMLVAATQ	96	1.3000	13.27
55	LKKLQSDET	203	1.3000	13.27
56	LTLDNDIQF	311	1.3000	13.27
57	LAMANDNTF	350	1.3000	13.27
58	YQMAGKTGT	586	1.3000	13.27
59	LFHNIAGWL	649	1.3000	13.27
60	LRRPPGAQE	20	1.2000	12.24
61	FFLQVSHAA	106	1.2000	12.24
62	MGGVTVHDA	415	1.2000	12.24
63	YDMLRKFGL	458	1.2000	12.24
64	INPGCGCYF	598	1.2000	12.24
65	VYLARAVDP	213	1.1000	11.22
66	VTVHDAWEH	418	1.1000	11.22
67	LVPPIDQWS	481	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	WITFAGIAT	611	5.3000	54.08

2	LRQYPGGSL	241	4.7000	47.96
3	YVIGIMLDN	625	4.4000	44.90
4	FRHRTGNAV	85	4.1000	41.84
5	VRQMLRAVV	558	3.5000	35.71
6	VMPYTTTGV	428	3.3600	34.29
7	VILVLMLVA	93	3.3000	33.67
8	FVFRHRTGN	83	3.1000	31.63
9	FHNIAGWLM	650	3.0800	31.43
10	FGLGQRTGV	464	3.0000	30.61
11	VVLTLDNDI	309	2.8000	28.57
12	LRKFGLGQR	461	2.8000	28.57
13	IQFYVQQQV	317	2.7000	27.55
14	LVLMLVAAT	95	2.6000	26.53
15	WDGHGLLGL	259	2.6000	26.53
16	LQVPGSIQM	407	2.5800	26.33
17	FVYLARAVD	212	2.5000	25.51
18	LPIGQGLSM	496	2.4800	25.31
19	LGLEDSLDA	265	2.4000	24.49
20	VVIPGSYRN	291	2.4000	24.49
21	IGQGLSMTL	498	2.3000	23.47
22	YQMAGKTGT	586	2.3000	23.47
23	IGIMLDNPA	627	2.3000	23.47
24	FFLQVSHAA	106	2.2000	22.45
25	VQPAARGSI	129	2.2000	22.45
26	YDMLRKFGL	458	2.2000	22.45
27	VRVPPRIIK	521	2.2000	22.45
28	LQMTGMYQA	507	2.1000	21.43
29	YQAIANDGV	513	2.1000	21.43
30	LMLVAATQL	97	2.0000	20.41
31	VQQAKNLSG	325	2.0000	20.41
32	YQQGTGPTA	573	2.0000	20.41
33	VVQRDPMGY	565	1.9000	19.39
34	LVAATQLFF	99	1.8000	18.37
35	LMQRENVPL	657	1.8000	18.37

36	FTIEARALT	147	1.7000	17.35
37	LLQMTGMYQ	506	1.6000	16.33
38	IRVVSAQTA	547	1.6000	16.33
39	VFRHRTGNA	84	1.5600	15.92
40	ILVLMLVAA	94	1.5000	15.31
41	YRNRHKAVH	297	1.5000	15.31
42	FEPGSVNKI	381	1.5000	15.31
43	VSHAAGLRA	110	1.3000	13.27
44	LFFLQVSHA	105	1.1000	11.22
45	YWITFAGIA	610	1.1000	11.22
46	VVSAQTAQT	549	1.0600	10.82
47	FGKSSNVGT	437	1.0000	10.20
48	LMLSQRVGP	446	1.0000	10.20
49	LGQRTGVGL	466	1.0000	10.20
50	LQVSHAAGL	108	0.9000	9.18
51	LRAQAAGQL	116	0.9000	9.18
52	VYWITFAGI	609	0.9000	9.18
53	MTLLQMTGM	504	0.8800	8.98
54	VAATQLFFL	100	0.8000	8.16
55	VLAMANDNT	349	0.8000	8.16
56	MLRKFGLGQ	460	0.8000	8.16
57	VVGGIDWDG	253	0.7000	7.14
58	YVQQQVQQA	320	0.7000	7.14
59	IVDRNNDRL	137	0.5000	5.10
60	WEHGVMPYT	424	0.5000	5.10
61	YYDMLRKFG	457	0.5000	5.10
62	LQSDETFVY	206	0.4600	4.69
63	VNKIVAASA	386	0.4000	4.08
64	IQMGGVTVH	413	0.4000	4.08
65	VGPERYYDM	452	0.3800	3.88
66	VGTRGASFV	76	0.3000	3.06
67	VLMLVAATQ	96	0.3000	3.06

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	LRQYPGGSL	241	5.7000	58.16
2	VRQMLRAVV	558	4.5000	45.92
3	VMPYTTTGV	428	4.3600	44.49
4	VILVLMLVA	93	4.3000	43.88
5	WITFAGIAT	611	4.3000	43.88
6	VVLTLDNDI	309	3.8000	38.78
7	LRKFGLGQR	461	3.8000	38.78
8	IQFYVQQQV	317	3.7000	37.76
9	LVLMLVAAT	95	3.6000	36.73
10	LQVPGSIQM	407	3.5800	36.53
11	LPIGQGLSM	496	3.4800	35.51
12	LGLEDSLDA	265	3.4000	34.69
13	VVIPGSYRN	291	3.4000	34.69
14	YVIGIMLDN	625	3.4000	34.69
15	IGQGLSMTL	498	3.3000	33.67
16	IGIMLDNPA	627	3.3000	33.67
17	VQPAARGSI	129	3.2000	32.65
18	VRVPPRIIK	521	3.2000	32.65
19	FRHRTGNAV	85	3.1000	31.63
20	LQMTGMYQA	507	3.1000	31.63
21	LMLVAATQL	97	3.0000	30.61
22	VQQAKNLSG	325	3.0000	30.61
23	VVQRDPMGY	565	2.9000	29.59
24	LVAATQLFF	99	2.8000	28.57
25	LMQRENVPL	657	2.8000	28.57
26	LLQMTGMYQ	506	2.6000	26.53
27	IRVVSAQTA	547	2.6000	26.53
28	VFRHRTGNA	84	2.5600	26.12
29	ILVLMLVAA	94	2.5000	25.51
30	VSHAAGLRA	110	2.3000	23.47
31	FVFRHRTGN	83	2.1000	21.43
32	LFFLQVSHA	105	2.1000	21.43

33	FHNIAGWLM	650	2.0800	21.22
34	VVSAQTAQT	549	2.0600	21.02
35	LMLSQRVGP	446	2.0000	20.41
36	FGLGQRTGV	464	2.0000	20.41
37	LGQRTGVGL	466	2.0000	20.41
38	LQVSHAAGL	108	1.9000	19.39
39	LRAQAAGQL	116	1.9000	19.39
40	VYWITFAGI	609	1.9000	19.39
41	MTLLQMTGM	504	1.8800	19.18
42	VAATQLFFL	100	1.8000	18.37
43	VLAMANDNT	349	1.8000	18.37
44	MLRKFGLGQ	460	1.8000	18.37
45	VVGGIDWDG	253	1.7000	17.35
46	WDGHGLLGL	259	1.6000	16.33
47	IVDRNNDRL	137	1.5000	15.31
48	FVYLARAVD	212	1.5000	15.31
49	LQSDETFVY	206	1.4600	14.90
50	VNKIVAASA	386	1.4000	14.29
51	IQMGGVTVH	413	1.4000	14.29
52	VGPERYYDM	452	1.3800	14.08
53	VGTRGASFV	76	1.3000	13.27
54	VLMLVAATQ	96	1.3000	13.27
55	LKKLQSDET	203	1.3000	13.27
56	LTLDNDIQF	311	1.3000	13.27
57	LAMANDNTF	350	1.3000	13.27
58	YQMAGKTGT	586	1.3000	13.27
59	LFHNIAGWL	649	1.3000	13.27
60	LRRPPGAQE	20	1.2000	12.24
61	FFLQVSHAA	106	1.2000	12.24
62	MGGVTVHDA	415	1.2000	12.24
63	YDMLRKFGL	458	1.2000	12.24
64	INPGCGCYF	598	1.2000	12.24
65	VYLARAVDP	213	1.1000	11.22
66	VTVHDAWEH	418	1.1000	11.22

67	LVPPIDQWS	481	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	LMLVAATQL	97	3.8000	38.78
2	IRVVSAQTA	547	3.5000	35.71
3	YTTTGVFGK	431	3.2000	32.65
4	FHNIAGWLM	650	3.2000	32.65
5	VRVPPRIIK	521	2.8000	28.57
6	VLMLVAATQ	96	2.7000	27.55
7	LRKFGLGQR	461	2.7000	27.55
8	LLQMTGMYQ	506	2.5000	25.51
9	LRAQAAGQL	116	2.4000	24.49
10	LVLMLVAAT	95	2.3000	23.47
11	YWITFAGIA	610	2.3000	23.47
12	LRQYPGGSL	241	2.2000	22.45
13	VVLTLDNDI	309	2.1000	21.43
14	YDMLRKFGL	458	2.0000	20.41
15	FFLQVSHAA	106	1.8000	18.37
16	VVIPGSYRN	291	1.8000	18.37
17	MLVAATQLF	98	1.6000	16.33
18	VIPGSYRNR	292	1.6000	16.33
19	LQMTGMYQA	507	1.6000	16.33
20	LVAATQLFF	99	1.5000	15.31
21	LQVSHAAGL	108	1.5000	15.31
22	VTDVQPAAR	126	1.5000	15.31
23	VQQQVQQAK	321	1.5000	15.31
24	VVDVGTRGA	73	1.4000	14.29
25	LTFQPKRIR	154	1.4000	14.29
26	VGTLMLSQR	443	1.4000	14.29
27	VRQMLRAVV	558	1.4000	14.29
28	LRAVVQRDP	562	1.4000	14.29
29	VILVLMLVA	93	1.3000	13.27

30	FLQVSHAAG	107	1.3000	13.27
31	VLQVPGSIQ	406	1.3000	13.27
32	YYDMLRKFG	457	1.3000	13.27
33	VVQRDPMGY	565	1.3000	13.27
34	YQMAGKTGT	586	1.2000	12.24
35	WITFAGIAT	611	1.2000	12.24
36	IGIMLDNPA	627	1.2000	12.24
37	VAATQLFFL	100	1.1000	11.22
38	VNKIVAASA	386	1.1000	11.22
39	YVIGIMLDN	625	1.1000	11.22
40	VQPAARGSI	129	1.0000	10.20
41	VSRAAPRRA	0	0.9000	9.18
42	IRRQLEEAR	161	0.8000	8.16
43	YVQQQVQQA	320	0.8000	8.16
44	MYQAIANDG	512	0.8000	8.16
45	FRHRTGNAV	85	0.7000	7.14
46	FVYLARAVD	212	0.7000	7.14
47	MGGVTVHDA	415	0.7000	7.14
48	FANLPIGQG	493	0.7000	7.14
49	VYWITFAGI	609	0.7000	7.14
50	FAGIATADN	614	0.7000	7.14
51	MPYTTTGVF	429	0.6000	6.12
52	LQSDETFVY	206	0.5000	5.10
53	VASAICAKY	223	0.5000	5.10
54	YRNRHKAVH	297	0.5000	5.10
55	FQPKRIRRQ	156	0.4000	4.08
56	LQVPGSIQM	407	0.4000	4.08
57	VAPAGRSTR	58	0.3000	3.06
58	LKVTDVQPA	124	0.3000	3.06
59	VVSAQTAQT	549	0.3000	3.06
60	FVFRHRTGN	83	0.2000	2.04
61	FDPSQDIGR	358	0.2000	2.04
62	IVAASAVIE	389	0.2000	2.04
63	IKATVAPDG	528	0.2000	2.04

64	LFHNIAGWL	649	0.2000	2.04
65	LAMANDNTF	350	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	LMLVAATQL	97	3.8000	38.78
2	IRVVSAQTA	547	3.5000	35.71
3	YTTTGVFGK	431	3.2000	32.65
4	FHNIAGWLM	650	3.2000	32.65
5	VRVPPRIIK	521	2.8000	28.57
6	VLMLVAATQ	96	2.7000	27.55
7	LRKFGLGQR	461	2.7000	27.55
8	LLQMTGMYQ	506	2.5000	25.51
9	LRAQAAGQL	116	2.4000	24.49
10	LVLMLVAAT	95	2.3000	23.47
11	YWITFAGIA	610	2.3000	23.47
12	LRQYPGGSL	241	2.2000	22.45
13	VVLTLDNDI	309	2.1000	21.43
14	YDMLRKFGL	458	2.0000	20.41
15	FFLQVSHAA	106	1.8000	18.37
16	VVIPGSYRN	291	1.8000	18.37
17	MLVAATQLF	98	1.6000	16.33
18	VIPGSYRNR	292	1.6000	16.33
19	LQMTGMYQA	507	1.6000	16.33
20	LVAATQLFF	99	1.5000	15.31
21	LQVSHAAGL	108	1.5000	15.31
22	VTDVQPAAR	126	1.5000	15.31
23	VQQQVQQAK	321	1.5000	15.31
24	VVDVGTRGA	73	1.4000	14.29
25	LTFQPKRIR	154	1.4000	14.29
26	VGTLMLSQR	443	1.4000	14.29
27	VRQMLRAVV	558	1.4000	14.29
28	LRAVVQRDP	562	1.4000	14.29

29	VILVLMLVA	93	1.3000	13.27
30	FLQVSHAAG	107	1.3000	13.27
31	VLQVPGSIQ	406	1.3000	13.27
32	YYDMLRKFG	457	1.3000	13.27
33	VVQRDPMGY	565	1.3000	13.27
34	YQMAGKTGT	586	1.2000	12.24
35	WITFAGIAT	611	1.2000	12.24
36	IGIMLDNPA	627	1.2000	12.24
37	VAATQLFFL	100	1.1000	11.22
38	VNKIVAASA	386	1.1000	11.22
39	YVIGIMLDN	625	1.1000	11.22
40	VQPAARGSI	129	1.0000	10.20
41	VSRAAPRRA	0	0.9000	9.18
42	IRRQLEEAR	161	0.8000	8.16
43	YVQQQVQQA	320	0.8000	8.16
44	MYQAIANDG	512	0.8000	8.16
45	FRHRTGNAV	85	0.7000	7.14
46	FVYLARAVD	212	0.7000	7.14
47	MGGVTVHDA	415	0.7000	7.14
48	FANLPIGQG	493	0.7000	7.14
49	VYWITFAGI	609	0.7000	7.14
50	FAGIATADN	614	0.7000	7.14
51	MPYTTTGVF	429	0.6000	6.12
52	LQSDETFVY	206	0.5000	5.10
53	VASAICAKY	223	0.5000	5.10
54	YRNRHKAVH	297	0.5000	5.10
55	FQPKRIRRQ	156	0.4000	4.08
56	LQVPGSIQM	407	0.4000	4.08
57	VAPAGRSTR	58	0.3000	3.06
58	LKVTDVQPA	124	0.3000	3.06
59	VVSAQTAQT	549	0.3000	3.06
60	FVFRHRTGN	83	0.2000	2.04
61	FDPSQDIGR	358	0.2000	2.04
62	IVAASAVIE	389	0.2000	2.04

63	IKATVAPDG	528	0.2000	2.04
64	LFHNIAGWL	649	0.2000	2.04
65	LAMANDNTF	350	0.1000	1.02