MHC Class-II Binding Peptide Prediction Results

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INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sat Feb 6 17:14:50 2010
Length of input sequence	525 amino acids
Number of nanomers from input sequence	517
Number of nanomers with obligatory P1 anchor residue	168
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	52

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	FVAATGANL	274	2.3000	38.33
2	FTLVEPLRL	368	1.5500	25.83
3	FGAQYAQLI	21	1.5000	25.00
4	YAQLIARRV	25	1.2900	21.50
5	FAGLGAQWT	198	1.1000	18.33
6	LGICYGFQA	89	1.0000	16.67
7	IRIVGEVTA	408	0.9500	15.83
8	LVLSGGPAS	60	0.8700	14.50
9	LVTVDAAET	282	0.8500	14.17

10	VVLLADVRS	447	0.7000	11.67
11	LEALSGVSA	292	0.4000	6.67
12	LRHADSIVR	422	0.4000	6.67
13	VLLADVRSV	448	0.2900	4.83
14	LRPVSSEDA	471	0.2500	4.17
15	IRARQPVAL	52	0.1000	1.67
16	YEVLERIST	489	0.1000	1.67
17	VVDFGAQYA	18	0.0800	1.33
18	IRAFEGAVR	313	-0.0200	0
19	LKVLGGKLH	119	-0.1000	0
20	VLSGGPASV	61	-0.4000	0
21	YGFQAMAQA	93	-0.4000	0
22	FLVQGTLYP	331	-0.4000	0
23	LGGIVAHTG	102	-0.5000	0
24	IVREELTAA	428	-0.5100	0
25	FQAMAQALG	95	-0.6000	0
26	LRLLFKDEV	374	-0.6000	0
27	VQRAIGDRL	244	-0.9000	0
28	LLDLGVPVL	81	-0.9300	0
29	LRAGERAQV	262	-1.0000	0
30	IWQCPVVLL	442	-1.0000	0
31	LERISTRIT	492	-1.0100	0
32	MSHGDAVTA	138	-1.1000	0
33	LKFTLVEPL	366	-1.3000	0
34	IVGEVTAKR	410	-1.3000	0
35	FIRAFEGAV	312	-1.4000	0
36	VSSEDAMTA	474	-1.4100	0
37	LHDFAGLGA	195	-1.4200	0
38	VGEVTAKRL	411	-1.4500	0
39	VRSVGVQGD	453	-1.4500	0
40	WTRVPYEVL	484	-1.4500	0
41	YGRTELKVL	114	-1.5000	0
42	VASSAGAPV	154	-1.5000	0
43	WQCPVVLLA	443	-1.5000	0

44	FEAFDRRLA	165	-1.5300	0
45	WTPANIANA	205	-1.6000	0
46	VDSAVAAAL	235	-1.6000	0
47	FVDHGLLRA	256	-1.6000	0
48	VAATGANLV	275	-1.6000	0
49	IKSHHNVGG	353	-1.6000	0
50	VAAFEAFDR	162	-1.6200	0
51	FSEVIPHTA	39	-1.6500	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	FVAATGANL	274	2.3000	38.33
2	LGICYGFQA	89	2.0000	33.33
3	IRIVGEVTA	408	1.9500	32.50
4	LVLSGGPAS	60	1.8700	31.17
5	LVTVDAAET	282	1.8500	30.83
6	VVLLADVRS	447	1.7000	28.33
7	FTLVEPLRL	368	1.5500	25.83
8	FGAQYAQLI	21	1.5000	25.00
9	LEALSGVSA	292	1.4000	23.33
10	LRHADSIVR	422	1.4000	23.33
11	VLLADVRSV	448	1.2900	21.50
12	LRPVSSEDA	471	1.2500	20.83
13	IRARQPVAL	52	1.1000	18.33
14	FAGLGAQWT	198	1.1000	18.33
15	VVDFGAQYA	18	1.0800	18.00
16	IRAFEGAVR	313	0.9800	16.33
17	LKVLGGKLH	119	0.9000	15.00
18	VLSGGPASV	61	0.6000	10.00
19	LGGIVAHTG	102	0.5000	8.33
20	IVREELTAA	428	0.4900	8.17
21	LRLLFKDEV	374	0.4000	6.67
22	YAQLIARRV	25	0.2900	4.83

23	VQRAIGDRL	244	0.1000	1.67
24	LLDLGVPVL	81	0.0700	1.17
25	LERISTRIT	492	-0.0100	0
26	MSHGDAVTA	138	-0.1000	0
27	LKFTLVEPL	366	-0.3000	0
28	IVGEVTAKR	410	-0.3000	0
29	FLVQGTLYP	331	-0.4000	0
30	VSSEDAMTA	474	-0.4100	0
31	LHDFAGLGA	195	-0.4200	0
32	VGEVTAKRL	411	-0.4500	0
33	VRSVGVQGD	453	-0.4500	0
34	VASSAGAPV	154	-0.5000	0
35	FQAMAQALG	95	-0.6000	0
36	VDSAVAAAL	235	-0.6000	0
37	VAATGANLV	275	-0.6000	0
38	IKSHHNVGG	353	-0.6000	0
39	VAAFEAFDR	162	-0.6200	0
40	IVARQPFPG	395	-0.7000	0
41	IVAHTGTRE	105	-0.7100	0
42	VVASSAGAP	153	-0.8000	0
43	LSGVSAPEG	295	-0.8800	0
44	MHTPHGQQV	182	-0.9000	0
45	VAAALVQRA	239	-0.9000	0
46	YEVLERIST	489	-0.9000	0
47	IGRQFIRAF	308	-0.9100	0
48	VYADGAPKL	69	-0.9300	0
49	LADVRSVGV	450	-0.9500	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	VVLDITSKP	509	5.9700	62.84
2	VQGDGRTYG	458	5.0000	52.63
3	LVLSGGPAS	60	4.9000	51.58

4	VQRDFVAAT	270	4.9000	51.58
5	LYPDVVESG	337	4.9000	51.58
6	LLADVRSVG	449	4.7700	50.21
7	LVVDFGAQY	17	4.5000	47.37
8	LRLLFKDEV	374	4.2000	44.21
9	LRAGERAQV	262	4.0000	42.11
10	VYADGAPKL	69	3.8600	40.63
11	LFKDEVRAV	377	3.7000	38.95
12	VFVDHGLLR	255	3.6000	37.89
13	VTVDAAETF	283	3.5000	36.84
14	LHSDLPEVQ	126	3.4000	35.79
15	VRAVGRELG	382	3.4000	35.79
16	LRHADSIVR	422	3.2000	33.68
17	IVLRPVSSE	469	3.0700	32.32
18	FLHDFAGLG	194	3.0000	31.58
19	VRSVGVQGD	453	2.9000	30.53
20	VVASSAGAP	153	2.6000	27.37
21	LGIRIVGEV	406	2.6000	27.37
22	IVGEVTAKR	410	2.6000	27.37
23	VLLADVRSV	448	2.6000	27.37
24	VLSGGPASV	61	2.5000	26.32
25	IVARQPFPG	395	2.5000	26.32
26	IRIVGEVTA	408	2.5000	26.32
27	VREARVFSE	33	2.4000	25.26
28	LVQRAIGDR	243	2.4000	25.26
29	LPDDLKFTL	362	2.2600	23.79
30	LRPVSSEDA	471	2.2000	23.16
31	LVQGTLYPD	332	2.1500	22.63
32	LVEPLRLLF	370	2.0000	21.05
33	VVLLADVRS	447	2.0000	21.05
34	IGRQFIRAF	308	1.9000	20.00
35	VLDGKTAEF	323	1.9000	20.00
36	IVREELTAA	428	1.9000	20.00
37	MTADWTRVP	480	1.9000	20.00

38	IRARQPVAL	52	1.8600	19.58
39	LKFTLVEPL	366	1.8600	19.58
40	LGICYGFQA	89	1.8000	18.95
41	LVTVDAAET	282	1.6000	16.84
42	LLDLGVPVL	81	1.5600	16.42
43	LGAQWTPAN	201	1.4000	14.74
44	LIEQVRTQI	214	1.4000	14.74
45	VVESGGGSG	341	1.4000	14.74
46	VQPADIDVP	1	1.3000	13.68
47	LDLGVPVLG	82	1.3000	13.68
48	IANALIEQV	210	1.3000	13.68
49	IKSHHNVGG	353	1.3000	13.68
50	IWQCPVVLL	442	1.2600	13.26
51	IEQVRTQIG	215	1.2000	12.63
52	FLVQGTLYP	331	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	VVLDITSKP	509	3.9700	43.63
2	LVLSGGPAS	60	3.5000	38.46
3	VQRDFVAAT	270	3.2000	35.16
4	LHSDLPEVQ	126	3.1000	34.07
5	FLHDFAGLG	194	2.6000	28.57
6	VQGDGRTYG	458	2.6000	28.57
7	LYPDVVESG	337	2.5000	27.47
8	LLADVRSVG	449	2.3700	26.04
9	LVVDFGAQY	17	2.2000	24.18
10	LRLLFKDEV	374	2.2000	24.18
11	LRAGERAQV	262	2.0000	21.98
12	VYADGAPKL	69	1.9000	20.88
13	LFKDEVRAV	377	1.7000	18.68
14	WQCPVVLLA	443	1.6000	17.58
15	IRIVGEVTA	408	1.5000	16.48

16	FVDHGLLRA	256	1.2000	13.19
17	FLVQGTLYP	331	1.2000	13.19
18	LRPVSSEDA	471	1.2000	13.19
19	VFVDHGLLR	255	1.1000	12.09
20	WTPANIANA	205	1.0000	10.99
21	VRAVGRELG	382	1.0000	10.99
22	IVREELTAA	428	0.9000	9.89
23	LGICYGFQA	89	0.8000	8.79
24	VRSVGVQGD	453	0.8000	8.79
25	YEVLERIST	489	0.8000	8.79
26	FTLVEPLRL	368	0.7000	7.69
27	LRHADSIVR	422	0.7000	7.69
28	IVLRPVSSE	469	0.6700	7.36
29	VVASSAGAP	153	0.6000	6.59
30	VTVDAAETF	283	0.6000	6.59
31	LGIRIVGEV	406	0.6000	6.59
32	VVLLADVRS	447	0.6000	6.59
33	VLLADVRSV	448	0.6000	6.59
34	VLSGGPASV	61	0.5000	5.49
35	FLEALSGVS	291	0.5000	5.49
36	YGFQAMAQA	93	0.4000	4.40
37	FVAATGANL	274	0.4000	4.40
38	LPDDLKFTL	362	0.3000	3.30
39	LDITSKPPA	511	0.2000	2.20
40	FGAQYAQLI	21	0.1000	1.10
41	VAAALVQRA	239	0.1000	1.10
42	IVARQPFPG	395	0.1000	1.10
43	IVGEVTAKR	410	0.1000	1.10
44	LVQGTLYPD	332	0.0500	0.55
45	VRTQIGDGH	218	-0.0200	0
46	IRARQPVAL	52	-0.1000	0
47	VLGICYGFQ	88	-0.1000	0
48	FQAMAQALG	95	-0.1000	0
49	LVQRAIGDR	243	-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	VVLDITSKP	509	4.7000	53.41
2	LHSDLPEVQ	126	4.5000	51.14
3	VQRDFVAAT	270	4.2000	47.73
4	LYPDVVESG	337	3.9000	44.32
5	VQGDGRTYG	458	3.6000	40.91
6	LRLLFKDEV	374	3.5000	39.77
7	LVVDFGAQY	17	3.2000	36.36
8	LVLSGGPAS	60	3.1000	35.23
9	LLADVRSVG	449	3.1000	35.23
10	LRAGERAQV	262	3.0000	34.09
11	VFVDHGLLR	255	2.6000	29.55
12	LRPVSSEDA	471	2.6000	29.55
13	LFKDEVRAV	377	2.4000	27.27
14	VRAVGRELG	382	2.4000	27.27
15	IRIVGEVTA	408	2.3800	27.05
16	VTVDAAETF	283	2.0000	22.73
17	IVREELTAA	428	1.9000	21.59
18	VRSVGVQGD	453	1.9000	21.59
19	VLSGGPASV	61	1.5000	17.05
20	VYADGAPKL	69	1.5000	17.05
21	VVLLADVRS	447	1.4800	16.82
22	IVLRPVSSE	469	1.4000	15.91
23	LRHADSIVR	422	1.3800	15.68
24	LKFTLVEPL	366	1.3000	14.77
25	VLLADVRSV	448	1.3000	14.77
26	VRTQIGDGH	218	1.2800	14.55
27	VAAALVQRA	239	1.2000	13.64
28	IVGEVTAKR	410	1.1000	12.50
29	WQCPVVLLA	443	1.1000	12.50
30	ICYGFQAMA	91	1.0000	11.36

31	VEPLRLLFK	371	1.0000	11.36
32	LVTVDAAET	282	0.9000	10.23
33	IRARQPVAL	52	0.7800	8.86
34	VQYHPEVMH	175	0.7600	8.64
35	IANALIEQV	210	0.7000	7.95
36	FVDHGLLRA	256	0.7000	7.95
37	FLVQGTLYP	331	0.7000	7.95
38	LKVLGGKLH	119	0.6800	7.73
39	VQPADIDVP	1	0.6000	6.82
40	LVEPLRLLF	370	0.6000	6.82
41	MTADWTRVP	480	0.6000	6.82
42	LIEQVRTQI	214	0.5000	5.68
43	MSHGDAVTA	138	0.4800	5.45
44	LTAAGLDNQ	433	0.4000	4.55
45	LGICYGFQA	89	0.3000	3.41
46	VWMSHGDAV	136	0.3000	3.41
47	LGGIVAHTG	102	0.2000	2.27
48	VLGGKLHSD	121	0.2000	2.27
49	VVASSAGAP	153	0.2000	2.27
50	FLHDFAGLG	194	0.2000	2.27
51	FTLVEPLRL	368	0.2000	2.27
52	LGIRIVGEV	406	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDITSKP	509	4.7000	53.41
2	LHSDLPEVQ	126	4.5000	51.14
3	VQRDFVAAT	270	4.2000	47.73
4	LYPDVVESG	337	3.9000	44.32
5	VQGDGRTYG	458	3.6000	40.91
6	LRLLFKDEV	374	3.5000	39.77
7	LVVDFGAQY	17	3.2000	36.36
8	LVLSGGPAS	60	3.1000	35.23

9	LLADVRSVG	449	3.1000	35.23
10	LRAGERAQV	262	3.0000	34.09
11	VFVDHGLLR	255	2.6000	29.55
12	LRPVSSEDA	471	2.6000	29.55
13	LFKDEVRAV	377	2.4000	27.27
14	VRAVGRELG	382	2.4000	27.27
15	IRIVGEVTA	408	2.3800	27.05
16	VTVDAAETF	283	2.0000	22.73
17	IVREELTAA	428	1.9000	21.59
18	VRSVGVQGD	453	1.9000	21.59
19	VLSGGPASV	61	1.5000	17.05
20	VYADGAPKL	69	1.5000	17.05
21	VVLLADVRS	447	1.4800	16.82
22	IVLRPVSSE	469	1.4000	15.91
23	LRHADSIVR	422	1.3800	15.68
24	LKFTLVEPL	366	1.3000	14.77
25	VLLADVRSV	448	1.3000	14.77
26	VRTQIGDGH	218	1.2800	14.55
27	VAAALVQRA	239	1.2000	13.64
28	IVGEVTAKR	410	1.1000	12.50
29	WQCPVVLLA	443	1.1000	12.50
30	ICYGFQAMA	91	1.0000	11.36
31	VEPLRLLFK	371	1.0000	11.36
32	LVTVDAAET	282	0.9000	10.23
33	IRARQPVAL	52	0.7800	8.86
34	VQYHPEVMH	175	0.7600	8.64
35	IANALIEQV	210	0.7000	7.95
36	FVDHGLLRA	256	0.7000	7.95
37	FLVQGTLYP	331	0.7000	7.95
38	LKVLGGKLH	119	0.6800	7.73
39	VQPADIDVP	1	0.6000	6.82
40	LVEPLRLLF	370	0.6000	6.82
41	MTADWTRVP	480	0.6000	6.82
42	LIEQVRTQI	214	0.5000	5.68

43	MSHGDAVTA	138	0.4800	5.45
44	LTAAGLDNQ	433	0.4000	4.55
45	LGICYGFQA	89	0.3000	3.41
46	VWMSHGDAV	136	0.3000	3.41
47	LGGIVAHTG	102	0.2000	2.27
48	VLGGKLHSD	121	0.2000	2.27
49	VVASSAGAP	153	0.2000	2.27
50	FLHDFAGLG	194	0.2000	2.27
51	FTLVEPLRL	368	0.2000	2.27
52	LGIRIVGEV	406	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDITSKP	509	4.7000	53.41
2	LHSDLPEVQ	126	4.5000	51.14
3	VQRDFVAAT	270	4.2000	47.73
4	LYPDVVESG	337	3.9000	44.32
5	VQGDGRTYG	458	3.6000	40.91
6	LRLLFKDEV	374	3.5000	39.77
7	LVVDFGAQY	17	3.2000	36.36
8	LVLSGGPAS	60	3.1000	35.23
9	LLADVRSVG	449	3.1000	35.23
10	LRAGERAQV	262	3.0000	34.09
11	VFVDHGLLR	255	2.6000	29.55
12	LRPVSSEDA	471	2.6000	29.55
13	LFKDEVRAV	377	2.4000	27.27
14	VRAVGRELG	382	2.4000	27.27
15	IRIVGEVTA	408	2.3800	27.05
16	VTVDAAETF	283	2.0000	22.73
17	IVREELTAA	428	1.9000	21.59
18	VRSVGVQGD	453	1.9000	21.59
19	VLSGGPASV	61	1.5000	17.05
20	VYADGAPKL	69	1.5000	17.05

21	VVLLADVRS	447	1.4800	16.82
22	IVLRPVSSE	469	1.4000	15.91
23	LRHADSIVR	422	1.3800	15.68
24	LKFTLVEPL	366	1.3000	14.77
25	VLLADVRSV	448	1.3000	14.77
26	VRTQIGDGH	218	1.2800	14.55
27	VAAALVQRA	239	1.2000	13.64
28	IVGEVTAKR	410	1.1000	12.50
29	WQCPVVLLA	443	1.1000	12.50
30	ICYGFQAMA	91	1.0000	11.36
31	VEPLRLLFK	371	1.0000	11.36
32	LVTVDAAET	282	0.9000	10.23
33	IRARQPVAL	52	0.7800	8.86
34	VQYHPEVMH	175	0.7600	8.64
35	IANALIEQV	210	0.7000	7.95
36	FVDHGLLRA	256	0.7000	7.95
37	FLVQGTLYP	331	0.7000	7.95
38	LKVLGGKLH	119	0.6800	7.73
39	VQPADIDVP	1	0.6000	6.82
40	LVEPLRLLF	370	0.6000	6.82
41	MTADWTRVP	480	0.6000	6.82
42	LIEQVRTQI	214	0.5000	5.68
43	MSHGDAVTA	138	0.4800	5.45
44	LTAAGLDNQ	433	0.4000	4.55
45	LGICYGFQA	89	0.3000	3.41
46	VWMSHGDAV	136	0.3000	3.41
47	LGGIVAHTG	102	0.2000	2.27
48	VLGGKLHSD	121	0.2000	2.27
49	VVASSAGAP	153	0.2000	2.27
50	FLHDFAGLG	194	0.2000	2.27
51	FTLVEPLRL	368	0.2000	2.27
52	LGIRIVGEV	406	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDITSKP	509	4.9700	52.32
2	FLHDFAGLG	194	4.0000	42.11
3	VQGDGRTYG	458	4.0000	42.11
4	LVLSGGPAS	60	3.9000	41.05
5	VQRDFVAAT	270	3.9000	41.05
6	LYPDVVESG	337	3.9000	41.05
7	LLADVRSVG	449	3.7700	39.68
8	LVVDFGAQY	17	3.5000	36.84
9	LRLLFKDEV	374	3.2000	33.68
10	LRAGERAQV	262	3.0000	31.58
11	VYADGAPKL	69	2.8600	30.11
12	LFKDEVRAV	377	2.7000	28.42
13	VFVDHGLLR	255	2.6000	27.37
14	VTVDAAETF	283	2.5000	26.32
15	LHSDLPEVQ	126	2.4000	25.26
16	VRAVGRELG	382	2.4000	25.26
17	FLVQGTLYP	331	2.2000	23.16
18	LRHADSIVR	422	2.2000	23.16
19	IVLRPVSSE	469	2.0700	21.79
20	VRSVGVQGD	453	1.9000	20.00
21	FTLVEPLRL	368	1.6600	17.47
22	VVASSAGAP	153	1.6000	16.84
23	LGIRIVGEV	406	1.6000	16.84
24	IVGEVTAKR	410	1.6000	16.84
25	WQCPVVLLA	443	1.6000	16.84
26	VLLADVRSV	448	1.6000	16.84
27	VLSGGPASV	61	1.5000	15.79
28	IVARQPFPG	395	1.5000	15.79
29	IRIVGEVTA	408	1.5000	15.79
30	YEVLERIST	489	1.5000	15.79
31	VREARVFSE	33	1.4000	14.74
32	LVQRAIGDR	243	1.4000	14.74

33	FVAATGANL	274	1.3600	14.32
34	FQAMAQALG	95	1.3000	13.68
35	LPDDLKFTL	362	1.2600	13.26
36	FVDHGLLRA	256	1.2000	12.63
37	LRPVSSEDA	471	1.2000	12.63
38	LVQGTLYPD	332	1.1500	12.11
39	FGAQYAQLI	21	1.0000	10.53
40	WTPANIANA	205	1.0000	10.53
41	LVEPLRLLF	370	1.0000	10.53
42	VVLLADVRS	447	1.0000	10.53
43	FLEALSGVS	291	0.9000	9.47
44	IGRQFIRAF	308	0.9000	9.47
45	VLDGKTAEF	323	0.9000	9.47
46	IVREELTAA	428	0.9000	9.47
47	MTADWTRVP	480	0.9000	9.47
48	IRARQPVAL	52	0.8600	9.05
49	LKFTLVEPL	366	0.8600	9.05
50	LGICYGFQA	89	0.8000	8.42
51	FIRAFEGAV	312	0.8000	8.42
52	YGHPIVLRP	465	0.8000	8.42

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDITSKP	509	4.7000	53.41
2	LHSDLPEVQ	126	4.5000	51.14
3	VQRDFVAAT	270	4.2000	47.73
4	LYPDVVESG	337	3.9000	44.32
5	VQGDGRTYG	458	3.6000	40.91
6	LRLLFKDEV	374	3.5000	39.77
7	LVVDFGAQY	17	3.2000	36.36
8	LVLSGGPAS	60	3.1000	35.23
9	LLADVRSVG	449	3.1000	35.23
10	LRAGERAQV	262	3.0000	34.09

11	VFVDHGLLR	255	2.6000	29.55
12	LRPVSSEDA	471	2.6000	29.55
13	LFKDEVRAV	377	2.4000	27.27
14	VRAVGRELG	382	2.4000	27.27
15	IRIVGEVTA	408	2.3800	27.05
16	VTVDAAETF	283	2.0000	22.73
17	IVREELTAA	428	1.9000	21.59
18	VRSVGVQGD	453	1.9000	21.59
19	VLSGGPASV	61	1.5000	17.05
20	VYADGAPKL	69	1.5000	17.05
21	VVLLADVRS	447	1.4800	16.82
22	IVLRPVSSE	469	1.4000	15.91
23	LRHADSIVR	422	1.3800	15.68
24	LKFTLVEPL	366	1.3000	14.77
25	VLLADVRSV	448	1.3000	14.77
26	VRTQIGDGH	218	1.2800	14.55
27	VAAALVQRA	239	1.2000	13.64
28	IVGEVTAKR	410	1.1000	12.50
29	WQCPVVLLA	443	1.1000	12.50
30	ICYGFQAMA	91	1.0000	11.36
31	VEPLRLLFK	371	1.0000	11.36
32	LVTVDAAET	282	0.9000	10.23
33	IRARQPVAL	52	0.7800	8.86
34	VQYHPEVMH	175	0.7600	8.64
35	IANALIEQV	210	0.7000	7.95
36	FVDHGLLRA	256	0.7000	7.95
37	FLVQGTLYP	331	0.7000	7.95
38	LKVLGGKLH	119	0.6800	7.73
39	VQPADIDVP	1	0.6000	6.82
40	LVEPLRLLF	370	0.6000	6.82
41	MTADWTRVP	480	0.6000	6.82
42	LIEQVRTQI	214	0.5000	5.68
43	MSHGDAVTA	138	0.4800	5.45
44	LTAAGLDNQ	433	0.4000	4.55

45	LGICYGFQA	89	0.3000	3.41
46	VWMSHGDAV	136	0.3000	3.41
47	LGGIVAHTG	102	0.2000	2.27
48	VLGGKLHSD	121	0.2000	2.27
49	VVASSAGAP	153	0.2000	2.27
50	FLHDFAGLG	194	0.2000	2.27
51	FTLVEPLRL	368	0.2000	2.27
52	LGIRIVGEV	406	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLDITSKP	509	3.9000	45.35
2	IVGEVTAKR	410	3.7000	43.02
3	FLVQGTLYP	331	3.6000	41.86
4	VVLLADVRS	447	2.5800	30.00
5	VREELTAAG	429	2.4000	27.91
6	LHSDLPEVQ	126	2.1000	24.42
7	IVREELTAA	428	2.1000	24.42
8	VQRDFVAAT	270	2.0000	23.26
9	LRPVSSEDA	471	1.8000	20.93
10	IKSHHNVGG	353	1.7800	20.70
11	LYPDVVESG	337	1.7000	19.77
12	LKFTLVEPL	366	1.7000	19.77
13	FVDHGLLRA	256	1.5000	17.44
14	LRHADSIVR	422	1.4800	17.21
15	LVLSGGPAS	60	1.4000	16.28
16	WQCPVVLLA	443	1.2000	13.95
17	VSSEDAMTA	474	1.2000	13.95
18	FGAQYAQLI	21	1.0000	11.63
19	YGFQAMAQA	93	1.0000	11.63
20	LVVDFGAQY	17	0.5000	5.81
21	FLHDFAGLG	194	0.3000	3.49
22	VRTQIGDGH	218	0.2800	3.26

23	YHPEVMHTP	177	0.2000	2.33
24	WTPANIANA	205	0.2000	2.33
25	FLEALSGVS	291	0.2000	2.33
26	LFKDEVRAV	377	0.2000	2.33
27	LPEEIVARQ	391	0.2000	2.33
28	WMSHGDAVT	137	0.1000	1.16
29	LGAQWTPAN	201	0.1000	1.16
30	VTVDAAETF	283	0.1000	1.16
31	LERISTRIT	492	0.1000	1.16
32	VAAALVQRA	239	-0.1000	0
33	VFVDHGLLR	255	-0.1000	0
34	VQYHPEVMH	175	-0.1400	0
35	FAGLGAQWT	198	-0.2000	0
36	FTLVEPLRL	368	-0.2000	0
37	MTADWTRVP	480	-0.2000	0
38	ITNEVAEVN	499	-0.2000	0
39	VRSVGVQGD	453	-0.3000	0
40	LKVLGGKLH	119	-0.3200	0
41	VIPHTASIE	42	-0.4000	0
42	VYADGAPKL	69	-0.4000	0
43	FQAMAQALG	95	-0.4000	0
44	VAHTGTREY	106	-0.4000	0
45	FVAATGANL	274	-0.4000	0
46	VAATGANLV	275	-0.4000	0
47	LRLLFKDEV	374	-0.4000	0
48	VPYEVLERI	487	-0.4000	0
49	VFSEVIPHT	38	-0.5000	0
50	LGGIVAHTG	102	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LIARRVREA	28	4.7000	48.96
2	VLLADVRSV	448	3.9000	40.62

3	LERISTRIT	492	3.2800	34.17
4	IKSHHNVGG	353	3.0000	31.25
5	LRHADSIVR	422	2.9000	30.21
6	IVLRPVSSE	469	2.9000	30.21
7	IVARQPFPG	395	2.6000	27.08
8	ISTRITNEV	495	2.5000	26.04
9	IRARQPVAL	52	2.4000	25.00
10	VAHTGTREY	106	2.3000	23.96
11	VVLLADVRS	447	2.3000	23.96
12	VVDFGAQYA	18	2.2000	22.92
13	VAAALVQRA	239	2.0000	20.83
14	VRSVGVQGD	453	2.0000	20.83
15	IIGRQFIRA	307	1.7000	17.71
16	FLVQGTLYP	331	1.7000	17.71
17	LRPVSSEDA	471	1.6000	16.67
18	VLERISTRI	491	1.6000	16.67
19	LLRAGERAQ	261	1.5000	15.62
20	IEQVRTQIG	215	1.4000	14.58
21	IGRQFIRAF	308	1.4000	14.58
22	IGDRLTCVF	248	1.1000	11.46
23	LGIRIVGEV	406	1.1000	11.46
24	VQYHPEVMH	175	1.0800	11.25
25	LGICYGFQA	89	1.0000	10.42
26	VVLDITSKP	509	1.0000	10.42
27	FVDHGLLRA	256	0.9000	9.38
28	IVGEVTAKR	410	0.9000	9.38
29	IRIVGEVTA	408	0.8000	8.33
30	WQCPVVLLA	443	0.8000	8.33
31	VREARVFSE	33	0.7000	7.29
32	VLSRFLHDF	190	0.6000	6.25
33	VIPHTASIE	42	0.5000	5.21
34	LFKDEVRAV	377	0.4000	4.17
35	LVLSGGPAS	60	0.3000	3.12
36	LGGIVAHTG	102	0.2800	2.92

37	IVAHTGTRE	105	0.2000	2.08
38	LVTVDAAET	282	0.2000	2.08
39	LKFTLVEPL	366	0.1000	1.04
40	FGAQYAQLI	21	-0.1000	0
41	LVQRAIGDR	243	-0.1000	0
42	VLDGKTAEF	323	-0.1000	0
43	VLSGGPASV	61	-0.2000	0
44	VAAFEAFDR	162	-0.2000	0
45	LLFKDEVRA	376	-0.3000	0
46	LGAQWTPAN	201	-0.4000	0
47	VREELTAAG	429	-0.4000	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	VVLLADVRS	447	3.6000	40.91
2	LRPVSSEDA	471	3.3000	37.50
3	VVLDITSKP	509	3.1000	35.23
4	LRHADSIVR	422	2.4800	28.18
5	IVGEVTAKR	410	2.1000	23.86
6	VRSVGVQGD	453	1.9000	21.59
7	IRIVGEVTA	408	1.7000	19.32
8	LERISTRIT	492	1.7000	19.32
9	VVDFGAQYA	18	1.6000	18.18
10	LVTVDAAET	282	1.4000	15.91
11	FLVQGTLYP	331	1.4000	15.91
12	IEQVRTQIG	215	1.3000	14.77
13	VLLADVRSV	448	1.3000	14.77
14	IVREELTAA	428	1.0000	11.36
15	VREELTAAG	429	0.8000	9.09
16	VAAALVQRA	239	0.7000	7.95
17	IRAFEGAVR	313	0.7000	7.95
18	LVLSGGPAS	60	0.6000	6.82
19	VQRDFVAAT	270	0.5000	5.68

20	IKSHHNVGG	353	0.5000	5.68
21	LGICYGFQA	89	0.4500	5.11
22	LGGIVAHTG	102	0.4000	4.55
23	VQPVWMSHG	133	0.4000	4.55
24	IVLRPVSSE	469	0.4000	4.55
25	VEPLRLLFK	371	0.3000	3.41
26	VLVVDFGAQ	16	0.2000	2.27
27	LKFTLVEPL	366	0.2000	2.27
28	VLRPVSSED	470	0.2000	2.27
29	VREARVFSE	33	0.1500	1.70
30	VLGICYGFQ	88	0.1000	1.14
31	WQCPVVLLA	443	0.1000	1.14
32	VAAFEAFDR	162	-0.0500	0
33	VPVLGICYG	86	-0.1000	0
34	LRLLFKDEV	374	-0.1000	0
35	LKVLGGKLH	119	-0.1200	0
36	FTLVEPLRL	368	-0.2000	0
37	LHSDLPEVQ	126	-0.3000	0
38	IWQCPVVLL	442	-0.3000	0
39	LLDLGVPVL	81	-0.4000	0
40	VRTQIGDGH	218	-0.4200	0
41	FQAMAQALG	95	-0.5000	0
42	LEALSGVSA	292	-0.5000	0
43	VSSEDAMTA	474	-0.5000	0
44	LADVRSVGV	450	-0.6000	0
45	VAHTGTREY	106	-0.7000	0
46	LHDFAGLGA	195	-0.7000	0
47	FLEALSGVS	291	-0.7000	0
48	LYPDVVESG	337	-0.7000	0
49	VIPHTASIE	42	-0.8000	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	VRSVGVQGD	453	3.6000	38.30
2	FLVQGTLYP	331	2.8000	29.79
3	VVLLADVRS	447	2.6000	27.66
4	VVLDITSKP	509	2.5000	26.60
5	IVLRPVSSE	469	2.4000	25.53
6	LRPVSSEDA	471	2.3000	24.47
7	VREARVFSE	33	2.1500	22.87
8	VLRPVSSED	470	1.9000	20.21
9	FQAMAQALG	95	1.8000	19.15
10	FTLVEPLRL	368	1.8000	19.15
11	IEQVRTQIG	215	1.6000	17.02
12	LERISTRIT	492	1.6000	17.02
13	FDVVASSAG	151	1.5000	15.96
14	LRHADSIVR	422	1.4800	15.74
15	LVTVDAAET	282	1.3000	13.83
16	VIPHTASIE	42	1.2000	12.77
17	IVGEVTAKR	410	1.1000	11.70
18	VREELTAAG	429	1.1000	11.70
19	WQCPVVLLA	443	1.1000	11.70
20	LGAQWTPAN	201	1.0000	10.64
21	VDAAETFLE	285	0.8500	9.04
22	IKSHHNVGG	353	0.8000	8.51
23	LGGIVAHTG	102	0.7000	7.45
24	VQPVWMSHG	133	0.7000	7.45
25	FAGLGAQWT	198	0.7000	7.45
26	IRIVGEVTA	408	0.7000	7.45
27	VVDFGAQYA	18	0.6000	6.38
28	FVAATGANL	274	0.6000	6.38
29	VLLADVRSV	448	0.6000	6.38
30	VQRDFVAAT	270	0.4000	4.26
31	IVAHTGTRE	105	0.3000	3.19
32	FLEALSGVS	291	0.3000	3.19
33	FGAQYAQLI	21	0.2000	2.13
34	VPVLGICYG	86	0.2000	2.13

35	YGFQAMAQA	93	0.2000	2.13
36	WTPANIANA	205	0.2000	2.13
37	LKFTLVEPL	366	0.2000	2.13
38	IPHTASIEE	43	0.1800	1.91
39	LKVLGGKLH	119	0.1000	1.06
40	VLGICYGFQ	88	-0.1000	0
41	VRTQIGDGH	218	-0.2000	0
42	YAQLIARRV	25	-0.3000	0
43	VAAALVQRA	239	-0.3000	0
44	IRAFEGAVR	313	-0.3000	0
45	IWQCPVVLL	442	-0.3000	0
46	YGHPIVLRP	465	-0.3000	0
47	LVLSGGPAS	60	-0.4000	0
48	LLDLGVPVL	81	-0.4000	0
49	LYPDVVESG	337	-0.4000	0

ALLELE: DRB1_0408	Threshold for 3 % with score: 1.2	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVLLADVRS	447	2.6000	29.55
2	FLVQGTLYP	331	2.4000	27.27
3	LRPVSSEDA	471	2.3000	26.14
4	VVLDITSKP	509	2.1000	23.86
5	LRHADSIVR	422	1.4800	16.82
6	IVGEVTAKR	410	1.1000	12.50
7	WQCPVVLLA	443	1.1000	12.50
8	VRSVGVQGD	453	0.9000	10.23
9	FTLVEPLRL	368	0.8000	9.09
10	IRIVGEVTA	408	0.7000	7.95
11	LERISTRIT	492	0.7000	7.95
12	VVDFGAQYA	18	0.6000	6.82
13	FQAMAQALG	95	0.5000	5.68
14	LVTVDAAET	282	0.4000	4.55
15	IEQVRTQIG	215	0.3000	3.41

16	FLEALSGVS	291	0.3000	3.41
17	VLLADVRSV	448	0.3000	3.41
18	YGFQAMAQA	93	0.2000	2.27
19	FDVVASSAG	151	0.2000	2.27
20	WTPANIANA	205	0.2000	2.27
21	FAGLGAQWT	198	-0.2000	0
22	VREELTAAG	429	-0.2000	0
23	VAAALVQRA	239	-0.3000	0
24	IRAFEGAVR	313	-0.3000	0
25	LVLSGGPAS	60	-0.4000	0
26	FVAATGANL	274	-0.4000	0
27	VQRDFVAAT	270	-0.5000	0
28	IKSHHNVGG	353	-0.5000	0
29	LGICYGFQA	89	-0.5500	0
30	YAQLIARRV	25	-0.6000	0
31	LGGIVAHTG	102	-0.6000	0
32	VQPVWMSHG	133	-0.6000	0
33	IVLRPVSSE	469	-0.6000	0
34	VEPLRLLFK	371	-0.7000	0
35	YGHPIVLRP	465	-0.7000	0
36	VLVVDFGAQ	16	-0.8000	0
37	LKFTLVEPL	366	-0.8000	0
38	VLRPVSSED	470	-0.8000	0
39	VREARVFSE	33	-0.8500	0
40	VLGICYGFQ	88	-0.9000	0
41	VALVLSGGP	58	-1.0000	0
42	LGAQWTPAN	201	-1.0000	0
43	FVDHGLLRA	256	-1.0000	0
44	VAAFEAFDR	162	-1.0500	0
45	VPVLGICYG	86	-1.1000	0
46	LRLLFKDEV	374	-1.1000	0
47	LKVLGGKLH	119	-1.1200	0
48	LHSDLPEVQ	126	-1.3000	0
49	IWQCPVVLL	442	-1.3000	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	VRSVGVQGD	453	4.6000	48.94
2	VVLLADVRS	447	3.6000	38.30
3	VVLDITSKP	509	3.5000	37.23
4	IVLRPVSSE	469	3.4000	36.17
5	LRPVSSEDA	471	3.3000	35.11
6	VREARVFSE	33	3.1500	33.51
7	VLRPVSSED	470	2.9000	30.85
8	IEQVRTQIG	215	2.6000	27.66
9	LERISTRIT	492	2.6000	27.66
10	LRHADSIVR	422	2.4800	26.38
11	LVTVDAAET	282	2.3000	24.47
12	VIPHTASIE	42	2.2000	23.40
13	IVGEVTAKR	410	2.1000	22.34
14	VREELTAAG	429	2.1000	22.34
15	LGAQWTPAN	201	2.0000	21.28
16	VDAAETFLE	285	1.8500	19.68
17	FLVQGTLYP	331	1.8000	19.15
18	IKSHHNVGG	353	1.8000	19.15
19	LGGIVAHTG	102	1.7000	18.09
20	VQPVWMSHG	133	1.7000	18.09
21	IRIVGEVTA	408	1.7000	18.09
22	VVDFGAQYA	18	1.6000	17.02
23	VLLADVRSV	448	1.6000	17.02
24	VQRDFVAAT	270	1.4000	14.89
25	IVAHTGTRE	105	1.3000	13.83
26	VPVLGICYG	86	1.2000	12.77
27	LKFTLVEPL	366	1.2000	12.77
28	IPHTASIEE	43	1.1800	12.55
29	LKVLGGKLH	119	1.1000	11.70
30	VLVVDFGAQ	16	1.0000	10.64

31	IVREELTAA	428	1.0000	10.64
32	VLGICYGFQ	88	0.9000	9.57
33	FQAMAQALG	95	0.8000	8.51
34	VRTQIGDGH	218	0.8000	8.51
35	FTLVEPLRL	368	0.8000	8.51
36	VAAALVQRA	239	0.7000	7.45
37	IRAFEGAVR	313	0.7000	7.45
38	IWQCPVVLL	442	0.7000	7.45
39	LVLSGGPAS	60	0.6000	6.38
40	LLDLGVPVL	81	0.6000	6.38
41	LYPDVVESG	337	0.6000	6.38
42	LHSDLPEVQ	126	0.5000	5.32
43	FDVVASSAG	151	0.5000	5.32
44	LTCVFVDHG	252	0.5000	5.32
45	LGICYGFQA	89	0.4500	4.79
46	VALVLSGGP	58	0.4000	4.26
47	VAHTGTREY	106	0.4000	4.26
48	LRLLFKDEV	374	0.2000	2.13
49	VGRELGLPE	385	0.2000	2.13
50	LVVDFGAQY	17	0.1000	1.06
51	LAGVQYHPE	172	0.1000	1.06
52	IGRQFIRAF	308	0.1000	1.06

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IVGEVTAKR	410	5.2000	57.78
2	VVLDITSKP	509	4.9000	54.44
3	FLVQGTLYP	331	4.6000	51.11
4	VREELTAAG	429	3.8000	42.22
5	IKSHHNVGG	353	3.1800	35.33
6	LYPDVVESG	337	3.1000	34.44
7	LRHADSIVR	422	2.9800	33.11
8	VVLLADVRS	447	2.9800	33.11

9	VQRDFVAAT	270	2.7000	30.00
10	LKFTLVEPL	366	2.6600	29.56
11	IVREELTAA	428	2.1000	23.33
12	VTVDAAETF	283	2.0000	22.22
13	FGAQYAQLI	21	1.9000	21.11
14	LVVDFGAQY	17	1.8000	20.00
15	LVLSGGPAS	60	1.8000	20.00
16	LRPVSSEDA	471	1.8000	20.00
17	FLHDFAGLG	194	1.7000	18.89
18	FVDHGLLRA	256	1.5000	16.67
19	LHSDLPEVQ	126	1.4000	15.56
20	VFVDHGLLR	255	1.4000	15.56
21	YHPEVMHTP	177	1.2000	13.33
22	LFKDEVRAV	377	1.2000	13.33
23	WQCPVVLLA	443	1.2000	13.33
24	VSSEDAMTA	474	1.2000	13.33
25	VIPHTASIE	42	1.0000	11.11
26	YGFQAMAQA	93	1.0000	11.11
27	FQAMAQALG	95	1.0000	11.11
28	VLLADVRSV	448	1.0000	11.11
29	LGGIVAHTG	102	0.9000	10.00
30	VAHTGTREY	106	0.9000	10.00
31	LGAQWTPAN	201	0.9000	10.00
32	WMSHGDAVT	137	0.8000	8.89
33	VRSVGVQGD	453	0.8000	8.89
34	MTADWTRVP	480	0.8000	8.89
35	LERISTRIT	492	0.8000	8.89
36	FTLVEPLRL	368	0.7600	8.44
37	VAATGANLV	275	0.6000	6.67
38	FLEALSGVS	291	0.6000	6.67
39	IGRQFIRAF	308	0.6000	6.67
40	LRLLFKDEV	374	0.6000	6.67
41	VGRELGLPE	385	0.6000	6.67
42	IVLRPVSSE	469	0.6000	6.67

43	ITNEVAEVN	499	0.6000	6.67
44	VYADGAPKL	69	0.5600	6.22
45	FVAATGANL	274	0.5600	6.22
46	FAGLGAQWT	198	0.5000	5.56
47	IEQVRTQIG	215	0.5000	5.56
48	VPYEVLERI	487	0.5000	5.56
49	YGRTELKVL	114	0.4600	5.11
50	YGHPIVLRP	465	0.4000	4.44
51	IVAHTGTRE	105	0.3000	3.33
52	VVASSAGAP	153	0.3000	3.33

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	VVLLADVRS	447	3.6000	40.91
2	LRPVSSEDA	471	3.3000	37.50
3	VVLDITSKP	509	3.1000	35.23
4	LRHADSIVR	422	2.4800	28.18
5	IVGEVTAKR	410	2.1000	23.86
6	VRSVGVQGD	453	1.9000	21.59
7	IRIVGEVTA	408	1.7000	19.32
8	LERISTRIT	492	1.7000	19.32
9	VVDFGAQYA	18	1.6000	18.18
10	LVTVDAAET	282	1.4000	15.91
11	FLVQGTLYP	331	1.4000	15.91
12	IEQVRTQIG	215	1.3000	14.77
13	VLLADVRSV	448	1.3000	14.77
14	IVREELTAA	428	1.0000	11.36
15	VREELTAAG	429	0.8000	9.09
16	VAAALVQRA	239	0.7000	7.95
17	IRAFEGAVR	313	0.7000	7.95
18	LVLSGGPAS	60	0.6000	6.82
19	VQRDFVAAT	270	0.5000	5.68
20	IKSHHNVGG	353	0.5000	5.68

21	LGICYGFQA	89	0.4500	5.11
22	LGGIVAHTG	102	0.4000	4.55
23	VQPVWMSHG	133	0.4000	4.55
24	IVLRPVSSE	469	0.4000	4.55
25	VEPLRLLFK	371	0.3000	3.41
26	VLVVDFGAQ	16	0.2000	2.27
27	LKFTLVEPL	366	0.2000	2.27
28	VLRPVSSED	470	0.2000	2.27
29	VREARVFSE	33	0.1500	1.70
30	VLGICYGFQ	88	0.1000	1.14
31	WQCPVVLLA	443	0.1000	1.14
32	VAAFEAFDR	162	-0.0500	0
33	VPVLGICYG	86	-0.1000	0
34	LRLLFKDEV	374	-0.1000	0
35	LKVLGGKLH	119	-0.1200	0
36	FTLVEPLRL	368	-0.2000	0
37	LHSDLPEVQ	126	-0.3000	0
38	IWQCPVVLL	442	-0.3000	0
39	LLDLGVPVL	81	-0.4000	0
40	VRTQIGDGH	218	-0.4200	0
41	FQAMAQALG	95	-0.5000	0
42	LEALSGVSA	292	-0.5000	0
43	VSSEDAMTA	474	-0.5000	0
44	LADVRSVGV	450	-0.6000	0
45	VAHTGTREY	106	-0.7000	0
46	LHDFAGLGA	195	-0.7000	0
47	FLEALSGVS	291	-0.7000	0
48	LYPDVVESG	337	-0.7000	0
49	VIPHTASIE	42	-0.8000	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	VVLDITSKP	509	3.9000	45.35

2	IVGEVTAKR	410	3.7000	43.02
3	FLVQGTLYP	331	3.6000	41.86
4	VVLLADVRS	447	2.5800	30.00
5	VREELTAAG	429	2.4000	27.91
6	LHSDLPEVQ	126	2.1000	24.42
7	IVREELTAA	428	2.1000	24.42
8	VQRDFVAAT	270	2.0000	23.26
9	LRPVSSEDA	471	1.8000	20.93
10	IKSHHNVGG	353	1.7800	20.70
11	LYPDVVESG	337	1.7000	19.77
12	LKFTLVEPL	366	1.7000	19.77
13	FVDHGLLRA	256	1.5000	17.44
14	LRHADSIVR	422	1.4800	17.21
15	LVLSGGPAS	60	1.4000	16.28
16	WQCPVVLLA	443	1.2000	13.95
17	VSSEDAMTA	474	1.2000	13.95
18	FGAQYAQLI	21	1.0000	11.63
19	YGFQAMAQA	93	1.0000	11.63
20	LVVDFGAQY	17	0.5000	5.81
21	FLHDFAGLG	194	0.3000	3.49
22	VRTQIGDGH	218	0.2800	3.26
23	YHPEVMHTP	177	0.2000	2.33
24	WTPANIANA	205	0.2000	2.33
25	FLEALSGVS	291	0.2000	2.33
26	LFKDEVRAV	377	0.2000	2.33
27	LPEEIVARQ	391	0.2000	2.33
28	WMSHGDAVT	137	0.1000	1.16
29	LGAQWTPAN	201	0.1000	1.16
30	VTVDAAETF	283	0.1000	1.16
31	LERISTRIT	492	0.1000	1.16
32	VAAALVQRA	239	-0.1000	0
33	VFVDHGLLR	255	-0.1000	0
34	VQYHPEVMH	175	-0.1400	0
35	FAGLGAQWT	198	-0.2000	0

36	FTLVEPLRL	368	-0.2000	0
37	MTADWTRVP	480	-0.2000	0
38	ITNEVAEVN	499	-0.2000	0
39	VRSVGVQGD	453	-0.3000	0
40	LKVLGGKLH	119	-0.3200	0
41	VIPHTASIE	42	-0.4000	0
42	VYADGAPKL	69	-0.4000	0
43	FQAMAQALG	95	-0.4000	0
44	VAHTGTREY	106	-0.4000	0
45	FVAATGANL	274	-0.4000	0
46	VAATGANLV	275	-0.4000	0
47	LRLLFKDEV	374	-0.4000	0
48	VPYEVLERI	487	-0.4000	0
49	VFSEVIPHT	38	-0.5000	0
50	LGGIVAHTG	102	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FTLVEPLRL	368	7.0000	60.34
2	LKFTLVEPL	366	6.7000	57.76
3	YGRTELKVL	114	5.6000	48.28
4	FVAATGANL	274	4.9000	42.24
5	WTRVPYEVL	484	4.9000	42.24
6	IRARQPVAL	52	4.6000	39.66
7	IWQCPVVLL	442	4.0000	34.48
8	LRPVSSEDA	471	3.9000	33.62
9	VAATGANLV	275	3.8000	32.76
10	VLLADVRSV	448	3.8000	32.76
11	LRHADSIVR	422	3.6000	31.03
12	FGAQYAQLI	21	3.5000	30.17
13	VGEVTAKRL	411	3.1000	26.72
14	IPHTASIEE	43	2.8000	24.14
15	LADVRSVGV	450	2.8000	24.14

16	IRIVGEVTA	408	2.7000	23.28
17	VQGTLYPDV	333	2.6000	22.41
18	VLERISTRI	491	2.6000	22.41
19	VAEVNRVVL	503	2.6000	22.41
20	LVLSGGPAS	60	2.5000	21.55
21	LGICYGFQA	89	2.5000	21.55
22	VQRAIGDRL	244	2.4000	20.69
23	LVTVDAAET	282	2.4000	20.69
24	VAHTGTREY	106	2.3200	20.00
25	WQCPVVLLA	443	2.3000	19.83
26	VRSVGVQGD	453	2.3000	19.83
27	FVDHGLLRA	256	2.2000	18.97
28	VASSAGAPV	154	2.1000	18.10
29	VVASSAGAP	153	2.0000	17.24
30	LGIRIVGEV	406	2.0000	17.24
31	LERISTRIT	492	1.9200	16.55
32	YAQLIARRV	25	1.9000	16.38
33	VREARVFSE	33	1.9000	16.38
34	VWMSHGDAV	136	1.9000	16.38
35	IANALIEQV	210	1.9000	16.38
36	LVEPLRLLF	370	1.9000	16.38
37	VVQPADIDV	0	1.8000	15.52
38	FLVQGTLYP	331	1.5200	13.10
39	VYADGAPKL	69	1.5000	12.93
40	YEVLERIST	489	1.5000	12.93
41	VPETPARPV	8	1.4000	12.07
42	LGGKLHSDL	122	1.4000	12.07
43	LPEVQPVWM	130	1.3000	11.21
44	VDSAVAAAL	235	1.3000	11.21
45	FIRAFEGAV	312	1.3000	11.21
46	FEGAVRDVL	316	1.3000	11.21
47	VRAVGRELG	382	1.3000	11.21
48	VPYEVLERI	487	1.3000	11.21
49	LLDLGVPVL	81	1.2000	10.34

50	IVAHTGTRE	105	1.2000	10.34
51	VLSRFLHDF	190	1.2000	10.34
52	YGHPIVLRP	465	1.2000	10.34

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	FTLVEPLRL	368	7.0000	60.34
2	LKFTLVEPL	366	6.7000	57.76
3	YGRTELKVL	114	5.6000	48.28
4	FVAATGANL	274	4.9000	42.24
5	WTRVPYEVL	484	4.9000	42.24
6	IRARQPVAL	52	4.6000	39.66
7	IWQCPVVLL	442	4.0000	34.48
8	LRPVSSEDA	471	3.9000	33.62
9	VAATGANLV	275	3.8000	32.76
10	VLLADVRSV	448	3.8000	32.76
11	LRHADSIVR	422	3.6000	31.03
12	FGAQYAQLI	21	3.5000	30.17
13	VGEVTAKRL	411	3.1000	26.72
14	IPHTASIEE	43	2.8000	24.14
15	LADVRSVGV	450	2.8000	24.14
16	IRIVGEVTA	408	2.7000	23.28
17	VQGTLYPDV	333	2.6000	22.41
18	VLERISTRI	491	2.6000	22.41
19	VAEVNRVVL	503	2.6000	22.41
20	LVLSGGPAS	60	2.5000	21.55
21	LGICYGFQA	89	2.5000	21.55
22	VQRAIGDRL	244	2.4000	20.69
23	LVTVDAAET	282	2.4000	20.69
24	VAHTGTREY	106	2.3200	20.00
25	WQCPVVLLA	443	2.3000	19.83
26	VRSVGVQGD	453	2.3000	19.83
27	FVDHGLLRA	256	2.2000	18.97

28	VASSAGAPV	154	2.1000	18.10
29	VVASSAGAP	153	2.0000	17.24
30	LGIRIVGEV	406	2.0000	17.24
31	LERISTRIT	492	1.9200	16.55
32	YAQLIARRV	25	1.9000	16.38
33	VREARVFSE	33	1.9000	16.38
34	VWMSHGDAV	136	1.9000	16.38
35	IANALIEQV	210	1.9000	16.38
36	LVEPLRLLF	370	1.9000	16.38
37	VVQPADIDV	0	1.8000	15.52
38	FLVQGTLYP	331	1.5200	13.10
39	VYADGAPKL	69	1.5000	12.93
40	YEVLERIST	489	1.5000	12.93
41	VPETPARPV	8	1.4000	12.07
42	LGGKLHSDL	122	1.4000	12.07
43	LPEVQPVWM	130	1.3000	11.21
44	VDSAVAAAL	235	1.3000	11.21
45	FIRAFEGAV	312	1.3000	11.21
46	FEGAVRDVL	316	1.3000	11.21
47	VRAVGRELG	382	1.3000	11.21
48	VPYEVLERI	487	1.3000	11.21
49	LLDLGVPVL	81	1.2000	10.34
50	IVAHTGTRE	105	1.2000	10.34
51	VLSRFLHDF	190	1.2000	10.34
52	YGHPIVLRP	465	1.2000	10.34

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	IVLRPVSSE	469	5.6000	65.12
2	LGIRIVGEV	406	3.6000	41.86
3	IVARQPFPG	395	3.3000	38.37
4	LIARRVREA	28	3.0000	34.88
5	IRARQPVAL	52	2.9000	33.72

6	VRSVGVQGD	453	2.7000	31.40
7	FQAMAQALG	95	2.6000	30.23
8	LVQRAIGDR	243	2.6000	30.23
9	FDRRLAGVQ	168	2.5000	29.07
10	ITSKPPATI	513	1.9000	22.09
11	VLSRFLHDF	190	1.7000	19.77
12	VREARVFSE	33	1.6000	18.60
13	FTLVEPLRL	368	1.5000	17.44
14	FVAATGANL	274	1.4000	16.28
15	LRLLFKDEV	374	1.4000	16.28
16	IGDRLTCVF	248	1.2000	13.95
17	VLLADVRSV	448	1.2000	13.95
18	YEVLERIST	489	1.2000	13.95
19	LKVLGGKLH	119	1.1000	12.79
20	LVTVDAAET	282	1.1000	12.79
21	WQCPVVLLA	443	1.1000	12.79
22	FEAFDRRLA	165	1.0000	11.63
23	WTPANIANA	205	1.0000	11.63
24	LRAGERAQV	262	0.8000	9.30
25	VQRDFVAAT	270	0.8000	9.30
26	VPVLGICYG	86	0.7000	8.14
27	LGGKLHSDL	122	0.6000	6.98
28	LLFKDEVRA	376	0.6000	6.98
29	IRIVGEVTA	408	0.5000	5.81
30	IIGRQFIRA	307	0.4000	4.65
31	VRAVGRELG	382	0.4000	4.65
32	VLVVDFGAQ	16	0.2000	2.33
33	LVQGTLYPD	332	0.2000	2.33
34	FLVQGTLYP	331	0.1000	1.16
35	FKDEVRAVG	378	0.1000	1.16
36	IVGEVTAKR	410	0.1000	1.16
37	VREELTAAG	429	0.1000	1.16
38	ISTRITNEV	495	0.1000	1.16
39	LVLSGGPAS	60	-0.1000	0

40	VLGICYGFQ	88	-0.1000	0
41	FLEALSGVS	291	-0.1000	0
42	YAQLIARRV	25	-0.3000	0
43	ICGLSGGVD	228	-0.3000	0
44	FVDHGLLRA	256	-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	LGIRIVGEV	406	3.3000	41.25
2	LIARRVREA	28	3.0000	37.50
3	LVQRAIGDR	243	2.6000	32.50
4	IVLRPVSSE	469	2.6000	32.50
5	IVARQPFPG	395	2.0000	25.00
6	IRARQPVAL	52	1.9000	23.75
7	FDRRLAGVQ	168	1.7000	21.25
8	ITSKPPATI	513	1.7000	21.25
9	FQAMAQALG	95	1.3000	16.25
10	LRLLFKDEV	374	1.1000	13.75
11	WQCPVVLLA	443	1.1000	13.75
12	FEAFDRRLA	165	1.0000	12.50
13	WTPANIANA	205	1.0000	12.50
14	VLLADVRSV	448	0.9000	11.25
15	VLSRFLHDF	190	0.8000	10.00
16	LLFKDEVRA	376	0.6000	7.50
17	LRAGERAQV	262	0.5000	6.25
18	FTLVEPLRL	368	0.5000	6.25
19	IRIVGEVTA	408	0.5000	6.25
20	FVAATGANL	274	0.4000	5.00
21	IIGRQFIRA	307	0.4000	5.00
22	IGDRLTCVF	248	0.3000	3.75
23	YEVLERIST	489	0.3000	3.75
24	LVTVDAAET	282	0.2000	2.50
25	IVGEVTAKR	410	0.1000	1.25

26	LVLSGGPAS	60	-0.1000	0
27	VQRDFVAAT	270	-0.1000	0
28	FLEALSGVS	291	-0.1000	0
29	LKVLGGKLH	119	-0.1200	0
30	ISTRITNEV	495	-0.2000	0
31	FVDHGLLRA	256	-0.3000	0
32	FLVQGTLYP	331	-0.3000	0
33	VEPLRLLFK	371	-0.3000	0
34	IARRVREAR	29	-0.4000	0
35	LGGKLHSDL	122	-0.4000	0
36	LRHADSIVR	422	-0.5000	0
37	VLVVDFGAQ	16	-0.6000	0
38	YAQLIARRV	25	-0.6000	0
39	VPVLGICYG	86	-0.6000	0
40	LGICYGFQA	89	-0.6000	0
41	YGFQAMAQA	93	-0.6000	0
42	YGHPIVLRP	465	-0.7000	0
43	LRPVSSEDA	471	-0.7000	0
44	VVLDITSKP	509	-0.7000	0
45	VMHTPHGQQ	181	-0.8000	0
46	LLRAGERAQ	261	-0.8000	0
47	FIRAFEGAV	312	-0.8000	0
48	VVDFGAQYA	18	-0.9000	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	LGIRIVGEV	406	4.3000	53.75
2	LIARRVREA	28	4.0000	50.00
3	LVQRAIGDR	243	3.6000	45.00
4	IVLRPVSSE	469	3.6000	45.00
5	IVARQPFPG	395	3.0000	37.50
6	IRARQPVAL	52	2.9000	36.25
7	ITSKPPATI	513	2.7000	33.75

8	LRLLFKDEV	374	2.1000	26.25
9	VLLADVRSV	448	1.9000	23.75
10	VLSRFLHDF	190	1.8000	22.50
11	LLFKDEVRA	376	1.6000	20.00
12	LRAGERAQV	262	1.5000	18.75
13	IRIVGEVTA	408	1.5000	18.75
14	IIGRQFIRA	307	1.4000	17.50
15	IGDRLTCVF	248	1.3000	16.25
16	LVTVDAAET	282	1.2000	15.00
17	IVGEVTAKR	410	1.1000	13.75
18	IRAFEGAVR	313	1.0000	12.50
19	VVLLADVRS	447	1.0000	12.50
20	VRSVGVQGD	453	1.0000	12.50
21	LVLSGGPAS	60	0.9000	11.25
22	VQRDFVAAT	270	0.9000	11.25
23	LKVLGGKLH	119	0.8800	11.00
24	ISTRITNEV	495	0.8000	10.00
25	FDRRLAGVQ	168	0.7000	8.75
26	VEPLRLLFK	371	0.7000	8.75
27	IARRVREAR	29	0.6000	7.50
28	LGGKLHSDL	122	0.6000	7.50
29	LRHADSIVR	422	0.5000	6.25
30	VLVVDFGAQ	16	0.4000	5.00
31	VPVLGICYG	86	0.4000	5.00
32	LGICYGFQA	89	0.4000	5.00
33	FQAMAQALG	95	0.3000	3.75
34	LRPVSSEDA	471	0.3000	3.75
35	VVLDITSKP	509	0.3000	3.75
36	VMHTPHGQQ	181	0.2000	2.50
37	LLRAGERAQ	261	0.2000	2.50
38	VVDFGAQYA	18	0.1000	1.25
39	VLGICYGFQ	88	0.1000	1.25
40	VRAVGRELG	382	0.1000	1.25
41	WQCPVVLLA	443	0.1000	1.25

42	LERISTRIT	492	0.1000	1.25
43	LVVDFGAQY	17	-0.1000	0
44	VREELTAAG	429	-0.2000	0
45	LGVPVLGIC	84	-0.3000	0
46	LFKDEVRAV	377	-0.3000	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	IVLRPVSSE	469	6.6000	76.74
2	LGIRIVGEV	406	4.6000	53.49
3	IVARQPFPG	395	4.3000	50.00
4	LIARRVREA	28	4.0000	46.51
5	IRARQPVAL	52	3.9000	45.35
6	VRSVGVQGD	453	3.7000	43.02
7	LVQRAIGDR	243	3.6000	41.86
8	ITSKPPATI	513	2.9000	33.72
9	VLSRFLHDF	190	2.7000	31.40
10	VREARVFSE	33	2.6000	30.23
11	LRLLFKDEV	374	2.4000	27.91
12	IGDRLTCVF	248	2.2000	25.58
13	VLLADVRSV	448	2.2000	25.58
14	LKVLGGKLH	119	2.1000	24.42
15	LVTVDAAET	282	2.1000	24.42
16	LRAGERAQV	262	1.8000	20.93
17	VQRDFVAAT	270	1.8000	20.93
18	VPVLGICYG	86	1.7000	19.77
19	FQAMAQALG	95	1.6000	18.60
20	LGGKLHSDL	122	1.6000	18.60
21	LLFKDEVRA	376	1.6000	18.60
22	FDRRLAGVQ	168	1.5000	17.44
23	IRIVGEVTA	408	1.5000	17.44
24	IIGRQFIRA	307	1.4000	16.28
25	VRAVGRELG	382	1.4000	16.28

26	VLVVDFGAQ	16	1.2000	13.95
27	LVQGTLYPD	332	1.2000	13.95
28	IVGEVTAKR	410	1.1000	12.79
29	VREELTAAG	429	1.1000	12.79
30	ISTRITNEV	495	1.1000	12.79
31	LVVDFGAQY	17	1.0000	11.63
32	VMHTPHGQQ	181	1.0000	11.63
33	LLRAGERAQ	261	1.0000	11.63
34	IRAFEGAVR	313	1.0000	11.63
35	VVLLADVRS	447	1.0000	11.63
36	LERISTRIT	492	1.0000	11.63
37	LVLSGGPAS	60	0.9000	10.47
38	VLGICYGFQ	88	0.9000	10.47
39	ICGLSGGVD	228	0.7000	8.14
40	VVLDITSKP	509	0.7000	8.14
41	IARRVREAR	29	0.6000	6.98
42	VLGGKLHSD	121	0.5000	5.81
43	FTLVEPLRL	368	0.5000	5.81
44	LVEPLRLLF	370	0.5000	5.81
45	VGRELGLPE	385	0.5000	5.81
46	LRHADSIVR	422	0.5000	5.81
47	VIPHTASIE	42	0.4000	4.65
48	LLDLGVPVL	81	0.4000	4.65
49	LGICYGFQA	89	0.4000	4.65
50	LGGIVAHTG	102	0.4000	4.65
51	FVAATGANL	274	0.4000	4.65
52	VLSGGPASV	61	0.3000	3.49

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	IVLRPVSSE	469	4.4000	50.57
2	IRARQPVAL	52	2.9000	33.33
3	IVARQPFPG	395	2.8500	32.76

4	LIARRVREA	28	2.7000	31.03
5	LGIRIVGEV	406	2.6000	29.89
6	LRLLFKDEV	374	2.3000	26.44
7	LVQRAIGDR	243	1.9000	21.84
8	ISTRITNEV	495	1.8000	20.69
9	WQCPVVLLA	443	1.7000	19.54
10	ITSKPPATI	513	1.7000	19.54
11	LLFKDEVRA	376	1.6000	18.39
12	IRIVGEVTA	408	1.5000	17.24
13	LGGKLHSDL	122	1.4000	16.09
14	IVREELTAA	428	1.4000	16.09
15	IARRVREAR	29	1.3000	14.94
16	FQAMAQALG	95	1.3000	14.94
17	VLSRFLHDF	190	1.3000	14.94
18	IIGRQFIRA	307	1.2800	14.71
19	YEVLERIST	489	1.1800	13.56
20	FTLVEPLRL	368	1.1000	12.64
21	VLERISTRI	491	1.1000	12.64
22	VVLDITSKP	509	1.1000	12.64
23	FDRRLAGVQ	168	1.0000	11.49
24	WTPANIANA	205	1.0000	11.49
25	VVLLADVRS	447	1.0000	11.49
26	VRSVGVQGD	453	1.0000	11.49
27	LRPVSSEDA	471	1.0000	11.49
28	VRAVGRELG	382	0.8000	9.20
29	FEAFDRRLA	165	0.7000	8.05
30	VLLADVRSV	448	0.6000	6.90
31	LRAGERAQV	262	0.5000	5.75
32	FVAATGANL	274	0.4000	4.60
33	LRHADSIVR	422	0.3800	4.37
34	IGDRLTCVF	248	0.3000	3.45
35	FVDHGLLRA	256	0.3000	3.45
36	FLVQGTLYP	331	0.3000	3.45
37	VEPLRLLFK	371	0.3000	3.45

38	LGICYGFQA	89	0.2500	2.87
39	LVTVDAAET	282	0.2000	2.30
40	VVDFGAQYA	18	0.1000	1.15
41	LVLSGGPAS	60	0.1000	1.15
42	IVGEVTAKR	410	0.1000	1.15
43	VQRDFVAAT	270	-0.1000	0
44	YGHPIVLRP	465	-0.1000	0
45	VQGDGRTYG	458	-0.2000	0
46	FAGLGAQWT	198	-0.5000	0
47	LLADVRSVG	449	-0.5000	0
48	VREARVFSE	33	-0.5500	0
49	VPVLGICYG	86	-0.6000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IVLRPVSSE	469	5.6000	55.45
2	IVARQPFPG	395	3.8000	37.62
3	LGIRIVGEV	406	3.7000	36.63
4	IRARQPVAL	52	3.4000	33.66
5	FTLVEPLRL	368	3.3000	32.67
6	LIARRVREA	28	3.2000	31.68
7	WQCPVVLLA	443	2.9000	28.71
8	VRSVGVQGD	453	2.8000	27.72
9	YEVLERIST	489	2.8000	27.72
10	LVQRAIGDR	243	2.7000	26.73
11	FQAMAQALG	95	2.6000	25.74
12	FDRRLAGVQ	168	2.6000	25.74
13	VLSRFLHDF	190	2.4000	23.76
14	VREARVFSE	33	2.1000	20.79
15	IIGRQFIRA	307	2.0000	19.80
16	FLVQGTLYP	331	1.9000	18.81
17	ITSKPPATI	513	1.9000	18.81
18	LKVLGGKLH	119	1.7000	16.83

19	FVDHGLLRA	256	1.5000	14.85
20	VRAVGRELG	382	1.5000	14.85
21	YGHPIVLRP	465	1.5000	14.85
22	FVAATGANL	274	1.4000	13.86
23	VLLADVRSV	448	1.4000	13.86
24	LVEPLRLLF	370	1.3000	12.87
25	VGRELGLPE	385	1.3000	12.87
26	FEAFDRRLA	165	1.2000	11.88
27	IGDRLTCVF	248	1.2000	11.88
28	LVTVDAAET	282	1.1000	10.89
29	LRLLFKDEV	374	1.1000	10.89
30	LLFKDEVRA	376	1.1000	10.89
31	LRHADSIVR	422	1.1000	10.89
32	LVLSGGPAS	60	1.0500	10.40
33	WTPANIANA	205	1.0000	9.90
34	IRIVGEVTA	408	1.0000	9.90
35	LVQGTLYPD	332	0.9000	8.91
36	LRAGERAQV	262	0.8000	7.92
37	VQRDFVAAT	270	0.8000	7.92
38	VEPLRLLFK	371	0.8000	7.92
39	IARRVREAR	29	0.7000	6.93
40	VPVLGICYG	86	0.7000	6.93
41	LGGKLHSDL	122	0.6000	5.94
42	LLDLGVPVL	81	0.5500	5.45
43	VVLLADVRS	447	0.5000	4.95
44	LRPVSSEDA	471	0.4000	3.96
45	ISTRITNEV	495	0.4000	3.96
46	VLVVDFGAQ	16	0.3000	2.97
47	YGRTELKVL	114	0.2000	1.98
48	VLGGKLHSD	121	0.2000	1.98
49	LLRAGERAQ	261	0.2000	1.98
50	LERISTRIT	492	0.2000	1.98
51	LGGIVAHTG	102	0.1000	0.99
52	VMHTPHGQQ	181	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	FTLVEPLRL	368	2.4000	28.92
2	YEVLERIST	489	2.3000	27.71
3	WQCPVVLLA	443	2.2000	26.51
4	FLVQGTLYP	331	2.1000	25.30
5	FVDHGLLRA	256	1.9000	22.89
6	VEPLRLLFK	371	1.9000	22.89
7	LVLSGGPAS	60	1.3500	16.27
8	LRLLFKDEV	374	1.2000	14.46
9	FEAFDRRLA	165	1.1000	13.25
10	IRIVGEVTA	408	1.1000	13.25
11	LRHADSIVR	422	1.1000	13.25
12	VLLADVRSV	448	1.1000	13.25
13	WTPANIANA	205	1.0000	12.05
14	FQAMAQALG	95	0.9000	10.84
15	VVLLADVRS	447	0.9000	10.84
16	LKVLGGKLH	119	0.8800	10.60
17	LRPVSSEDA	471	0.5000	6.02
18	FVAATGANL	274	0.4000	4.82
19	LGIRIVGEV	406	0.4000	4.82
20	YGHPIVLRP	465	0.4000	4.82
21	LVTVDAAET	282	0.3000	3.61
22	VRAVGRELG	382	0.3000	3.61
23	LIARRVREA	28	0.2000	2.41
24	VRSVGVQGD	453	0.2000	2.41
25	LLDLGVPVL	81	-0.0500	0
26	LGICYGFQA	89	-0.1000	0
27	IRAFEGAVR	313	-0.1000	0
28	LERISTRIT	492	-0.1000	0
29	LDITSKPPA	511	-0.1500	0
30	VPVLGICYG	86	-0.2000	0

31	VLGICYGFQ	88	-0.2000	0
32	LRAGERAQV	262	-0.2000	0
33	VMHTPHGQQ	181	-0.3000	0
34	LHDFAGLGA	195	-0.3000	0
35	LVQRAIGDR	243	-0.3000	0
36	LVEPLRLLF	370	-0.3000	0
37	VLVVDFGAQ	16	-0.4000	0
38	YGRTELKVL	114	-0.4000	0
39	IVLRPVSSE	469	-0.4000	0
40	IVARQPFPG	395	-0.5000	0
41	IRARQPVAL	52	-0.6000	0
42	LGGIVAHTG	102	-0.6000	0
43	LLRAGERAQ	261	-0.6000	0
44	IVGEVTAKR	410	-0.6000	0
45	LDTLRHADS	419	-0.6000	0
46	FIRAFEGAV	312	-0.7000	0
47	FSEVIPHTA	39	-0.8000	0
48	VQRDFVAAT	270	-0.8000	0

ALLELE: DRB1_1102	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	LIARRVREA	28	3.7000	44.05
2	VLLADVRSV	448	3.7000	44.05
3	IGRQFIRAF	308	2.7000	32.14
4	LRLLFKDEV	374	2.7000	32.14
5	IVARQPFPG	395	2.4000	28.57
6	FEAFDRRLA	165	2.1000	25.00
7	VQYHPEVMH	175	2.0800	24.76
8	LVLSGGPAS	60	2.0000	23.81
9	LLRAGERAQ	261	2.0000	23.81
10	LGICYGFQA	89	1.9000	22.62
11	FVDHGLLRA	256	1.9000	22.62
12	IVLRPVSSE	469	1.9000	22.62

13	IRARQPVAL	52	1.8000	21.43
14	VVLLADVRS	447	1.7000	20.24
15	LKVLGGKLH	119	1.3800	16.43
16	IRAFEGAVR	313	1.3000	15.48
17	IRIVGEVTA	408	1.3000	15.48
18	VVDFGAQYA	18	1.2000	14.29
19	LGIRIVGEV	406	1.2000	14.29
20	ITSKPPATI	513	1.2000	14.29
21	VREARVFSE	33	1.1000	13.10
22	IKSHHNVGG	353	1.1000	13.10
23	VEPLRLLFK	371	1.1000	13.10
24	LLFKDEVRA	376	1.1000	13.10
25	LFKDEVRAV	377	1.1000	13.10
26	LRAGERAQV	262	1.0000	11.90
27	FLVQGTLYP	331	1.0000	11.90
28	IVGEVTAKR	410	1.0000	11.90
29	IVREELTAA	428	1.0000	11.90
30	LERISTRIT	492	1.0000	11.90
31	VLSRFLHDF	190	0.9000	10.71
32	VAAALVQRA	239	0.8000	9.52
33	LRHADSIVR	422	0.8000	9.52
34	VRTQIGDGH	218	0.6800	8.10
35	VRSVGVQGD	453	0.6000	7.14
36	LVQRAIGDR	243	0.5000	5.95
37	VQRDFVAAT	270	0.5000	5.95
38	LRPVSSEDA	471	0.5000	5.95
39	VAAFEAFDR	162	0.4000	4.76
40	VIPHTASIE	42	0.3000	3.57
41	IVAHTGTRE	105	0.3000	3.57
42	LIEQVRTQI	214	0.3000	3.57
43	VRAVGRELG	382	0.3000	3.57
44	WQCPVVLLA	443	0.3000	3.57
45	VVLDITSKP	509	0.3000	3.57
46	VPVLGICYG	86	0.1000	1.19

47	VAHTGTREY	106	0.1000	1.19
48	ISTRITNEV	495	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	VEPLRLLFK	371	2.9000	34.94
2	LVLSGGPAS	60	2.3500	28.31
3	LRLLFKDEV	374	2.2000	26.51
4	IRIVGEVTA	408	2.1000	25.30
5	LRHADSIVR	422	2.1000	25.30
6	VLLADVRSV	448	2.1000	25.30
7	VVLLADVRS	447	1.9000	22.89
8	LKVLGGKLH	119	1.8800	22.65
9	LRPVSSEDA	471	1.5000	18.07
10	FTLVEPLRL	368	1.4000	16.87
11	LGIRIVGEV	406	1.4000	16.87
12	LVTVDAAET	282	1.3000	15.66
13	VRAVGRELG	382	1.3000	15.66
14	YEVLERIST	489	1.3000	15.66
15	LIARRVREA	28	1.2000	14.46
16	WQCPVVLLA	443	1.2000	14.46
17	VRSVGVQGD	453	1.2000	14.46
18	FLVQGTLYP	331	1.1000	13.25
19	LLDLGVPVL	81	0.9500	11.45
20	LGICYGFQA	89	0.9000	10.84
21	FVDHGLLRA	256	0.9000	10.84
22	IRAFEGAVR	313	0.9000	10.84
23	LERISTRIT	492	0.9000	10.84
24	LDITSKPPA	511	0.8500	10.24
25	VPVLGICYG	86	0.8000	9.64
26	VLGICYGFQ	88	0.8000	9.64
27	LRAGERAQV	262	0.8000	9.64
28	VMHTPHGQQ	181	0.7000	8.43

29	LHDFAGLGA	195	0.7000	8.43
30	LVQRAIGDR	243	0.7000	8.43
31	LVEPLRLLF	370	0.7000	8.43
32	VLVVDFGAQ	16	0.6000	7.23
33	IVLRPVSSE	469	0.6000	7.23
34	IVARQPFPG	395	0.5000	6.02
35	IRARQPVAL	52	0.4000	4.82
36	LGGIVAHTG	102	0.4000	4.82
37	LLRAGERAQ	261	0.4000	4.82
38	IVGEVTAKR	410	0.4000	4.82
39	LDTLRHADS	419	0.4000	4.82
40	VQRDFVAAT	270	0.2000	2.41
41	LKFTLVEPL	366	0.2000	2.41
42	VVDFGAQYA	18	0.1000	1.20
43	VREARVFSE	33	0.1000	1.20
44	FEAFDRRLA	165	0.1000	1.20
45	VAAALVQRA	239	0.1000	1.20
46	IGRQFIRAF	308	0.1000	1.20
47	FQAMAQALG	95	-0.1000	0
48	LEALSGVSA	292	-0.1000	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	VEPLRLLFK	371	2.9000	34.94
2	LVLSGGPAS	60	2.3500	28.31
3	LRLLFKDEV	374	2.2000	26.51
4	IRIVGEVTA	408	2.1000	25.30
5	LRHADSIVR	422	2.1000	25.30
6	VLLADVRSV	448	2.1000	25.30
7	VVLLADVRS	447	1.9000	22.89
8	LKVLGGKLH	119	1.8800	22.65
9	LRPVSSEDA	471	1.5000	18.07
10	FTLVEPLRL	368	1.4000	16.87

11	LGIRIVGEV	406	1.4000	16.87
12	LVTVDAAET	282	1.3000	15.66
13	VRAVGRELG	382	1.3000	15.66
14	YEVLERIST	489	1.3000	15.66
15	LIARRVREA	28	1.2000	14.46
16	WQCPVVLLA	443	1.2000	14.46
17	VRSVGVQGD	453	1.2000	14.46
18	FLVQGTLYP	331	1.1000	13.25
19	LLDLGVPVL	81	0.9500	11.45
20	LGICYGFQA	89	0.9000	10.84
21	FVDHGLLRA	256	0.9000	10.84
22	IRAFEGAVR	313	0.9000	10.84
23	LERISTRIT	492	0.9000	10.84
24	LDITSKPPA	511	0.8500	10.24
25	VPVLGICYG	86	0.8000	9.64
26	VLGICYGFQ	88	0.8000	9.64
27	LRAGERAQV	262	0.8000	9.64
28	VMHTPHGQQ	181	0.7000	8.43
29	LHDFAGLGA	195	0.7000	8.43
30	LVQRAIGDR	243	0.7000	8.43
31	LVEPLRLLF	370	0.7000	8.43
32	VLVVDFGAQ	16	0.6000	7.23
33	IVLRPVSSE	469	0.6000	7.23
34	IVARQPFPG	395	0.5000	6.02
35	IRARQPVAL	52	0.4000	4.82
36	LGGIVAHTG	102	0.4000	4.82
37	LLRAGERAQ	261	0.4000	4.82
38	IVGEVTAKR	410	0.4000	4.82
39	LDTLRHADS	419	0.4000	4.82
40	VQRDFVAAT	270	0.2000	2.41
41	LKFTLVEPL	366	0.2000	2.41
42	VVDFGAQYA	18	0.1000	1.20
43	VREARVFSE	33	0.1000	1.20
44	FEAFDRRLA	165	0.1000	1.20

45	VAAALVQRA	239	0.1000	1.20
46	IGRQFIRAF	308	0.1000	1.20
47	FQAMAQALG	95	-0.1000	0
48	LEALSGVSA	292	-0.1000	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	VVLDITSKP	509	4.9700	54.62
2	LVLSGGPAS	60	4.5000	49.45
3	VQRDFVAAT	270	4.2000	46.15
4	LHSDLPEVQ	126	4.1000	45.05
5	VQGDGRTYG	458	3.6000	39.56
6	LYPDVVESG	337	3.5000	38.46
7	LLADVRSVG	449	3.3700	37.03
8	LVVDFGAQY	17	3.2000	35.16
9	LRLLFKDEV	374	3.2000	35.16
10	LRAGERAQV	262	3.0000	32.97
11	VYADGAPKL	69	2.9000	31.87
12	LFKDEVRAV	377	2.7000	29.67
13	IRIVGEVTA	408	2.5000	27.47
14	LRPVSSEDA	471	2.2000	24.18
15	VFVDHGLLR	255	2.1000	23.08
16	VRAVGRELG	382	2.0000	21.98
17	IVREELTAA	428	1.9000	20.88
18	LGICYGFQA	89	1.8000	19.78
19	VRSVGVQGD	453	1.8000	19.78
20	LRHADSIVR	422	1.7000	18.68
21	IVLRPVSSE	469	1.6700	18.35
22	VVASSAGAP	153	1.6000	17.58
23	FLHDFAGLG	194	1.6000	17.58
24	VTVDAAETF	283	1.6000	17.58
25	LGIRIVGEV	406	1.6000	17.58
26	VVLLADVRS	447	1.6000	17.58

27	VLLADVRSV	448	1.6000	17.58
28	VLSGGPASV	61	1.5000	16.48
29	LPDDLKFTL	362	1.3000	14.29
30	LDITSKPPA	511	1.2000	13.19
31	VAAALVQRA	239	1.1000	12.09
32	IVARQPFPG	395	1.1000	12.09
33	IVGEVTAKR	410	1.1000	12.09
34	LVQGTLYPD	332	1.0500	11.54
35	VREARVFSE	33	1.0000	10.99
36	ICYGFQAMA	91	1.0000	10.99
37	VRTQIGDGH	218	0.9800	10.77
38	IRARQPVAL	52	0.9000	9.89
39	VLGICYGFQ	88	0.9000	9.89
40	LVQRAIGDR	243	0.9000	9.89
41	LVTVDAAET	282	0.9000	9.89
42	LKFTLVEPL	366	0.9000	9.89
43	MTADWTRVP	480	0.9000	9.89
44	VQYHPEVMH	175	0.8800	9.67
45	VMHTPHGQQ	181	0.8000	8.79
46	VLVVDFGAQ	16	0.7000	7.69
47	LLDLGVPVL	81	0.6000	6.59
48	MSHGDAVTA	138	0.6000	6.59
49	LGAQWTPAN	201	0.6000	6.59
50	WQCPVVLLA	443	0.6000	6.59
51	LIEQVRTQI	214	0.5000	5.49
52	VEPLRLLFK	371	0.5000	5.49

ALLELE: DRB1_1114	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	FEAFDRRLA	165	3.1000	36.90
2	FVDHGLLRA	256	2.9000	34.52
3	LIARRVREA	28	2.7000	32.14
4	VLLADVRSV	448	2.7000	32.14

5	FLVQGTLYP	331	2.0000	23.81
6	IGRQFIRAF	308	1.7000	20.24
7	LRLLFKDEV	374	1.7000	20.24
8	IVARQPFPG	395	1.4000	16.67
9	WQCPVVLLA	443	1.3000	15.48
10	VQYHPEVMH	175	1.0800	12.86
11	LVLSGGPAS	60	1.0000	11.90
12	YGFQAMAQA	93	1.0000	11.90
13	WTPANIANA	205	1.0000	11.90
14	LLRAGERAQ	261	1.0000	11.90
15	YAQLIARRV	25	0.9000	10.71
16	LGICYGFQA	89	0.9000	10.71
17	IVLRPVSSE	469	0.9000	10.71
18	IRARQPVAL	52	0.8000	9.52
19	FQAMAQALG	95	0.7000	8.33
20	VVLLADVRS	447	0.7000	8.33
21	FGAQYAQLI	21	0.4000	4.76
22	FVAATGANL	274	0.4000	4.76
23	LKVLGGKLH	119	0.3800	4.52
24	IRAFEGAVR	313	0.3000	3.57
25	IRIVGEVTA	408	0.3000	3.57
26	YEVLERIST	489	0.3000	3.57
27	VVDFGAQYA	18	0.2000	2.38
28	LGIRIVGEV	406	0.2000	2.38
29	ITSKPPATI	513	0.2000	2.38
30	VREARVFSE	33	0.1000	1.19
31	IKSHHNVGG	353	0.1000	1.19
32	VEPLRLLFK	371	0.1000	1.19
33	LLFKDEVRA	376	0.1000	1.19
34	LFKDEVRAV	377	0.1000	1.19
35	VLSRFLHDF	190	-0.1000	0
36	VAAALVQRA	239	-0.2000	0
37	LRHADSIVR	422	-0.2000	0
38	VRTQIGDGH	218	-0.3200	0

39	VRSVGVQGD	453	-0.4000	0
40	LVQRAIGDR	243	-0.5000	0
41	VQRDFVAAT	270	-0.5000	0
42	YGHPIVLRP	465	-0.5000	0
43	LRPVSSEDA	471	-0.5000	0
44	VAAFEAFDR	162	-0.6000	0
45	VIPHTASIE	42	-0.7000	0
46	IVAHTGTRE	105	-0.7000	0

ALLELE: DRB1_1120	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VLLADVRSV	448	3.7000	42.05
2	IGRQFIRAF	308	3.6000	40.91
3	FEAFDRRLA	165	3.1000	35.23
4	FLVQGTLYP	331	3.0000	34.09
5	FVDHGLLRA	256	2.9000	32.95
6	IVARQPFPG	395	2.8000	31.82
7	LIARRVREA	28	2.7000	30.68
8	LRLLFKDEV	374	2.7000	30.68
9	IVLRPVSSE	469	2.3000	26.14
10	FQAMAQALG	95	2.1000	23.86
11	YAQLIARRV	25	1.9000	21.59
12	VLSRFLHDF	190	1.8000	20.45
13	IRAFEGAVR	313	1.8000	20.45
14	IRARQPVAL	52	1.7600	20.00
15	VREARVFSE	33	1.5000	17.05
16	IKSHHNVGG	353	1.5000	17.05
17	IVGEVTAKR	410	1.5000	17.05
18	LVLSGGPAS	60	1.4000	15.91
19	FVAATGANL	274	1.3600	15.45
20	FGAQYAQLI	21	1.3000	14.77
21	LRHADSIVR	422	1.3000	14.77
22	WQCPVVLLA	443	1.3000	14.77

23	LGIRIVGEV	406	1.2000	13.64
24	LFKDEVRAV	377	1.1000	12.50
25	VVLLADVRS	447	1.1000	12.50
26	ITSKPPATI	513	1.1000	12.50
27	YGFQAMAQA	93	1.0000	11.36
28	WTPANIANA	205	1.0000	11.36
29	LVQRAIGDR	243	1.0000	11.36
30	LRAGERAQV	262	1.0000	11.36
31	YEVLERIST	489	1.0000	11.36
32	FTLVEPLRL	368	0.9600	10.91
33	LGICYGFQA	89	0.9000	10.23
34	VAAFEAFDR	162	0.9000	10.23
35	VIPHTASIE	42	0.7000	7.95
36	IVAHTGTRE	105	0.7000	7.95
37	LVEPLRLLF	370	0.7000	7.95
38	VRAVGRELG	382	0.7000	7.95
39	VRSVGVQGD	453	0.7000	7.95
40	LERISTRIT	492	0.7000	7.95
41	VPVLGICYG	86	0.5000	5.68
42	VQYHPEVMH	175	0.5000	5.68
43	YGHPIVLRP	465	0.5000	5.68
44	IARRVREAR	29	0.4000	4.55
45	VAHTGTREY	106	0.4000	4.55
46	LLRAGERAQ	261	0.3000	3.41
47	IRIVGEVTA	408	0.3000	3.41
48	VVLDITSKP	509	0.3000	3.41
49	YGRTELKVL	114	0.2600	2.95
50	VVDFGAQYA	18	0.2000	2.27
51	LIEQVRTQI	214	0.2000	2.27
52	VQRDFVAAT	270	0.2000	2.27

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	LIARRVREA	28	3.7000	44.05
2	VLLADVRSV	448	3.7000	44.05
3	IGRQFIRAF	308	2.7000	32.14
4	LRLLFKDEV	374	2.7000	32.14
5	IVARQPFPG	395	2.4000	28.57
6	FEAFDRRLA	165	2.1000	25.00
7	VQYHPEVMH	175	2.0800	24.76
8	LVLSGGPAS	60	2.0000	23.81
9	LLRAGERAQ	261	2.0000	23.81
10	LGICYGFQA	89	1.9000	22.62
11	FVDHGLLRA	256	1.9000	22.62
12	IVLRPVSSE	469	1.9000	22.62
13	IRARQPVAL	52	1.8000	21.43
14	VVLLADVRS	447	1.7000	20.24
15	LKVLGGKLH	119	1.3800	16.43
16	IRAFEGAVR	313	1.3000	15.48
17	IRIVGEVTA	408	1.3000	15.48
18	VVDFGAQYA	18	1.2000	14.29
19	LGIRIVGEV	406	1.2000	14.29
20	ITSKPPATI	513	1.2000	14.29
21	VREARVFSE	33	1.1000	13.10
22	IKSHHNVGG	353	1.1000	13.10
23	VEPLRLLFK	371	1.1000	13.10
24	LLFKDEVRA	376	1.1000	13.10
25	LFKDEVRAV	377	1.1000	13.10
26	LRAGERAQV	262	1.0000	11.90
27	FLVQGTLYP	331	1.0000	11.90
28	IVGEVTAKR	410	1.0000	11.90
29	IVREELTAA	428	1.0000	11.90
30	LERISTRIT	492	1.0000	11.90
31	VLSRFLHDF	190	0.9000	10.71
32	VAAALVQRA	239	0.8000	9.52
33	LRHADSIVR	422	0.8000	9.52
34	VRTQIGDGH	218	0.6800	8.10

35	VRSVGVQGD	453	0.6000	7.14
36	LVQRAIGDR	243	0.5000	5.95
37	VQRDFVAAT	270	0.5000	5.95
38	LRPVSSEDA	471	0.5000	5.95
39	VAAFEAFDR	162	0.4000	4.76
40	VIPHTASIE	42	0.3000	3.57
41	IVAHTGTRE	105	0.3000	3.57
42	LIEQVRTQI	214	0.3000	3.57
43	VRAVGRELG	382	0.3000	3.57
44	WQCPVVLLA	443	0.3000	3.57
45	VVLDITSKP	509	0.3000	3.57
46	VPVLGICYG	86	0.1000	1.19
47	VAHTGTREY	106	0.1000	1.19
48	ISTRITNEV	495	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	FTLVEPLRL	368	3.3600	38.62
2	FLVQGTLYP	331	3.1000	35.63
3	YEVLERIST	489	3.0000	34.48
4	LRHADSIVR	422	2.6000	29.89
5	FQAMAQALG	95	2.3000	26.44
6	LRLLFKDEV	374	2.2000	25.29
7	WQCPVVLLA	443	2.2000	25.29
8	VLLADVRSV	448	2.1000	24.14
9	VEPLRLLFK	371	2.0000	22.99
10	FVDHGLLRA	256	1.9000	21.84
11	LVLSGGPAS	60	1.7500	20.11
12	VRAVGRELG	382	1.7000	19.54
13	LVEPLRLLF	370	1.6000	18.39
14	IRAFEGAVR	313	1.4000	16.09
15	LGIRIVGEV	406	1.4000	16.09
16	YGHPIVLRP	465	1.4000	16.09

17	FVAATGANL	274	1.3600	15.63
18	VVLLADVRS	447	1.3000	14.94
19	VRSVGVQGD	453	1.3000	14.94
20	VPVLGICYG	86	1.2000	13.79
21	LVQRAIGDR	243	1.2000	13.79
22	FEAFDRRLA	165	1.1000	12.64
23	IRIVGEVTA	408	1.1000	12.64
24	YAQLIARRV	25	1.0000	11.49
25	WTPANIANA	205	1.0000	11.49
26	LVTVDAAET	282	1.0000	11.49
27	IGRQFIRAF	308	1.0000	11.49
28	IVLRPVSSE	469	1.0000	11.49
29	LLDLGVPVL	81	0.9100	10.46
30	IVARQPFPG	395	0.9000	10.34
31	IVGEVTAKR	410	0.9000	10.34
32	LGGIVAHTG	102	0.8000	9.20
33	LRAGERAQV	262	0.8000	9.20
34	LERISTRIT	492	0.6000	6.90
35	YGRTELKVL	114	0.5600	6.44
36	VREARVFSE	33	0.5000	5.75
37	LRPVSSEDA	471	0.5000	5.75
38	VLSRFLHDF	190	0.4000	4.60
39	FLEALSGVS	291	0.4000	4.60
40	IRARQPVAL	52	0.3600	4.14
41	LKVLGGKLH	119	0.3000	3.45
42	FIRAFEGAV	312	0.3000	3.45
43	LIARRVREA	28	0.2000	2.30
44	LKFTLVEPL	366	0.1600	1.84
45	LGICYGFQA	89	-0.1000	0
46	VFVDHGLLR	255	-0.1000	0
47	VQRDFVAAT	270	-0.1000	0
48	LDITSKPPA	511	-0.1500	0
49	LDTLRHADS	419	-0.2000	0
50	ITSKPPATI	513	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VLLADVRSV	448	4.7000	53.41
2	IGRQFIRAF	308	4.6000	52.27
3	IVARQPFPG	395	3.8000	43.18
4	LIARRVREA	28	3.7000	42.05
5	LRLLFKDEV	374	3.7000	42.05
6	IVLRPVSSE	469	3.3000	37.50
7	VLSRFLHDF	190	2.8000	31.82
8	IRAFEGAVR	313	2.8000	31.82
9	IRARQPVAL	52	2.7600	31.36
10	VREARVFSE	33	2.5000	28.41
11	IKSHHNVGG	353	2.5000	28.41
12	IVGEVTAKR	410	2.5000	28.41
13	LVLSGGPAS	60	2.4000	27.27
14	LRHADSIVR	422	2.3000	26.14
15	LGIRIVGEV	406	2.2000	25.00
16	FEAFDRRLA	165	2.1000	23.86
17	LFKDEVRAV	377	2.1000	23.86
18	VVLLADVRS	447	2.1000	23.86
19	ITSKPPATI	513	2.1000	23.86
20	LVQRAIGDR	243	2.0000	22.73
21	LRAGERAQV	262	2.0000	22.73
22	FLVQGTLYP	331	2.0000	22.73
23	LGICYGFQA	89	1.9000	21.59
24	VAAFEAFDR	162	1.9000	21.59
25	FVDHGLLRA	256	1.9000	21.59
26	VIPHTASIE	42	1.7000	19.32
27	IVAHTGTRE	105	1.7000	19.32
28	LVEPLRLLF	370	1.7000	19.32
29	VRAVGRELG	382	1.7000	19.32
30	VRSVGVQGD	453	1.7000	19.32

31	LERISTRIT	492	1.7000	19.32
32	VPVLGICYG	86	1.5000	17.05
33	VQYHPEVMH	175	1.5000	17.05
34	IARRVREAR	29	1.4000	15.91
35	VAHTGTREY	106	1.4000	15.91
36	LLRAGERAQ	261	1.3000	14.77
37	IRIVGEVTA	408	1.3000	14.77
38	VVLDITSKP	509	1.3000	14.77
39	VVDFGAQYA	18	1.2000	13.64
40	LIEQVRTQI	214	1.2000	13.64
41	VQRDFVAAT	270	1.2000	13.64
42	VEPLRLLFK	371	1.2000	13.64
43	FQAMAQALG	95	1.1000	12.50
44	IGDRLTCVF	248	1.1000	12.50
45	LLFKDEVRA	376	1.1000	12.50
46	VREELTAAG	429	1.1000	12.50
47	ISTRITNEV	495	1.1000	12.50
48	IVREELTAA	428	1.0000	11.36
49	LKFTLVEPL	366	0.9600	10.91
50	IWQCPVVLL	442	0.9600	10.91
51	YAQLIARRV	25	0.9000	10.23
52	LVVDFGAQY	17	0.8000	9.09

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	VLLADVRSV	448	3.7000	42.05
2	IGRQFIRAF	308	3.6000	40.91
3	FEAFDRRLA	165	3.1000	35.23
4	FLVQGTLYP	331	3.0000	34.09
5	FVDHGLLRA	256	2.9000	32.95
6	IVARQPFPG	395	2.8000	31.82
7	LIARRVREA	28	2.7000	30.68
8	LRLLFKDEV	374	2.7000	30.68

9	IVLRPVSSE	469	2.3000	26.14
10	FQAMAQALG	95	2.1000	23.86
11	YAQLIARRV	25	1.9000	21.59
12	VLSRFLHDF	190	1.8000	20.45
13	IRAFEGAVR	313	1.8000	20.45
14	IRARQPVAL	52	1.7600	20.00
15	VREARVFSE	33	1.5000	17.05
16	IKSHHNVGG	353	1.5000	17.05
17	IVGEVTAKR	410	1.5000	17.05
18	LVLSGGPAS	60	1.4000	15.91
19	FVAATGANL	274	1.3600	15.45
20	FGAQYAQLI	21	1.3000	14.77
21	LRHADSIVR	422	1.3000	14.77
22	WQCPVVLLA	443	1.3000	14.77
23	LGIRIVGEV	406	1.2000	13.64
24	LFKDEVRAV	377	1.1000	12.50
25	VVLLADVRS	447	1.1000	12.50
26	ITSKPPATI	513	1.1000	12.50
27	YGFQAMAQA	93	1.0000	11.36
28	WTPANIANA	205	1.0000	11.36
29	LVQRAIGDR	243	1.0000	11.36
30	LRAGERAQV	262	1.0000	11.36
31	YEVLERIST	489	1.0000	11.36
32	FTLVEPLRL	368	0.9600	10.91
33	LGICYGFQA	89	0.9000	10.23
34	VAAFEAFDR	162	0.9000	10.23
35	VIPHTASIE	42	0.7000	7.95
36	IVAHTGTRE	105	0.7000	7.95
37	LVEPLRLLF	370	0.7000	7.95
38	VRAVGRELG	382	0.7000	7.95
39	VRSVGVQGD	453	0.7000	7.95
40	LERISTRIT	492	0.7000	7.95
41	VPVLGICYG	86	0.5000	5.68
42	VQYHPEVMH	175	0.5000	5.68

43	YGHPIVLRP	465	0.5000	5.68
44	IARRVREAR	29	0.4000	4.55
45	VAHTGTREY	106	0.4000	4.55
46	LLRAGERAQ	261	0.3000	3.41
47	IRIVGEVTA	408	0.3000	3.41
48	VVLDITSKP	509	0.3000	3.41
49	YGRTELKVL	114	0.2600	2.95
50	VVDFGAQYA	18	0.2000	2.27
51	LIEQVRTQI	214	0.2000	2.27
52	VQRDFVAAT	270	0.2000	2.27

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	IVLRPVSSE	469	4.9000	54.44
2	VREARVFSE	33	4.1000	45.56
3	VLLADVRSV	448	4.0000	44.44
4	LIARRVREA	28	3.7000	41.11
5	IVARQPFPG	395	3.7000	41.11
6	IGRQFIRAF	308	3.6000	40.00
7	VIPHTASIE	42	3.3000	36.67
8	IVAHTGTRE	105	3.3000	36.67
9	VQYHPEVMH	175	3.3000	36.67
10	VRSVGVQGD	453	3.3000	36.67
11	LRLLFKDEV	374	3.0000	33.33
12	IRARQPVAL	52	2.8000	31.11
13	LLRAGERAQ	261	2.8000	31.11
14	LKVLGGKLH	119	2.6000	28.89
15	IKSHHNVGG	353	2.4000	26.67
16	FEAFDRRLA	165	2.1000	23.33
17	LVLSGGPAS	60	2.0000	22.22
18	LGAQWTPAN	201	2.0000	22.22
19	LGICYGFQA	89	1.9000	21.11
20	VRTQIGDGH	218	1.9000	21.11

21	FVDHGLLRA	256	1.9000	21.11
22	LERISTRIT	492	1.9000	21.11
23	VLSRFLHDF	190	1.8000	20.00
24	VVLLADVRS	447	1.7000	18.89
25	LVQGTLYPD	332	1.6000	17.78
26	VRAVGRELG	382	1.6000	17.78
27	LGIRIVGEV	406	1.5000	16.67
28	VPVLGICYG	86	1.4000	15.56
29	VQRDFVAAT	270	1.4000	15.56
30	VDAAETFLE	285	1.4000	15.56
31	FLVQGTLYP	331	1.4000	15.56
32	LFKDEVRAV	377	1.4000	15.56
33	ITSKPPATI	513	1.4000	15.56
34	LRAGERAQV	262	1.3000	14.44
35	IRAFEGAVR	313	1.3000	14.44
36	IRIVGEVTA	408	1.3000	14.44
37	VVDFGAQYA	18	1.2000	13.33
38	VAHTGTREY	106	1.2000	13.33
39	VLGGKLHSD	121	1.2000	13.33
40	LLFKDEVRA	376	1.1000	12.22
41	VGRELGLPE	385	1.1000	12.22
42	FQAMAQALG	95	1.0000	11.11
43	LKFTLVEPL	366	1.0000	11.11
44	IVGEVTAKR	410	1.0000	11.11
45	IVREELTAA	428	1.0000	11.11
46	VREELTAAG	429	1.0000	11.11
47	IWQCPVVLL	442	1.0000	11.11
48	LVTVDAAET	282	0.9000	10.00
49	LLDLGVPVL	81	0.8000	8.89
50	VAAALVQRA	239	0.8000	8.89
51	LRHADSIVR	422	0.8000	8.89
52	LGGIVAHTG	102	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	FTLVEPLRL	368	3.3600	38.62
2	FLVQGTLYP	331	3.1000	35.63
3	YEVLERIST	489	3.0000	34.48
4	LRHADSIVR	422	2.6000	29.89
5	FQAMAQALG	95	2.3000	26.44
6	LRLLFKDEV	374	2.2000	25.29
7	WQCPVVLLA	443	2.2000	25.29
8	VLLADVRSV	448	2.1000	24.14
9	VEPLRLLFK	371	2.0000	22.99
10	FVDHGLLRA	256	1.9000	21.84
11	LVLSGGPAS	60	1.7500	20.11
12	VRAVGRELG	382	1.7000	19.54
13	LVEPLRLLF	370	1.6000	18.39
14	IRAFEGAVR	313	1.4000	16.09
15	LGIRIVGEV	406	1.4000	16.09
16	YGHPIVLRP	465	1.4000	16.09
17	FVAATGANL	274	1.3600	15.63
18	VVLLADVRS	447	1.3000	14.94
19	VRSVGVQGD	453	1.3000	14.94
20	VPVLGICYG	86	1.2000	13.79
21	LVQRAIGDR	243	1.2000	13.79
22	FEAFDRRLA	165	1.1000	12.64
23	IRIVGEVTA	408	1.1000	12.64
24	YAQLIARRV	25	1.0000	11.49
25	WTPANIANA	205	1.0000	11.49
26	LVTVDAAET	282	1.0000	11.49
27	IGRQFIRAF	308	1.0000	11.49
28	IVLRPVSSE	469	1.0000	11.49
29	LLDLGVPVL	81	0.9100	10.46
30	IVARQPFPG	395	0.9000	10.34
31	IVGEVTAKR	410	0.9000	10.34
32	LGGIVAHTG	102	0.8000	9.20

33	LRAGERAQV	262	0.8000	9.20
34	LERISTRIT	492	0.6000	6.90
35	YGRTELKVL	114	0.5600	6.44
36	VREARVFSE	33	0.5000	5.75
37	LRPVSSEDA	471	0.5000	5.75
38	VLSRFLHDF	190	0.4000	4.60
39	FLEALSGVS	291	0.4000	4.60
40	IRARQPVAL	52	0.3600	4.14
41	LKVLGGKLH	119	0.3000	3.45
42	FIRAFEGAV	312	0.3000	3.45
43	LIARRVREA	28	0.2000	2.30
44	LKFTLVEPL	366	0.1600	1.84
45	LGICYGFQA	89	-0.1000	0
46	VFVDHGLLR	255	-0.1000	0
47	VQRDFVAAT	270	-0.1000	0
48	LDITSKPPA	511	-0.1500	0
49	LDTLRHADS	419	-0.2000	0
50	ITSKPPATI	513	-0.2000	0

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRLLFKDEV	374	1.5000	22.06
2	WTPANIANA	205	1.0000	14.71
3	FQAMAQALG	95	0.9000	13.24
4	FEAFDRRLA	165	0.9000	13.24
5	VLLADVRSV	448	0.9000	13.24
6	YEVLERIST	489	0.7000	10.29
7	FTLVEPLRL	368	0.6000	8.82
8	IRIVGEVTA	408	0.6000	8.82
9	FVAATGANL	274	0.4000	5.88
10	WQCPVVLLA	443	0.4000	5.88
11	VVLLADVRS	447	0.4000	5.88
12	LVTVDAAET	282	0.3000	4.41

13	FLVQGTLYP	331	0.3000	4.41
14	LGIRIVGEV	406	0.3000	4.41
15	LKVLGGKLH	119	0.2800	4.12
16	LVLSGGPAS	60	0.2000	2.94
17	FVDHGLLRA	256	0.1000	1.47
18	VEPLRLLFK	371	0.1000	1.47
19	VRSVGVQGD	453	0.1000	1.47
20	FLEALSGVS	291	-0.1000	0
21	IRAFEGAVR	313	-0.1000	0
22	YAQLIARRV	25	-0.2000	0
23	VPVLGICYG	86	-0.2000	0
24	LRAGERAQV	262	-0.2000	0
25	VLGICYGFQ	88	-0.3000	0
26	LERISTRIT	492	-0.3000	0
27	VMHTPHGQQ	181	-0.4000	0
28	LVQRAIGDR	243	-0.4000	0
29	IVLRPVSSE	469	-0.4000	0
30	VLVVDFGAQ	16	-0.5000	0
31	LRHADSIVR	422	-0.5000	0
32	LGICYGFQA	89	-0.6000	0
33	IVGEVTAKR	410	-0.6000	0
34	LDTLRHADS	419	-0.6000	0
35	LRPVSSEDA	471	-0.6000	0
36	LLRAGERAQ	261	-0.8000	0
37	VQRDFVAAT	270	-0.8000	0
38	FIRAFEGAV	312	-0.8000	0
39	VRAVGRELG	382	-0.8000	0
40	VVDFGAQYA	18	-1.0000	0
41	YGRTELKVL	114	-1.0000	0
42	VAAALVQRA	239	-1.0000	0
43	IVARQPFPG	395	-1.0000	0
44	IRARQPVAL	52	-1.1000	0
45	FAGLGAQWT	198	-1.1000	0
46	IGRQFIRAF	308	-1.1000	0

47	ITSKPPATI	513	-1.1000	0
48	LLDLGVPVL	81	-1.2000	0
49	LGGIVAHTG	102	-1.3000	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	VEPLRLLFK	371	2.9000	34.94
2	LVLSGGPAS	60	2.3500	28.31
3	LRLLFKDEV	374	2.2000	26.51
4	IRIVGEVTA	408	2.1000	25.30
5	LRHADSIVR	422	2.1000	25.30
6	VLLADVRSV	448	2.1000	25.30
7	VVLLADVRS	447	1.9000	22.89
8	LKVLGGKLH	119	1.8800	22.65
9	LRPVSSEDA	471	1.5000	18.07
10	FTLVEPLRL	368	1.4000	16.87
11	LGIRIVGEV	406	1.4000	16.87
12	LVTVDAAET	282	1.3000	15.66
13	VRAVGRELG	382	1.3000	15.66
14	YEVLERIST	489	1.3000	15.66
15	LIARRVREA	28	1.2000	14.46
16	WQCPVVLLA	443	1.2000	14.46
17	VRSVGVQGD	453	1.2000	14.46
18	FLVQGTLYP	331	1.1000	13.25
19	LLDLGVPVL	81	0.9500	11.45
20	LGICYGFQA	89	0.9000	10.84
21	FVDHGLLRA	256	0.9000	10.84
22	IRAFEGAVR	313	0.9000	10.84
23	LERISTRIT	492	0.9000	10.84
24	LDITSKPPA	511	0.8500	10.24
25	VPVLGICYG	86	0.8000	9.64
26	VLGICYGFQ	88	0.8000	9.64
27	LRAGERAQV	262	0.8000	9.64

28	VMHTPHGQQ	181	0.7000	8.43
29	LHDFAGLGA	195	0.7000	8.43
30	LVQRAIGDR	243	0.7000	8.43
31	LVEPLRLLF	370	0.7000	8.43
32	VLVVDFGAQ	16	0.6000	7.23
33	IVLRPVSSE	469	0.6000	7.23
34	IVARQPFPG	395	0.5000	6.02
35	IRARQPVAL	52	0.4000	4.82
36	LGGIVAHTG	102	0.4000	4.82
37	LLRAGERAQ	261	0.4000	4.82
38	IVGEVTAKR	410	0.4000	4.82
39	LDTLRHADS	419	0.4000	4.82
40	VQRDFVAAT	270	0.2000	2.41
41	LKFTLVEPL	366	0.2000	2.41
42	VVDFGAQYA	18	0.1000	1.20
43	VREARVFSE	33	0.1000	1.20
44	FEAFDRRLA	165	0.1000	1.20
45	VAAALVQRA	239	0.1000	1.20
46	IGRQFIRAF	308	0.1000	1.20
47	FQAMAQALG	95	-0.1000	0
48	LEALSGVSA	292	-0.1000	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	FTLVEPLRL	368	3.4000	38.20
2	YEVLERIST	489	3.2000	35.96
3	VRSVGVQGD	453	2.9000	32.58
4	IVLRPVSSE	469	2.6000	29.21
5	FLVQGTLYP	331	2.5000	28.09
6	FQAMAQALG	95	2.2000	24.72
7	WQCPVVLLA	443	2.2000	24.72
8	VREARVFSE	33	2.1000	23.60
9	LKVLGGKLH	119	2.1000	23.60

10	FVDHGLLRA	256	1.9000	21.35
11	VRAVGRELG	382	1.6000	17.98
12	LRLLFKDEV	374	1.5000	16.85
13	FVAATGANL	274	1.4000	15.73
14	VLLADVRSV	448	1.4000	15.73
15	LVLSGGPAS	60	1.3500	15.17
16	LVTVDAAET	282	1.2000	13.48
17	VEPLRLLFK	371	1.2000	13.48
18	VPVLGICYG	86	1.1000	12.36
19	FEAFDRRLA	165	1.1000	12.36
20	IRIVGEVTA	408	1.1000	12.36
21	LRHADSIVR	422	1.1000	12.36
22	WTPANIANA	205	1.0000	11.24
23	LLDLGVPVL	81	0.9500	10.67
24	VVLLADVRS	447	0.9000	10.11
25	IVARQPFPG	395	0.8000	8.99
26	YGHPIVLRP	465	0.8000	8.99
27	LERISTRIT	492	0.8000	8.99
28	LGGIVAHTG	102	0.7000	7.87
29	LGIRIVGEV	406	0.7000	7.87
30	VLGICYGFQ	88	0.6000	6.74
31	YGRTELKVL	114	0.6000	6.74
32	LVEPLRLLF	370	0.6000	6.74
33	VGRELGLPE	385	0.6000	6.74
34	VMHTPHGQQ	181	0.5000	5.62
35	LRPVSSEDA	471	0.5000	5.62
36	LGAQWTPAN	201	0.4500	5.06
37	VLVVDFGAQ	16	0.4000	4.49
38	IRARQPVAL	52	0.4000	4.49
39	YAQLIARRV	25	0.3000	3.37
40	LIARRVREA	28	0.2000	2.25
41	ICGLSGGVD	228	0.2000	2.25
42	LLRAGERAQ	261	0.2000	2.25
43	LVQGTLYPD	332	0.2000	2.25

44	LKFTLVEPL	366	0.2000	2.25
45	IPHTASIEE	43	0.1000	1.12
46	LRAGERAQV	262	0.1000	1.12
47	VQRDFVAAT	270	0.1000	1.12
48	LGICYGFQA	89	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LIARRVREA	28	3.7000	44.05
2	VLLADVRSV	448	3.7000	44.05
3	IGRQFIRAF	308	2.7000	32.14
4	LRLLFKDEV	374	2.7000	32.14
5	IVARQPFPG	395	2.4000	28.57
6	FEAFDRRLA	165	2.1000	25.00
7	VQYHPEVMH	175	2.0800	24.76
8	LVLSGGPAS	60	2.0000	23.81
9	LLRAGERAQ	261	2.0000	23.81
10	LGICYGFQA	89	1.9000	22.62
11	FVDHGLLRA	256	1.9000	22.62
12	IVLRPVSSE	469	1.9000	22.62
13	IRARQPVAL	52	1.8000	21.43
14	VVLLADVRS	447	1.7000	20.24
15	LKVLGGKLH	119	1.3800	16.43
16	IRAFEGAVR	313	1.3000	15.48
17	IRIVGEVTA	408	1.3000	15.48
18	VVDFGAQYA	18	1.2000	14.29
19	LGIRIVGEV	406	1.2000	14.29
20	ITSKPPATI	513	1.2000	14.29
21	VREARVFSE	33	1.1000	13.10
22	IKSHHNVGG	353	1.1000	13.10
23	VEPLRLLFK	371	1.1000	13.10
24	LLFKDEVRA	376	1.1000	13.10
25	LFKDEVRAV	377	1.1000	13.10

26	LRAGERAQV	262	1.0000	11.90
27	FLVQGTLYP	331	1.0000	11.90
28	IVGEVTAKR	410	1.0000	11.90
29	IVREELTAA	428	1.0000	11.90
30	LERISTRIT	492	1.0000	11.90
31	VLSRFLHDF	190	0.9000	10.71
32	VAAALVQRA	239	0.8000	9.52
33	LRHADSIVR	422	0.8000	9.52
34	VRTQIGDGH	218	0.6800	8.10
35	VRSVGVQGD	453	0.6000	7.14
36	LVQRAIGDR	243	0.5000	5.95
37	VQRDFVAAT	270	0.5000	5.95
38	LRPVSSEDA	471	0.5000	5.95
39	VAAFEAFDR	162	0.4000	4.76
40	VIPHTASIE	42	0.3000	3.57
41	IVAHTGTRE	105	0.3000	3.57
42	LIEQVRTQI	214	0.3000	3.57
43	VRAVGRELG	382	0.3000	3.57
44	WQCPVVLLA	443	0.3000	3.57
45	VVLDITSKP	509	0.3000	3.57
46	VPVLGICYG	86	0.1000	1.19
47	VAHTGTREY	106	0.1000	1.19
48	ISTRITNEV	495	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	FEAFDRRLA	165	3.1000	36.90
2	FVDHGLLRA	256	2.9000	34.52
3	LIARRVREA	28	2.7000	32.14
4	VLLADVRSV	448	2.7000	32.14
5	FLVQGTLYP	331	2.0000	23.81
6	IGRQFIRAF	308	1.7000	20.24
7	LRLLFKDEV	374	1.7000	20.24

8	IVARQPFPG	395	1.4000	16.67
9	WQCPVVLLA	443	1.3000	15.48
10	VQYHPEVMH	175	1.0800	12.86
11	LVLSGGPAS	60	1.0000	11.90
12	YGFQAMAQA	93	1.0000	11.90
13	WTPANIANA	205	1.0000	11.90
14	LLRAGERAQ	261	1.0000	11.90
15	YAQLIARRV	25	0.9000	10.71
16	LGICYGFQA	89	0.9000	10.71
17	IVLRPVSSE	469	0.9000	10.71
18	IRARQPVAL	52	0.8000	9.52
19	FQAMAQALG	95	0.7000	8.33
20	VVLLADVRS	447	0.7000	8.33
21	FGAQYAQLI	21	0.4000	4.76
22	FVAATGANL	274	0.4000	4.76
23	LKVLGGKLH	119	0.3800	4.52
24	IRAFEGAVR	313	0.3000	3.57
25	IRIVGEVTA	408	0.3000	3.57
26	YEVLERIST	489	0.3000	3.57
27	VVDFGAQYA	18	0.2000	2.38
28	LGIRIVGEV	406	0.2000	2.38
29	ITSKPPATI	513	0.2000	2.38
30	VREARVFSE	33	0.1000	1.19
31	IKSHHNVGG	353	0.1000	1.19
32	VEPLRLLFK	371	0.1000	1.19
33	LLFKDEVRA	376	0.1000	1.19
34	LFKDEVRAV	377	0.1000	1.19
35	VLSRFLHDF	190	-0.1000	0
36	VAAALVQRA	239	-0.2000	0
37	LRHADSIVR	422	-0.2000	0
38	VRTQIGDGH	218	-0.3200	0
39	VRSVGVQGD	453	-0.4000	0
40	LVQRAIGDR	243	-0.5000	0
41	VQRDFVAAT	270	-0.5000	0

42	YGHPIVLRP	465	-0.5000	0
43	LRPVSSEDA	471	-0.5000	0
44	VAAFEAFDR	162	-0.6000	0
45	VIPHTASIE	42	-0.7000	0
46	IVAHTGTRE	105	-0.7000	0

ALLELE: DRB1_1327	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VLLADVRSV	448	4.7000	53.41
2	IGRQFIRAF	308	4.6000	52.27
3	IVARQPFPG	395	3.8000	43.18
4	LIARRVREA	28	3.7000	42.05
5	LRLLFKDEV	374	3.7000	42.05
6	IVLRPVSSE	469	3.3000	37.50
7	VLSRFLHDF	190	2.8000	31.82
8	IRAFEGAVR	313	2.8000	31.82
9	IRARQPVAL	52	2.7600	31.36
10	VREARVFSE	33	2.5000	28.41
11	IKSHHNVGG	353	2.5000	28.41
12	IVGEVTAKR	410	2.5000	28.41
13	LVLSGGPAS	60	2.4000	27.27
14	LRHADSIVR	422	2.3000	26.14
15	LGIRIVGEV	406	2.2000	25.00
16	FEAFDRRLA	165	2.1000	23.86
17	LFKDEVRAV	377	2.1000	23.86
18	VVLLADVRS	447	2.1000	23.86
19	ITSKPPATI	513	2.1000	23.86
20	LVQRAIGDR	243	2.0000	22.73
21	LRAGERAQV	262	2.0000	22.73
22	FLVQGTLYP	331	2.0000	22.73
23	LGICYGFQA	89	1.9000	21.59
24	VAAFEAFDR	162	1.9000	21.59
25	FVDHGLLRA	256	1.9000	21.59

26	VIPHTASIE	42	1.7000	19.32
27	IVAHTGTRE	105	1.7000	19.32
28	LVEPLRLLF	370	1.7000	19.32
29	VRAVGRELG	382	1.7000	19.32
30	VRSVGVQGD	453	1.7000	19.32
31	LERISTRIT	492	1.7000	19.32
32	VPVLGICYG	86	1.5000	17.05
33	VQYHPEVMH	175	1.5000	17.05
34	IARRVREAR	29	1.4000	15.91
35	VAHTGTREY	106	1.4000	15.91
36	LLRAGERAQ	261	1.3000	14.77
37	IRIVGEVTA	408	1.3000	14.77
38	VVLDITSKP	509	1.3000	14.77
39	VVDFGAQYA	18	1.2000	13.64
40	LIEQVRTQI	214	1.2000	13.64
41	VQRDFVAAT	270	1.2000	13.64
42	VEPLRLLFK	371	1.2000	13.64
43	FQAMAQALG	95	1.1000	12.50
44	IGDRLTCVF	248	1.1000	12.50
45	LLFKDEVRA	376	1.1000	12.50
46	VREELTAAG	429	1.1000	12.50
47	ISTRITNEV	495	1.1000	12.50
48	IVREELTAA	428	1.0000	11.36
49	LKFTLVEPL	366	0.9600	10.91
50	IWQCPVVLL	442	0.9600	10.91
51	YAQLIARRV	25	0.9000	10.23
52	LVVDFGAQY	17	0.8000	9.09

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	VLLADVRSV	448	4.7000	53.41
2	IGRQFIRAF	308	4.6000	52.27
3	IVARQPFPG	395	3.8000	43.18

4	LIARRVREA	28	3.7000	42.05
5	LRLLFKDEV	374	3.7000	42.05
6	IVLRPVSSE	469	3.3000	37.50
7	VLSRFLHDF	190	2.8000	31.82
8	IRAFEGAVR	313	2.8000	31.82
9	IRARQPVAL	52	2.7600	31.36
10	VREARVFSE	33	2.5000	28.41
11	IKSHHNVGG	353	2.5000	28.41
12	IVGEVTAKR	410	2.5000	28.41
13	LVLSGGPAS	60	2.4000	27.27
14	LRHADSIVR	422	2.3000	26.14
15	LGIRIVGEV	406	2.2000	25.00
16	FEAFDRRLA	165	2.1000	23.86
17	LFKDEVRAV	377	2.1000	23.86
18	VVLLADVRS	447	2.1000	23.86
19	ITSKPPATI	513	2.1000	23.86
20	LVQRAIGDR	243	2.0000	22.73
21	LRAGERAQV	262	2.0000	22.73
22	FLVQGTLYP	331	2.0000	22.73
23	LGICYGFQA	89	1.9000	21.59
24	VAAFEAFDR	162	1.9000	21.59
25	FVDHGLLRA	256	1.9000	21.59
26	VIPHTASIE	42	1.7000	19.32
27	IVAHTGTRE	105	1.7000	19.32
28	LVEPLRLLF	370	1.7000	19.32
29	VRAVGRELG	382	1.7000	19.32
30	VRSVGVQGD	453	1.7000	19.32
31	LERISTRIT	492	1.7000	19.32
32	VPVLGICYG	86	1.5000	17.05
33	VQYHPEVMH	175	1.5000	17.05
34	IARRVREAR	29	1.4000	15.91
35	VAHTGTREY	106	1.4000	15.91
36	LLRAGERAQ	261	1.3000	14.77
37	IRIVGEVTA	408	1.3000	14.77

38	VVLDITSKP	509	1.3000	14.77
39	VVDFGAQYA	18	1.2000	13.64
40	LIEQVRTQI	214	1.2000	13.64
41	VQRDFVAAT	270	1.2000	13.64
42	VEPLRLLFK	371	1.2000	13.64
43	FQAMAQALG	95	1.1000	12.50
44	IGDRLTCVF	248	1.1000	12.50
45	LLFKDEVRA	376	1.1000	12.50
46	VREELTAAG	429	1.1000	12.50
47	ISTRITNEV	495	1.1000	12.50
48	IVREELTAA	428	1.0000	11.36
49	LKFTLVEPL	366	0.9600	10.91
50	IWQCPVVLL	442	0.9600	10.91
51	YAQLIARRV	25	0.9000	10.23
52	LVVDFGAQY	17	0.8000	9.09

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	LHDFAGLGA	195	4.3000	43.88
2	IRAFEGAVR	313	4.1000	41.84
3	LGICYGFQA	89	3.9000	39.80
4	LRAGERAQV	262	3.5000	35.71
5	LRHADSIVR	422	3.5000	35.71
6	LVLSGGPAS	60	3.3000	33.67
7	VVQPADIDV	0	3.2000	32.65
8	IRIVGEVTA	408	3.2000	32.65
9	VVLLADVRS	447	3.2000	32.65
10	LVEPLRLLF	370	3.1000	31.63
11	IRARQPVAL	52	3.0000	30.61
12	FVDHGLLRA	256	3.0000	30.61
13	LRLLFKDEV	374	3.0000	30.61
14	VVDFGAQYA	18	2.9000	29.59
15	VAAFEAFDR	162	2.8000	28.57

16	IIGRQFIRA	307	2.7000	27.55
17	IVARQPFPG	395	2.7000	27.55
18	IKSHHNVGG	353	2.6000	26.53
19	IVREELTAA	428	2.6000	26.53
20	LRPVSSEDA	471	2.6000	26.53
21	FTLVEPLRL	368	2.4000	24.49
22	YEVLERIST	489	2.4000	24.49
23	VFVDHGLLR	255	2.3000	23.47
24	VQRAIGDRL	244	2.2000	22.45
25	LGIRIVGEV	406	2.2000	22.45
26	FVAATGANL	274	2.1000	21.43
27	LVTVDAAET	282	2.1000	21.43
28	VQGTLYPDV	333	2.1000	21.43
29	IVAHTGTRE	105	2.0000	20.41
30	FEAFDRRLA	165	2.0000	20.41
31	VRAVGRELG	382	1.9000	19.39
32	VVLDITSKP	509	1.8600	18.98
33	LVVDFGAQY	17	1.8000	18.37
34	VLSRFLHDF	190	1.8000	18.37
35	LGLPEEIVA	389	1.7000	17.35
36	LSRFLHDFA	191	1.6000	16.33
37	WQCPVVLLA	443	1.5000	15.31
38	VLLADVRSV	448	1.5000	15.31
39	VLERISTRI	491	1.5000	15.31
40	LEALSGVSA	292	1.4000	14.29
41	VQGDGRTYG	458	1.4000	14.29
42	IVLRPVSSE	469	1.4000	14.29
43	LVQRAIGDR	243	1.3500	13.78
44	VLSGGPASV	61	1.3000	13.27
45	VYADGAPKL	69	1.3000	13.27
46	VQPVWMSHG	133	1.3000	13.27
47	VQYHPEVMH	175	1.3000	13.27
48	VEPLRLLFK	371	1.3000	13.27
49	LKVLGGKLH	119	1.2000	12.24

50	LGGIVAHTG	102	1.1000	11.22
51	VWMSHGDAV	136	1.1000	11.22
52	LVQGTLYPD	332	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	FVDHGLLRA	256	4.0000	40.82
2	FTLVEPLRL	368	3.4000	34.69
3	YEVLERIST	489	3.4000	34.69
4	LHDFAGLGA	195	3.3000	33.67
5	FVAATGANL	274	3.1000	31.63
6	IRAFEGAVR	313	3.1000	31.63
7	FEAFDRRLA	165	3.0000	30.61
8	LGICYGFQA	89	2.9000	29.59
9	LRAGERAQV	262	2.5000	25.51
10	LRHADSIVR	422	2.5000	25.51
11	WQCPVVLLA	443	2.5000	25.51
12	LVLSGGPAS	60	2.3000	23.47
13	VVQPADIDV	0	2.2000	22.45
14	IRIVGEVTA	408	2.2000	22.45
15	VVLLADVRS	447	2.2000	22.45
16	LVEPLRLLF	370	2.1000	21.43
17	IRARQPVAL	52	2.0000	20.41
18	LRLLFKDEV	374	2.0000	20.41
19	VVDFGAQYA	18	1.9000	19.39
20	WMSHGDAVT	137	1.8000	18.37
21	VAAFEAFDR	162	1.8000	18.37
22	IIGRQFIRA	307	1.7000	17.35
23	IVARQPFPG	395	1.7000	17.35
24	IKSHHNVGG	353	1.6000	16.33
25	IVREELTAA	428	1.6000	16.33
26	LRPVSSEDA	471	1.6000	16.33
27	FLVQGTLYP	331	1.4600	14.90

28	YGRTELKVL	114	1.3000	13.27
29	VFVDHGLLR	255	1.3000	13.27
30	VQRAIGDRL	244	1.2000	12.24
31	LGIRIVGEV	406	1.2000	12.24
32	LVTVDAAET	282	1.1000	11.22
33	FIRAFEGAV	312	1.1000	11.22
34	FEGAVRDVL	316	1.1000	11.22
35	VQGTLYPDV	333	1.1000	11.22
36	WTRVPYEVL	484	1.1000	11.22
37	IVAHTGTRE	105	1.0000	10.20
38	VRAVGRELG	382	0.9000	9.18
39	YGHPIVLRP	465	0.9000	9.18
40	VVLDITSKP	509	0.8600	8.78
41	LVVDFGAQY	17	0.8000	8.16
42	VLSRFLHDF	190	0.8000	8.16
43	LGLPEEIVA	389	0.7000	7.14
44	YGFQAMAQA	93	0.6000	6.12
45	FQAMAQALG	95	0.6000	6.12
46	LSRFLHDFA	191	0.6000	6.12
47	VLLADVRSV	448	0.5000	5.10
48	VLERISTRI	491	0.5000	5.10
49	LEALSGVSA	292	0.4000	4.08
50	VQGDGRTYG	458	0.4000	4.08
51	IVLRPVSSE	469	0.4000	4.08
52	WTPANIANA	205	0.3500	3.57

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	LHDFAGLGA	195	4.3000	43.88
2	IRAFEGAVR	313	4.1000	41.84
3	LGICYGFQA	89	3.9000	39.80
4	LRAGERAQV	262	3.5000	35.71
5	LRHADSIVR	422	3.5000	35.71

6	LVLSGGPAS	60	3.3000	33.67
7	VVQPADIDV	0	3.2000	32.65
8	IRIVGEVTA	408	3.2000	32.65
9	VVLLADVRS	447	3.2000	32.65
10	LVEPLRLLF	370	3.1000	31.63
11	IRARQPVAL	52	3.0000	30.61
12	FVDHGLLRA	256	3.0000	30.61
13	LRLLFKDEV	374	3.0000	30.61
14	VVDFGAQYA	18	2.9000	29.59
15	VAAFEAFDR	162	2.8000	28.57
16	IIGRQFIRA	307	2.7000	27.55
17	IVARQPFPG	395	2.7000	27.55
18	IKSHHNVGG	353	2.6000	26.53
19	IVREELTAA	428	2.6000	26.53
20	LRPVSSEDA	471	2.6000	26.53
21	FTLVEPLRL	368	2.4000	24.49
22	YEVLERIST	489	2.4000	24.49
23	VFVDHGLLR	255	2.3000	23.47
24	VQRAIGDRL	244	2.2000	22.45
25	LGIRIVGEV	406	2.2000	22.45
26	FVAATGANL	274	2.1000	21.43
27	LVTVDAAET	282	2.1000	21.43
28	VQGTLYPDV	333	2.1000	21.43
29	IVAHTGTRE	105	2.0000	20.41
30	FEAFDRRLA	165	2.0000	20.41
31	VRAVGRELG	382	1.9000	19.39
32	VVLDITSKP	509	1.8600	18.98
33	LVVDFGAQY	17	1.8000	18.37
34	VLSRFLHDF	190	1.8000	18.37
35	LGLPEEIVA	389	1.7000	17.35
36	LSRFLHDFA	191	1.6000	16.33
37	WQCPVVLLA	443	1.5000	15.31
38	VLLADVRSV	448	1.5000	15.31
39	VLERISTRI	491	1.5000	15.31

40	LEALSGVSA	292	1.4000	14.29
41	VQGDGRTYG	458	1.4000	14.29
42	IVLRPVSSE	469	1.4000	14.29
43	LVQRAIGDR	243	1.3500	13.78
44	VLSGGPASV	61	1.3000	13.27
45	VYADGAPKL	69	1.3000	13.27
46	VQPVWMSHG	133	1.3000	13.27
47	VQYHPEVMH	175	1.3000	13.27
48	VEPLRLLFK	371	1.3000	13.27
49	LKVLGGKLH	119	1.2000	12.24
50	LGGIVAHTG	102	1.1000	11.22
51	VWMSHGDAV	136	1.1000	11.22
52	LVQGTLYPD	332	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	LRHADSIVR	422	4.6000	46.94
2	FTLVEPLRL	368	4.2000	42.86
3	FVAATGANL	274	3.1000	31.63
4	LKVLGGKLH	119	2.8000	28.57
5	IRAFEGAVR	313	2.8000	28.57
6	YGRTELKVL	114	2.7000	27.55
7	LGGIVAHTG	102	2.6000	26.53
8	VAAFEAFDR	162	2.4000	24.49
9	VEPLRLLFK	371	2.3000	23.47
10	LGICYGFQA	89	2.2000	22.45
11	LVTVDAAET	282	2.0000	20.41
12	FQAMAQALG	95	1.9000	19.39
13	VLGICYGFQ	88	1.8000	18.37
14	FGAQYAQLI	21	1.7000	17.35
15	YAQLIARRV	25	1.7000	17.35
16	IVGEVTAKR	410	1.7000	17.35
17	VGEVTAKRL	411	1.6000	16.33

18	IVARQPFPG	395	1.5000	15.31
19	IRIVGEVTA	408	1.5000	15.31
20	LVLSGGPAS	60	1.4000	14.29
21	LERISTRIT	492	1.4000	14.29
22	VAHTGTREY	106	1.3000	13.27
23	FAGLGAQWT	198	1.3000	13.27
24	VLVVDFGAQ	16	1.2000	12.24
25	VFVDHGLLR	255	1.2000	12.24
26	LRPVSSEDA	471	1.2000	12.24
27	WTRVPYEVL	484	1.2000	12.24
28	LVQRAIGDR	243	1.1000	11.22
29	VVLLADVRS	447	1.1000	11.22
30	FSEVIPHTA	39	1.0000	10.20
31	YEVLERIST	489	0.9000	9.18
32	VLLADVRSV	448	0.8000	8.16
33	LVVDFGAQY	17	0.7000	7.14
34	IRARQPVAL	52	0.7000	7.14
35	VMHTPHGQQ	181	0.7000	7.14
36	LLRAGERAQ	261	0.7000	7.14
37	FLEALSGVS	291	0.6000	6.12
38	IGRQFIRAF	308	0.6000	6.12
39	IEQVRTQIG	215	0.5000	5.10
40	VSAPEGKRK	298	0.5000	5.10
41	VRAVGRELG	382	0.5000	5.10
42	VALVLSGGP	58	0.4000	4.08
43	VVASSAGAP	153	0.4000	4.08
44	VQRAIGDRL	244	0.4000	4.08
45	VRSVGVQGD	453	0.4000	4.08
46	VQPVWMSHG	133	0.3000	3.06
47	FLHDFAGLG	194	0.3000	3.06
48	LKFTLVEPL	366	0.3000	3.06
49	FPGPGLGIR	401	0.3000	3.06
50	FIRAFEGAV	312	0.2000	2.04
51	VVESGGGSG	341	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	LRHADSIVR	422	4.6000	46.94
2	FTLVEPLRL	368	4.2000	42.86
3	FVAATGANL	274	3.1000	31.63
4	LKVLGGKLH	119	2.8000	28.57
5	IRAFEGAVR	313	2.8000	28.57
6	YGRTELKVL	114	2.7000	27.55
7	LGGIVAHTG	102	2.6000	26.53
8	VAAFEAFDR	162	2.4000	24.49
9	VEPLRLLFK	371	2.3000	23.47
10	LGICYGFQA	89	2.2000	22.45
11	LVTVDAAET	282	2.0000	20.41
12	FQAMAQALG	95	1.9000	19.39
13	VLGICYGFQ	88	1.8000	18.37
14	FGAQYAQLI	21	1.7000	17.35
15	YAQLIARRV	25	1.7000	17.35
16	IVGEVTAKR	410	1.7000	17.35
17	VGEVTAKRL	411	1.6000	16.33
18	IVARQPFPG	395	1.5000	15.31
19	IRIVGEVTA	408	1.5000	15.31
20	LVLSGGPAS	60	1.4000	14.29
21	LERISTRIT	492	1.4000	14.29
22	VAHTGTREY	106	1.3000	13.27
23	FAGLGAQWT	198	1.3000	13.27
24	VLVVDFGAQ	16	1.2000	12.24
25	VFVDHGLLR	255	1.2000	12.24
26	LRPVSSEDA	471	1.2000	12.24
27	WTRVPYEVL	484	1.2000	12.24
28	LVQRAIGDR	243	1.1000	11.22
29	VVLLADVRS	447	1.1000	11.22
30	FSEVIPHTA	39	1.0000	10.20

31	YEVLERIST	489	0.9000	9.18
32	VLLADVRSV	448	0.8000	8.16
33	LVVDFGAQY	17	0.7000	7.14
34	IRARQPVAL	52	0.7000	7.14
35	VMHTPHGQQ	181	0.7000	7.14
36	LLRAGERAQ	261	0.7000	7.14
37	FLEALSGVS	291	0.6000	6.12
38	IGRQFIRAF	308	0.6000	6.12
39	IEQVRTQIG	215	0.5000	5.10
40	VSAPEGKRK	298	0.5000	5.10
41	VRAVGRELG	382	0.5000	5.10
42	VALVLSGGP	58	0.4000	4.08
43	VVASSAGAP	153	0.4000	4.08
44	VQRAIGDRL	244	0.4000	4.08
45	VRSVGVQGD	453	0.4000	4.08
46	VQPVWMSHG	133	0.3000	3.06
47	FLHDFAGLG	194	0.3000	3.06
48	LKFTLVEPL	366	0.3000	3.06
49	FPGPGLGIR	401	0.3000	3.06
50	FIRAFEGAV	312	0.2000	2.04
51	VVESGGGSG	341	0.1000	1.02