MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Fri Feb 5 17:21:43 2010
Length of input sequence	874 amino acids
Number of nanomers from input sequence	866
Number of nanomers with obligatory P1 anchor residue	268
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	87

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	LRLASGREV	457	2.2900	38.17
2	MVIVAARPG	220	1.8400	30.67
3	YGRQPPQDL	19	1.8000	30.00
4	VRFLRHVGV	686	1.7000	28.33
5	LRMVARPMI	436	1.5200	25.33
6	LRRIGGAPY	93	1.2000	20.00
7	VMRLLSAEA	263	1.1000	18.33
8	LRHLWSAGG	616	0.9000	15.00
9	LRQLKGPVR	706	0.8700	14.50
10	MRLLSAEAK	264	0.8000	13.33
11	YGYAGAEGA	141	0.7000	11.67
12	VHGAEAVAA	694	0.7000	11.67
13	FLRHVGVHG	688	0.6000	10.00
14	YLAARVPSL	558	0.4700	7.83

15	YYGSTSRRL	638	0.3900	6.50
16	LRHVGVHGA	689	0.3500	5.83
17	YGRGEPADA	72	0.3000	5.00
18	VILLHRPDA	823	0.2700	4.50
19	LRRLVEAGT	128	0.2000	3.33
20	YAGAEGADV	143	0.2000	3.33
21	YASIVAEKA	118	0.1000	1.67
22	WLAGLGLFT	584	0.1000	1.67
23	YRPAHQNVY	57	-0.1000	0
24	FRLRLASGR	455	-0.1000	0
25	IRHRMASVI	244	-0.2000	0
26	FMKFEGWTP	473	-0.3000	0
27	LRESGCLTA	394	-0.4000	0
28	WTRLARRMS	288	-0.4100	0
29	VVILLHRPD	822	-0.5100	0
30	LDFMRSCSI	236	-0.6000	0
31	LRVGIFSWI	655	-0.6000	0
32	LIVVDYLQL	331	-0.6500	0
33	LPRGRCTPI	573	-0.7100	0
34	MRSGERPMV	421	-0.7300	0
35	WITHAPKLG	662	-0.8000	0
36	LISTVPTAA	105	-0.8100	0
37	FILAKHRNG	844	-0.8100	0
38	VIVAARPGV	221	-0.8300	0
39	MINVFPSGR	443	-0.8500	0
40	VVAISQLNR	371	-0.9000	0
41	LHTLISTVP	102	-0.9100	0
42	LVEAGTRVV	131	-0.9100	0
43	WKHSPSRSR	749	-0.9100	0
44	LERLRPGDF	48	-1.0000	0
45	FVALEDLLQ	174	-1.0000	0
46	IVAARPGVG	222	-1.0000	0
47	LKLIVVDYL	329	-1.0000	0
48	VGVHGAEAV	692	-1.0000	0
49	IQLHEPTMW	741	-1.0100	0
50	FVANGISLH	805	-1.0600	0
51	LEMSKSEIV	255	-1.1000	0
52	LLLRVGIFS	653	-1.1000	0
53	LFIDDSPNL	303	-1.1300	0
54	LGGHDSWRL	669	-1.1800	0
55	LRQKANLKL	323	-1.2000	0

56	YLQLMTSGK	336	-1.2000	0
57	LRADTGAEV	407	-1.2000	0
58	LHIHGAKDQ	677	-1.2000	0
59	LKVGDRIAA	485	-1.3000	0
60	LARGVATGF	197	-1.3100	0
61	MKFEGWTPL	474	-1.3100	0
62	LISLARMIG	511	-1.3100	0
63	LRPARQRLP	566	-1.3100	0
64	YGSTSRRLI	639	-1.3100	0
65	WAQVRNRLS	726	-1.3600	0
66	LHPGQMVIV	215	-1.4000	0
67	IFSLEMSKS	252	-1.4000	0
68	LQLMTSGKK	337	-1.4000	0
69	VFRLRLASG	454	-1.4000	0
70	MRSCSIRHR	239	-1.4100	0
71	IRYEPVDEA	529	-1.5000	0
72	VVEITSIGD	783	-1.5000	0
73	VTVAHQLHL	857	-1.5000	0
74	YEPVDEANL	531	-1.5500	0
75	YLHTLISTV	101	-1.6000	0
76	LLSAEAKIK	266	-1.7000	0
77	MMEIRAKAR	313	-1.8000	0
78	VGIFSWITH	657	-1.8200	0
79	LRPGDFYRP	51	-1.9000	0
80	MVARPMINV	438	-1.9000	0
81	LHLSRFANM	863	-1.9200	0
82	FYRPAHQNV	56	-2.0000	0
83	VVQYGYAGA	138	-2.0000	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	LRLASGREV	457	3.2900	54.83
2	MVIVAARPG	220	2.8400	47.33
3	VRFLRHVGV	686	2.7000	45.00
4	LRMVARPMI	436	2.5200	42.00
5	LRRIGGAPY	93	2.2000	36.67

6	VMRLLSAEA	263	2.1000	35.00
7	LRHLWSAGG	616	1.9000	31.67
8	LRQLKGPVR	706	1.8700	31.17
9	MRLLSAEAK	264	1.8000	30.00
10	VHGAEAVAA	694	1.7000	28.33
11	LRHVGVHGA	689	1.3500	22.50
12	VILLHRPDA	823	1.2700	21.17
13	LRRLVEAGT	128	1.2000	20.00
14	IVAEKALLR	121	1.0000	16.67
15	YGRQPPQDL	19	0.8000	13.33
16	IRHRMASVI	244	0.8000	13.33
17	LRESGCLTA	394	0.6000	10.00
18	FLRHVGVHG	688	0.6000	10.00
19	VVILLHRPD	822	0.4900	8.17
20	LDFMRSCSI	236	0.4000	6.67
21	LRVGIFSWI	655	0.4000	6.67
22	LIVVDYLQL	331	0.3500	5.83
23	LPRGRCTPI	573	0.2900	4.83
24	MRSGERPMV	421	0.2700	4.50
25	LISTVPTAA	105	0.1900	3.17
26	VIVAARPGV	221	0.1700	2.83
27	MINVFPSGR	443	0.1500	2.50
28	VVAISQLNR	371	0.1000	1.67
29	LHTLISTVP	102	0.0900	1.50
30	LVEAGTRVV	131	0.0900	1.50
31	IQLHEPTMW	741	-0.0100	0
32	LEMSKSEIV	255	-0.1000	0
33	FRLRLASGR	455	-0.1000	0
34	LLLRVGIFS	653	-0.1000	0
35	LFIDDSPNL	303	-0.1300	0
36	LGGHDSWRL	669	-0.1800	0
37	LRQKANLKL	323	-0.2000	0
38	LRADTGAEV	407	-0.2000	0
39	LHIHGAKDQ	677	-0.2000	0
40	YGYAGAEGA	141	-0.3000	0
41	FMKFEGWTP	473	-0.3000	0
42	LKVGDRIAA	485	-0.3000	0
43	LARGVATGF	197	-0.3100	0
44	MKFEGWTPL	474	-0.3100	0
45	LISLARMIG	511	-0.3100	0
46	LRPARQRLP	566	-0.3100	0

47	LHPGQMVIV	215	-0.4000	0
48	IFSLEMSKS	252	-0.4000	0
49	LQLMTSGKK	337	-0.4000	0
50	VFRLRLASG	454	-0.4000	0
51	MRSCSIRHR	239	-0.4100	0
52	IRYEPVDEA	529	-0.5000	0
53	VVEITSIGD	783	-0.5000	0
54	VTVAHQLHL	857	-0.5000	0
55	YLAARVPSL	558	-0.5300	0
56	YYGSTSRRL	638	-0.6100	0
57	YGRGEPADA	72	-0.7000	0
58	LLSAEAKIK	266	-0.7000	0
59	YAGAEGADV	143	-0.8000	0
60	MMEIRAKAR	313	-0.8000	0
61	FILAKHRNG	844	-0.8100	0
62	VGIFSWITH	657	-0.8200	0
63	LRPGDFYRP	51	-0.9000	0
64	YASIVAEKA	118	-0.9000	0
65	MVARPMINV	438	-0.9000	0
66	WLAGLGLFT	584	-0.9000	0
67	LHLSRFANM	863	-0.9200	0
68	VVQYGYAGA	138	-1.0000	0
69	FVALEDLLQ	174	-1.0000	0
70	WTPLAQLKV	479	-1.0000	0
71	MLRQLKGPV	705	-1.0000	0
72	FVANGISLH	805	-1.0600	0
73	LAAEQSVLG	27	-1.1000	0
74	YRPAHQNVY	57	-1.1000	0
75	LARMIGDGS	514	-1.1000	0
76	LHRPDAFDR	826	-1.1000	0
77	IKLSDMRSG	273	-1.1100	0
78	LMRSGERPM	420	-1.1300	0
79	IGGAPYLHT	96	-1.2000	0
80	VPSLRPARQ	563	-1.2000	0
81	VWAQVRNRL	725	-1.2000	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	IVVDYLQLM	332	6.1000	64.21
2	LRMVARPMI	436	5.9000	62.11
3	LFIDDSPNL	303	5.1600	54.32
4	VRWDPTNGQ	626	5.0100	52.74
5	VVDDLAPGM	2	4.9000	51.58
6	MRSGERPMV	421	4.9000	51.58
7	MLADLRESG	390	4.5000	47.37
8	WSLDERLRM	430	4.3000	45.26
9	LRADTGAEV	407	4.1000	43.16
10	IRDDYLAAR	554	3.9000	41.05
11	LISLARMIG	511	3.8000	40.00
12	VILLHRPDA	823	3.8000	40.00
13	VAFGELMRS	415	3.7000	38.95
14	VIVAARPGV	221	3.6000	37.89
15	VYYGSTSRR	637	3.5700	37.58
16	LKVGDRIAA	485	3.5000	36.84
17	VRFLRHVGV	686	3.4000	35.79
18	MLRQLKGPV	705	3.4000	35.79
19	MIGDGSCLK	517	3.3000	34.74
20	LKLIVVDYL	329	3.1600	33.26
21	MVIVAARPG	220	3.1000	32.63
22	IVAARPGVG	222	3.1000	32.63
23	MTSGKKYES	340	3.0500	32.11
24	LSKDAIADV	39	3.0000	31.58
25	LRRIGGAPY	93	3.0000	31.58
26	VVAISQLNR	371	3.0000	31.58
27	LKLLAKELE	360	2.9000	30.53
28	MRLLSAEAK	264	2.8000	29.47
29	LRHVGVHGA	689	2.8000	29.47
30	ILLHRPDAF	824	2.8000	29.47
31	VAISQLNRG	372	2.7100	28.53
32	MRSCSIRHR	239	2.7000	28.42
33	LRHLWSAGG	616	2.7000	28.42
34	LRQLKGPVR	706	2.7000	28.42
35	MINVFPSGR	443	2.6700	28.11
36	LTASTRILR	400	2.6000	27.37
37	IRYEPVDEA	529	2.6000	27.37
38	IVMRLLSAE	262	2.4700	26.00
39	LRVGIFSWI	655	2.4700	26.00
40	MEIRAKARR	314	2.4000	25.26

41	LERLRPGDF	48	2.3000	24.21
42	VQYGYAGAE	139	2.3000	24.21
43	ILRADTGAE	406	2.3000	24.21
44	LEMSKSEIV	255	2.2000	23.16
45	VFPSGRKEV	446	2.2000	23.16
46	LHLSRFANM	863	2.2000	23.16
47	LLRRLVEAG	127	2.1000	22.11
48	VIFSLEMSK	251	2.1000	22.11
49	VFRLRLASG	454	2.1000	22.11
50	ITHAPKLGG	663	2.1000	22.11
51	IRHRMASVI	244	2.0700	21.79
52	LARGVATGF	197	2.0000	21.05
53	LGLDFMRSC	234	2.0000	21.05
54	LQLMTSGKK	337	2.0000	21.05
55	WRLHIHGAK	675	2.0000	21.05
56	VVILLHRPD	822	2.0000	21.05
57	LIDDVAQLL	646	1.9600	20.63
58	VLGGMLLSK	33	1.9000	20.00
59	VDYLQLMTS	334	1.9000	20.00
60	LMTSGKKYE	339	1.9000	20.00
61	LEVPVVAIS	367	1.9000	20.00
62	LRESGCLTA	394	1.9000	20.00
63	LRLASGREV	457	1.9000	20.00
64	LLRVGIFSW	654	1.9000	20.00
65	YLAARVPSL	558	1.8600	19.58
66	IVAEKALLR	121	1.8000	18.95
67	MSKSEIVMR	257	1.8000	18.95
68	IRAKARRLR	316	1.8000	18.95
69	LAQLKVGDR	482	1.8000	18.95
70	LLLRVGIFS	653	1.8000	18.95
71	FRLRLASGR	455	1.7700	18.63
72	LSEDFVALE	170	1.7000	17.89
73	VMRLLSAEA	263	1.7000	17.89
74	YYASIVAEK	117	1.6000	16.84
75	VEAGTRVVQ	132	1.6000	16.84
76	IQLHEPTMW	741	1.6000	16.84
77	MWKHSPSRS	748	1.5700	16.53
78	FVANGISLH	805	1.5700	16.53
79	LHRPDAFDR	826	1.5000	15.79
80	MRSGRMSDD	278	1.4700	15.47
81	YRPAHQNVY	57	1.4100	14.84

82	VTNGLHPGQ	211	1.4000	14.74
83	IKLSDMRSG	273	1.4000	14.74
84	VRNRLSAKQ	729	1.4000	14.74
85	FMRSCSIRH	238	1.3000	13.68
86	LMRSGERPM	420	1.3000	13.68
87	VRNPNLDSA	713	1.3000	13.68

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	VRWDPTNGQ	626	4.7100	51.76
2	LRMVARPMI	436	4.0000	43.96
3	WSLDERLRM	430	3.8000	41.76
4	IVVDYLQLM	332	3.6000	39.56
5	LFIDDSPNL	303	3.2000	35.16
6	FVANGISLH	805	3.1500	34.62
7	MRSGERPMV	421	2.9000	31.87
8	WRLHIHGAK	675	2.9000	31.87
9	FMRSCSIRH	238	2.8800	31.65
10	VILLHRPDA	823	2.8000	30.77
11	YYASIVAEK	117	2.5000	27.47
12	LKVGDRIAA	485	2.5000	27.47
13	VVDDLAPGM	2	2.4000	26.37
14	VAFGELMRS	415	2.3000	25.27
15	YGRGEPADA	72	2.2000	24.18
16	MIGDGSCLK	517	2.2000	24.18
17	MLADLRESG	390	2.1000	23.08
18	LRADTGAEV	407	2.1000	23.08
19	FSRHLKLLA	356	1.9000	20.88
20	YLAARVPSL	558	1.9000	20.88
21	LRHVGVHGA	689	1.8000	19.78
22	MRLLSAEAK	264	1.7000	18.68
23	MTSGKKYES	340	1.6500	18.13
24	VIVAARPGV	221	1.6000	17.58
25	IRYEPVDEA	529	1.6000	17.58
26	YLQLMTSGK	336	1.5700	17.25
27	WTRLARRMS	288	1.5000	16.48

28	LISLARMIG	511	1.4000	15.38
29	IRDDYLAAR	554	1.4000	15.38
30	VRFLRHVGV	686	1.4000	15.38
31	MLRQLKGPV	705	1.4000	15.38
32	FIDDSPNLT	304	1.3100	14.40
33	VEAGTRVVQ	132	1.3000	14.29
34	FRLRLASGR	455	1.2700	13.96
35	LKLIVVDYL	329	1.2000	13.19
36	YRPAHQNVY	57	1.1100	12.20
37	YGYAGAEGA	141	1.1000	12.09
38	VTNGLHPGQ	211	1.1000	12.09
39	VRNRLSAKQ	729	1.1000	12.09
40	VYYGSTSRR	637	1.0700	11.76
41	LSKDAIADV	39	1.0000	10.99
42	LGLDFMRSC	234	1.0000	10.99
43	VIFSLEMSK	251	1.0000	10.99
44	YESRQVEVS	346	1.0000	10.99
45	LQLMTSGKK	337	0.9000	9.89
46	LRESGCLTA	394	0.9000	9.89
47	LLRVGIFSW	654	0.9000	9.89
48	LHIHGAKDQ	677	0.9000	9.89
49	VEITSIGDQ	784	0.9000	9.89
50	VLGGMLLSK	33	0.8000	8.79
51	LRRIGGAPY	93	0.7000	7.69
52	MVIVAARPG	220	0.7000	7.69
53	IVAARPGVG	222	0.7000	7.69
54	VMRLLSAEA	263	0.7000	7.69
55	YGRQPPQDL	19	0.6000	6.59
56	IQLHEPTMW	741	0.6000	6.59
57	LRVGIFSWI	655	0.5700	6.26
58	YASIVAEKA	118	0.5000	5.49
59	VDYLQLMTS	334	0.5000	5.49
60	LKLLAKELE	360	0.5000	5.49
61	LEVPVVAIS	367	0.5000	5.49
62	VVAISQLNR	371	0.5000	5.49
63	FEGWTPLAQ	476	0.5000	5.49
64	FVALEDLLQ	174	0.4000	4.40
65	LLLRVGIFS	653	0.4000	4.40
66	VAISQLNRG	372	0.3100	3.41
67	FPSGRKEVF	447	0.3000	3.30
68	LRHLWSAGG	616	0.3000	3.30

69	VRNPNLDSA	713	0.3000	3.30
70	ISLHNSLEQ	810	0.3000	3.30
71	FDRDDPRGG	832	0.3000	3.30
72	YLHTLISTV	101	0.2700	2.97
73	LAAVTVSAA	539	0.2700	2.97
74	MRSCSIRHR	239	0.2000	2.20
75	LEMSKSEIV	255	0.2000	2.20
76	VFPSGRKEV	446	0.2000	2.20
77	FLRHVGVHG	688	0.2000	2.20
78	VHGAEAVAA	694	0.2000	2.20
79	LRQLKGPVR	706	0.2000	2.20
80	IRHRMASVI	244	0.1700	1.87
81	MINVFPSGR	443	0.1700	1.87
82	MWKHSPSRS	748	0.1700	1.87
83	LTASTRILR	400	0.1000	1.10
84	FILAKHRNG	844	0.1000	1.10
85	IVMRLLSAE	262	0.0700	0.77

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRWDPTNGQ	626	6.4000	72.73
2	IVVDYLQLM	332	4.7000	53.41
3	LRMVARPMI	436	3.6000	40.91
4	LRHVGVHGA	689	3.6000	40.91
5	MLADLRESG	390	3.5000	39.77
6	WSLDERLRM	430	3.3000	37.50
7	MIGDGSCLK	517	3.2000	36.36
8	LKVGDRIAA	485	3.1800	36.14
9	MRLLSAEAK	264	3.1000	35.23
10	LRADTGAEV	407	3.1000	35.23
11	VAFGELMRS	415	3.0000	34.09
12	IRYEPVDEA	529	2.9000	32.95
13	LFIDDSPNL	303	2.8000	31.82
14	LKLIVVDYL	329	2.5000	28.41
15	MRSGERPMV	421	2.5000	28.41
16	LHIHGAKDQ	677	2.5000	28.41

17	LRESGCLTA	394	2.4000	27.27
18	IRDDYLAAR	554	2.4000	27.27
19	VILLHRPDA	823	2.4000	27.27
20	VLGGMLLSK	33	2.3000	26.14
21	VRFLRHVGV	686	2.2800	25.91
22	VEAGTRVVQ	132	2.1800	24.77
23	LISLARMIG	511	2.1000	23.86
24	VRNRLSAKQ	729	2.1000	23.86
25	VVDDLAPGM	2	2.0000	22.73
26	LSKDAIADV	39	2.0000	22.73
27	VVAISQLNR	371	2.0000	22.73
28	VAISQLNRG	372	2.0000	22.73
29	LKLLAKELE	360	1.9000	21.59
30	FVANGISLH	805	1.8800	21.36
31	VFPSGRKEV	446	1.8000	20.45
32	VYYGSTSRR	637	1.8000	20.45
33	ISLHNSLEQ	810	1.8000	20.45
34	LRRIGGAPY	93	1.7000	19.32
35	LGLDFMRSC	234	1.7000	19.32
36	VIFSLEMSK	251	1.7000	19.32
37	VMRLLSAEA	263	1.7000	19.32
38	LEMSKSEIV	255	1.6000	18.18
39	VRNPNLDSA	713	1.6000	18.18
40	IQLHEPTMW	741	1.6000	18.18
41	FMRSCSIRH	238	1.5600	17.73
42	YYASIVAEK	117	1.5000	17.05
43	MTSGKKYES	340	1.5000	17.05
44	LEVPVVAIS	367	1.5000	17.05
45	MVIVAARPG	220	1.4000	15.91
46	FSRHLKLLA	356	1.4000	15.91
47	LRHLWSAGG	616	1.3000	14.77
48	LRVGIFSWI	655	1.3000	14.77
49	YGRGEPADA	72	1.2000	13.64
50	VIVAARPGV	221	1.2000	13.64
51	VDYLQLMTS	334	1.2000	13.64
52	ITHAPKLGG	663	1.2000	13.64
53	ILLHRPDAF	824	1.2000	13.64
54	LLRRLVEAG	127	1.1000	12.50
55	LMTSGKKYE	339	1.1000	12.50
56	LIDDVAQLL	646	1.1000	12.50
57	LLLRVGIFS	653	1.0800	12.27

58	VHGAEAVAA	694	1.0800	12.27
59	FIDDSPNLT	304	1.0000	11.36
60	LAAVTVSAA	539	1.0000	11.36
61	MLRQLKGPV	705	1.0000	11.36
62	MRSCSIRHR	239	0.9000	10.23
63	IRHRMASVI	244	0.9000	10.23
64	MEIRAKARR	314	0.9000	10.23
65	MINVFPSGR	443	0.9000	10.23
66	MWKHSPSRS	748	0.9000	10.23
67	YRPAHQNVY	57	0.8000	9.09
68	IVAEKALLR	121	0.8000	9.09
69	IVMRLLSAE	262	0.8000	9.09
70	LTASTRILR	400	0.7800	8.86
71	LISTVPTAA	105	0.7000	7.95
72	VTNGLHPGQ	211	0.7000	7.95
73	VFRLRLASG	454	0.7000	7.95
74	VPSLRPARQ	563	0.7000	7.95
75	LHLSRFANM	863	0.7000	7.95
76	LGLFTKRSH	588	0.6800	7.73
77	IFSLEMSKS	252	0.6000	6.82
78	LLSAEAKIK	266	0.6000	6.82
79	LTMMEIRAK	311	0.6000	6.82
80	LRLASGREV	457	0.6000	6.82
81	LHNSLEQDA	812	0.6000	6.82
82	VVILLHRPD	822	0.6000	6.82
83	YGYAGAEGA	141	0.5000	5.68
84	LARRMSEIS	291	0.5000	5.68
85	LQLMTSGKK	337	0.5000	5.68
86	WRLHIHGAK	675	0.5000	5.68
87	VGVHGAEAV	692	0.5000	5.68

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	VRWDPTNGQ	626	6.4000	72.73
2	IVVDYLQLM	332	4.7000	53.41
3	LRMVARPMI	436	3.6000	40.91

4	LRHVGVHGA	689	3.6000	40.91
5	MLADLRESG	390	3.5000	39.77
6	WSLDERLRM	430	3.3000	37.50
7	MIGDGSCLK	517	3.2000	36.36
8	LKVGDRIAA	485	3.1800	36.14
9	MRLLSAEAK	264	3.1000	35.23
10	LRADTGAEV	407	3.1000	35.23
11	VAFGELMRS	415	3.0000	34.09
12	IRYEPVDEA	529	2.9000	32.95
13	LFIDDSPNL	303	2.8000	31.82
14	LKLIVVDYL	329	2.5000	28.41
15	MRSGERPMV	421	2.5000	28.41
16	LHIHGAKDQ	677	2.5000	28.41
17	LRESGCLTA	394	2.4000	27.27
18	IRDDYLAAR	554	2.4000	27.27
19	VILLHRPDA	823	2.4000	27.27
20	VLGGMLLSK	33	2.3000	26.14
21	VRFLRHVGV	686	2.2800	25.91
22	VEAGTRVVQ	132	2.1800	24.77
23	LISLARMIG	511	2.1000	23.86
24	VRNRLSAKQ	729	2.1000	23.86
25	VVDDLAPGM	2	2.0000	22.73
26	LSKDAIADV	39	2.0000	22.73
27	VVAISQLNR	371	2.0000	22.73
28	VAISQLNRG	372	2.0000	22.73
29	LKLLAKELE	360	1.9000	21.59
30	FVANGISLH	805	1.8800	21.36
31	VFPSGRKEV	446	1.8000	20.45
32	VYYGSTSRR	637	1.8000	20.45
33	ISLHNSLEQ	810	1.8000	20.45
34	LRRIGGAPY	93	1.7000	19.32
35	LGLDFMRSC	234	1.7000	19.32
36	VIFSLEMSK	251	1.7000	19.32
37	VMRLLSAEA	263	1.7000	19.32
38	LEMSKSEIV	255	1.6000	18.18
39	VRNPNLDSA	713	1.6000	18.18
40	IQLHEPTMW	741	1.6000	18.18
41	FMRSCSIRH	238	1.5600	17.73
42	YYASIVAEK	117	1.5000	17.05
43	MTSGKKYES	340	1.5000	17.05
44	LEVPVVAIS	367	1.5000	17.05

45	MVIVAARPG	220	1.4000	15.91
46	FSRHLKLLA	356	1.4000	15.91
47	LRHLWSAGG	616	1.3000	14.77
48	LRVGIFSWI	655	1.3000	14.77
49	YGRGEPADA	72	1.2000	13.64
50	VIVAARPGV	221	1.2000	13.64
51	VDYLQLMTS	334	1.2000	13.64
52	ITHAPKLGG	663	1.2000	13.64
53	ILLHRPDAF	824	1.2000	13.64
54	LLRRLVEAG	127	1.1000	12.50
55	LMTSGKKYE	339	1.1000	12.50
56	LIDDVAQLL	646	1.1000	12.50
57	LLLRVGIFS	653	1.0800	12.27
58	VHGAEAVAA	694	1.0800	12.27
59	FIDDSPNLT	304	1.0000	11.36
60	LAAVTVSAA	539	1.0000	11.36
61	MLRQLKGPV	705	1.0000	11.36
62	MRSCSIRHR	239	0.9000	10.23
63	IRHRMASVI	244	0.9000	10.23
64	MEIRAKARR	314	0.9000	10.23
65	MINVFPSGR	443	0.9000	10.23
66	MWKHSPSRS	748	0.9000	10.23
67	YRPAHQNVY	57	0.8000	9.09
68	IVAEKALLR	121	0.8000	9.09
69	IVMRLLSAE	262	0.8000	9.09
70	LTASTRILR	400	0.7800	8.86
71	LISTVPTAA	105	0.7000	7.95
72	VTNGLHPGQ	211	0.7000	7.95
73	VFRLRLASG	454	0.7000	7.95
74	VPSLRPARQ	563	0.7000	7.95
75	LHLSRFANM	863	0.7000	7.95
76	LGLFTKRSH	588	0.6800	7.73
77	IFSLEMSKS	252	0.6000	6.82
78	LLSAEAKIK	266	0.6000	6.82
79	LTMMEIRAK	311	0.6000	6.82
80	LRLASGREV	457	0.6000	6.82
81	LHNSLEQDA	812	0.6000	6.82
82	VVILLHRPD	822	0.6000	6.82
83	YGYAGAEGA	141	0.5000	5.68
84	LARRMSEIS	291	0.5000	5.68
85	LQLMTSGKK	337	0.5000	5.68

86	WRLHIHGAK	675	0.5000	5.68
87	VGVHGAEAV	692	0.5000	5.68

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	VRWDPTNGQ	626	6.4000	72.73
2	IVVDYLQLM	332	4.7000	53.41
3	LRMVARPMI	436	3.6000	40.91
4	LRHVGVHGA	689	3.6000	40.91
5	MLADLRESG	390	3.5000	39.77
6	WSLDERLRM	430	3.3000	37.50
7	MIGDGSCLK	517	3.2000	36.36
8	LKVGDRIAA	485	3.1800	36.14
9	MRLLSAEAK	264	3.1000	35.23
10	LRADTGAEV	407	3.1000	35.23
11	VAFGELMRS	415	3.0000	34.09
12	IRYEPVDEA	529	2.9000	32.95
13	LFIDDSPNL	303	2.8000	31.82
14	LKLIVVDYL	329	2.5000	28.41
15	MRSGERPMV	421	2.5000	28.41
16	LHIHGAKDQ	677	2.5000	28.41
17	LRESGCLTA	394	2.4000	27.27
18	IRDDYLAAR	554	2.4000	27.27
19	VILLHRPDA	823	2.4000	27.27
20	VLGGMLLSK	33	2.3000	26.14
21	VRFLRHVGV	686	2.2800	25.91
22	VEAGTRVVQ	132	2.1800	24.77
23	LISLARMIG	511	2.1000	23.86
24	VRNRLSAKQ	729	2.1000	23.86
25	VVDDLAPGM	2	2.0000	22.73
26	LSKDAIADV	39	2.0000	22.73
27	VVAISQLNR	371	2.0000	22.73
28	VAISQLNRG	372	2.0000	22.73
29	LKLLAKELE	360	1.9000	21.59
30	FVANGISLH	805	1.8800	21.36
31	VFPSGRKEV	446	1.8000	20.45

32	VYYGSTSRR	637	1.8000	20.45
33	ISLHNSLEQ	810	1.8000	20.45
34	LRRIGGAPY	93	1.7000	19.32
35	LGLDFMRSC	234	1.7000	19.32
36	VIFSLEMSK	251	1.7000	19.32
37	VMRLLSAEA	263	1.7000	19.32
38	LEMSKSEIV	255	1.6000	18.18
39	VRNPNLDSA	713	1.6000	18.18
40	IQLHEPTMW	741	1.6000	18.18
41	FMRSCSIRH	238	1.5600	17.73
42	YYASIVAEK	117	1.5000	17.05
43	MTSGKKYES	340	1.5000	17.05
44	LEVPVVAIS	367	1.5000	17.05
45	MVIVAARPG	220	1.4000	15.91
46	FSRHLKLLA	356	1.4000	15.91
47	LRHLWSAGG	616	1.3000	14.77
48	LRVGIFSWI	655	1.3000	14.77
49	YGRGEPADA	72	1.2000	13.64
50	VIVAARPGV	221	1.2000	13.64
51	VDYLQLMTS	334	1.2000	13.64
52	ITHAPKLGG	663	1.2000	13.64
53	ILLHRPDAF	824	1.2000	13.64
54	LLRRLVEAG	127	1.1000	12.50
55	LMTSGKKYE	339	1.1000	12.50
56	LIDDVAQLL	646	1.1000	12.50
57	LLLRVGIFS	653	1.0800	12.27
58	VHGAEAVAA	694	1.0800	12.27
59	FIDDSPNLT	304	1.0000	11.36
60	LAAVTVSAA	539	1.0000	11.36
61	MLRQLKGPV	705	1.0000	11.36
62	MRSCSIRHR	239	0.9000	10.23
63	IRHRMASVI	244	0.9000	10.23
64	MEIRAKARR	314	0.9000	10.23
65	MINVFPSGR	443	0.9000	10.23
66	MWKHSPSRS	748	0.9000	10.23
67	YRPAHQNVY	57	0.8000	9.09
68	IVAEKALLR	121	0.8000	9.09
69	IVMRLLSAE	262	0.8000	9.09
70	LTASTRILR	400	0.7800	8.86
71	LISTVPTAA	105	0.7000	7.95
72	VTNGLHPGQ	211	0.7000	7.95

73	VFRLRLASG	454	0.7000	7.95
74	VPSLRPARQ	563	0.7000	7.95
75	LHLSRFANM	863	0.7000	7.95
76	LGLFTKRSH	588	0.6800	7.73
77	IFSLEMSKS	252	0.6000	6.82
78	LLSAEAKIK	266	0.6000	6.82
79	LTMMEIRAK	311	0.6000	6.82
80	LRLASGREV	457	0.6000	6.82
81	LHNSLEQDA	812	0.6000	6.82
82	VVILLHRPD	822	0.6000	6.82
83	YGYAGAEGA	141	0.5000	5.68
84	LARRMSEIS	291	0.5000	5.68
85	LQLMTSGKK	337	0.5000	5.68
86	WRLHIHGAK	675	0.5000	5.68
87	VGVHGAEAV	692	0.5000	5.68

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	WSLDERLRM	430	5.3000	55.79
2	IVVDYLQLM	332	5.1000	53.68
3	LRMVARPMI	436	4.9000	51.58
4	LFIDDSPNL	303	4.1600	43.79
5	VRWDPTNGQ	626	4.0100	42.21
6	VVDDLAPGM	2	3.9000	41.05
7	MRSGERPMV	421	3.9000	41.05
8	MLADLRESG	390	3.5000	36.84
9	LRADTGAEV	407	3.1000	32.63
10	WRLHIHGAK	675	3.0000	31.58
11	IRDDYLAAR	554	2.9000	30.53
12	YLAARVPSL	558	2.8600	30.11
13	LISLARMIG	511	2.8000	29.47
14	VILLHRPDA	823	2.8000	29.47
15	FRLRLASGR	455	2.7700	29.16
16	VAFGELMRS	415	2.7000	28.42
17	YYASIVAEK	117	2.6000	27.37
18	VIVAARPGV	221	2.6000	27.37

19	VYYGSTSRR	637	2.5700	27.05
20	FVANGISLH	805	2.5700	27.05
21	LKVGDRIAA	485	2.5000	26.32
22	YRPAHQNVY	57	2.4100	25.37
23	VRFLRHVGV	686	2.4000	25.26
24	MLRQLKGPV	705	2.4000	25.26
25	FMRSCSIRH	238	2.3000	24.21
26	MIGDGSCLK	517	2.3000	24.21
27	YGRGEPADA	72	2.2000	23.16
28	FPSGRKEVF	447	2.2000	23.16
29	LKLIVVDYL	329	2.1600	22.74
30	MVIVAARPG	220	2.1000	22.11
31	IVAARPGVG	222	2.1000	22.11
32	MTSGKKYES	340	2.0500	21.58
33	FIDDSPNLT	304	2.0100	21.16
34	LSKDAIADV	39	2.0000	21.05
35	LRRIGGAPY	93	2.0000	21.05
36	VVAISQLNR	371	2.0000	21.05
37	WTRLARRMS	288	1.9000	20.00
38	FSRHLKLLA	356	1.9000	20.00
39	LKLLAKELE	360	1.9000	20.00
40	MRLLSAEAK	264	1.8000	18.95
41	LRHVGVHGA	689	1.8000	18.95
42	ILLHRPDAF	824	1.8000	18.95
43	VAISQLNRG	372	1.7100	18.00
44	MRSCSIRHR	239	1.7000	17.89
45	LRHLWSAGG	616	1.7000	17.89
46	LRQLKGPVR	706	1.7000	17.89
47	FDRDDPRGG	832	1.7000	17.89
48	YLQLMTSGK	336	1.6700	17.58
49	MINVFPSGR	443	1.6700	17.58
50	LTASTRILR	400	1.6000	16.84
51	IRYEPVDEA	529	1.6000	16.84
52	FLRHVGVHG	688	1.6000	16.84
53	YGRQPPQDL	19	1.5600	16.42
54	WKHSPSRSR	749	1.5000	15.79
55	FILAKHRNG	844	1.5000	15.79
56	IVMRLLSAE	262	1.4700	15.47
57	LRVGIFSWI	655	1.4700	15.47
58	MEIRAKARR	314	1.4000	14.74
59	YESRQVEVS	346	1.4000	14.74

60	LERLRPGDF	48	1.3000	13.68
61	VQYGYAGAE	139	1.3000	13.68
62	ILRADTGAE	406	1.3000	13.68
63	YLHTLISTV	101	1.2700	13.37
64	LEMSKSEIV	255	1.2000	12.63
65	VFPSGRKEV	446	1.2000	12.63
66	LHLSRFANM	863	1.2000	12.63
67	LLRRLVEAG	127	1.1000	11.58
68	YGYAGAEGA	141	1.1000	11.58
69	VIFSLEMSK	251	1.1000	11.58
70	VFRLRLASG	454	1.1000	11.58
71	WITHAPKLG	662	1.1000	11.58
72	ITHAPKLGG	663	1.1000	11.58
73	IRHRMASVI	244	1.0700	11.26
74	LARGVATGF	197	1.0000	10.53
75	LGLDFMRSC	234	1.0000	10.53
76	LQLMTSGKK	337	1.0000	10.53
77	VVILLHRPD	822	1.0000	10.53
78	LIDDVAQLL	646	0.9600	10.11
79	VLGGMLLSK	33	0.9000	9.47
80	VDYLQLMTS	334	0.9000	9.47
81	LMTSGKKYE	339	0.9000	9.47
82	LEVPVVAIS	367	0.9000	9.47
83	LRESGCLTA	394	0.9000	9.47
84	LRLASGREV	457	0.9000	9.47
85	LLRVGIFSW	654	0.9000	9.47
86	IVAEKALLR	121	0.8000	8.42
87	MSKSEIVMR	257	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	VRWDPTNGQ	626	6.4000	72.73
2	IVVDYLQLM	332	4.7000	53.41
3	LRMVARPMI	436	3.6000	40.91
4	LRHVGVHGA	689	3.6000	40.91
5	MLADLRESG	390	3.5000	39.77

6	WSLDERLRM	430	3.3000	37.50
7	MIGDGSCLK	517	3.2000	36.36
8	LKVGDRIAA	485	3.1800	36.14
9	MRLLSAEAK	264	3.1000	35.23
10	LRADTGAEV	407	3.1000	35.23
11	VAFGELMRS	415	3.0000	34.09
12	IRYEPVDEA	529	2.9000	32.95
13	LFIDDSPNL	303	2.8000	31.82
14	LKLIVVDYL	329	2.5000	28.41
15	MRSGERPMV	421	2.5000	28.41
16	LHIHGAKDQ	677	2.5000	28.41
17	LRESGCLTA	394	2.4000	27.27
18	IRDDYLAAR	554	2.4000	27.27
19	VILLHRPDA	823	2.4000	27.27
20	VLGGMLLSK	33	2.3000	26.14
21	VRFLRHVGV	686	2.2800	25.91
22	VEAGTRVVQ	132	2.1800	24.77
23	LISLARMIG	511	2.1000	23.86
24	VRNRLSAKQ	729	2.1000	23.86
25	VVDDLAPGM	2	2.0000	22.73
26	LSKDAIADV	39	2.0000	22.73
27	VVAISQLNR	371	2.0000	22.73
28	VAISQLNRG	372	2.0000	22.73
29	LKLLAKELE	360	1.9000	21.59
30	FVANGISLH	805	1.8800	21.36
31	VFPSGRKEV	446	1.8000	20.45
32	VYYGSTSRR	637	1.8000	20.45
33	ISLHNSLEQ	810	1.8000	20.45
34	LRRIGGAPY	93	1.7000	19.32
35	LGLDFMRSC	234	1.7000	19.32
36	VIFSLEMSK	251	1.7000	19.32
37	VMRLLSAEA	263	1.7000	19.32
38	LEMSKSEIV	255	1.6000	18.18
39	VRNPNLDSA	713	1.6000	18.18
40	IQLHEPTMW	741	1.6000	18.18
41	FMRSCSIRH	238	1.5600	17.73
42	YYASIVAEK	117	1.5000	17.05
43	MTSGKKYES	340	1.5000	17.05
44	LEVPVVAIS	367	1.5000	17.05
45	MVIVAARPG	220	1.4000	15.91
46	FSRHLKLLA	356	1.4000	15.91

47	LRHLWSAGG	616	1.3000	14.77
48	LRVGIFSWI	655	1.3000	14.77
49	YGRGEPADA	72	1.2000	13.64
50	VIVAARPGV	221	1.2000	13.64
51	VDYLQLMTS	334	1.2000	13.64
52	ITHAPKLGG	663	1.2000	13.64
53	ILLHRPDAF	824	1.2000	13.64
54	LLRRLVEAG	127	1.1000	12.50
55	LMTSGKKYE	339	1.1000	12.50
56	LIDDVAQLL	646	1.1000	12.50
57	LLLRVGIFS	653	1.0800	12.27
58	VHGAEAVAA	694	1.0800	12.27
59	FIDDSPNLT	304	1.0000	11.36
60	LAAVTVSAA	539	1.0000	11.36
61	MLRQLKGPV	705	1.0000	11.36
62	MRSCSIRHR	239	0.9000	10.23
63	IRHRMASVI	244	0.9000	10.23
64	MEIRAKARR	314	0.9000	10.23
65	MINVFPSGR	443	0.9000	10.23
66	MWKHSPSRS	748	0.9000	10.23
67	YRPAHQNVY	57	0.8000	9.09
68	IVAEKALLR	121	0.8000	9.09
69	IVMRLLSAE	262	0.8000	9.09
70	LTASTRILR	400	0.7800	8.86
71	LISTVPTAA	105	0.7000	7.95
72	VTNGLHPGQ	211	0.7000	7.95
73	VFRLRLASG	454	0.7000	7.95
74	VPSLRPARQ	563	0.7000	7.95
75	LHLSRFANM	863	0.7000	7.95
76	LGLFTKRSH	588	0.6800	7.73
77	IFSLEMSKS	252	0.6000	6.82
78	LLSAEAKIK	266	0.6000	6.82
79	LTMMEIRAK	311	0.6000	6.82
80	LRLASGREV	457	0.6000	6.82
81	LHNSLEQDA	812	0.6000	6.82
82	VVILLHRPD	822	0.6000	6.82
83	YGYAGAEGA	141	0.5000	5.68
84	LARRMSEIS	291	0.5000	5.68
85	LQLMTSGKK	337	0.5000	5.68
86	WRLHIHGAK	675	0.5000	5.68
87	VGVHGAEAV	692	0.5000	5.68

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	VRWDPTNGQ	626	5.6000	65.12
2	IRYEPVDEA	529	4.1000	47.67
3	FMRSCSIRH	238	3.7600	43.72
4	YLQLMTSGK	336	3.2000	37.21
5	FVALEDLLQ	174	3.0000	34.88
6	ISLHNSLEQ	810	3.0000	34.88
7	MRLLSAEAK	264	2.9000	33.72
8	FVANGISLH	805	2.7800	32.33
9	VMRLLSAEA	263	2.6000	30.23
10	LHIHGAKDQ	677	2.6000	30.23
11	MIGDGSCLK	517	2.4000	27.91
12	YYASIVAEK	117	2.3000	26.74
13	IVAEKALLR	121	2.3000	26.74
14	LRHLWSAGG	616	2.2000	25.58
15	LFIDDSPNL	303	2.0000	23.26
16	LEMSKSEIV	255	1.8000	20.93
17	YGYAGAEGA	141	1.5000	17.44
18	LKLIVVDYL	329	1.5000	17.44
19	IVVDYLQLM	332	1.5000	17.44
20	LQLMTSGKK	337	1.5000	17.44
21	LRESGCLTA	394	1.5000	17.44
22	LRHVGVHGA	689	1.4000	16.28
23	WRLHIHGAK	675	1.3000	15.12
24	VRNRLSAKQ	729	1.3000	15.12
25	YASIVAEKA	118	1.2000	13.95
26	FSLEMSKSE	253	1.2000	13.95
27	IQLHEPTMW	741	1.2000	13.95
28	YGRQPPQDL	19	1.0000	11.63
29	YLHTLISTV	101	0.9000	10.47
30	LISTVPTAA	105	0.9000	10.47
31	WITHAPKLG	662	0.9000	10.47
32	WKHSPSRSR	749	0.9000	10.47
33	VFRAPNDQV	604	0.8000	9.30
34	ILLHRPDAF	824	0.8000	9.30

35	VRFLRHVGV	686	0.7800	9.07
36	MLLSKDAIA	37	0.7000	8.14
37	YYGSTSRRL	638	0.7000	8.14
38	YRPAHQNVY	57	0.6000	6.98
39	FIDDSPNLT	304	0.6000	6.98
40	FLRHLWSAG	615	0.6000	6.98
41	VGVHGAEAV	692	0.6000	6.98
42	LAAEQSVLG	27	0.5800	6.74
43	LRQKANLKL	323	0.5000	5.81
44	MWKHSPSRS	748	0.5000	5.81
45	LRADTGAEV	407	0.4000	4.65
46	VEITSIGDQ	784	0.4000	4.65
47	FLRHVGVHG	688	0.3800	4.42
48	MKFEGWTPL	474	0.3000	3.49
49	FEGWTPLAQ	476	0.3000	3.49
50	LRRIGGAPY	93	0.2000	2.33
51	LHTLISTVP	102	0.2000	2.33
52	IFSLEMSKS	252	0.2000	2.33
53	YESRQVEVS	346	0.2000	2.33
54	YLAARVPSL	558	0.2000	2.33
55	VVDDLAPGM	2	0.1000	1.16
56	LDFMRSCSI	236	0.1000	1.16
57	VVAISQLNR	371	0.1000	1.16
58	FRLRLASGR	455	0.1000	1.16
59	LHLSRFANM	863	0.1000	1.16
60	VHGAEAVAA	694	0.0800	0.93
61	VVEITSIGD	783	0.0800	0.93
62	LVEAGTRVV	131	-0.1000	0
63	VAAQEMLRQ	700	-0.1000	0
64	WAQVRNRLS	726	-0.1000	0
65	VSGTHNFVA	799	-0.1000	0
66	VALEDLLQP	175	-0.2000	0
67	VIFSLEMSK	251	-0.2000	0
68	FSRHLKLLA	356	-0.2000	0
69	VAISQLNRG	372	-0.2000	0
70	VEATGSHPF	465	-0.2000	0
71	VYYGSTSRR	637	-0.2000	0
72	LARRMSEIS	291	-0.3000	0
73	LTMMEIRAK	311	-0.3000	0
74	VDYLQLMTS	334	-0.3000	0
75	YGRGEPADA	72	-0.4000	0

76	LGLDFMRSC	234	-0.4000	0
77	LLSAEAKIK	266	-0.4000	0
78	LEVPVVAIS	367	-0.4000	0
79	ILRADTGAE	406	-0.4000	0
80	WTPLAQLKV	479	-0.4000	0
81	LSRFANMAR	865	-0.4000	0
82	MVIVAARPG	220	-0.5000	0
83	LARMIGDGS	514	-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	VRNRLSAKQ	729	5.2000	54.17
2	ISLHNSLEQ	810	4.4000	45.83
3	LHIHGAKDQ	677	4.0000	41.67
4	LVEAGTRVV	131	3.8000	39.58
5	IFSWITHAP	659	3.7000	38.54
6	MVIVAARPG	220	3.6000	37.50
7	LRQKANLKL	323	3.6000	37.50
8	LTMMEIRAK	311	3.3000	34.38
9	LGGHDSWRL	669	3.3000	34.38
10	LFLRHLWSA	614	3.1000	32.29
11	LRHVGVHGA	689	3.1000	32.29
12	MRSCSIRHR	239	3.0000	31.25
13	VRWDPTNGQ	626	2.9000	30.21
14	IRHRMASVI	244	2.7000	28.13
15	LRLASGREV	457	2.7000	28.13
16	LLLRVGIFS	653	2.7000	28.13
17	IQLHEPTMW	741	2.5000	26.04
18	FEGWTPLAQ	476	2.4000	25.00
19	VMRLLSAEA	263	2.2000	22.92
20	LARRMSEIS	291	2.2000	22.92
21	LFTKRSHEK	590	2.1000	21.88
22	WAQVRNRLS	726	2.0000	20.83
23	VGIFSWITH	657	1.8800	19.58
24	MVARPMINV	438	1.8000	18.75
25	FRLRLASGR	455	1.8000	18.75

26	LRHLWSAGG	616	1.8000	18.75
27	LSRFANMAR	865	1.8000	18.75
28	VVILLHRPD	822	1.6000	16.67
29	VYYGSTSRR	637	1.5000	15.62
30	LLRRLVEAG	127	1.4000	14.58
31	LQLMTSGKK	337	1.4000	14.58
32	LRPARQRLP	566	1.4000	14.58
33	MWKHSPSRS	748	1.4000	14.58
34	FMRSCSIRH	238	1.3800	14.37
35	IVMRLLSAE	262	1.3000	13.54
36	VHGAEAVAA	694	1.2000	12.50
37	VSGTHNFVA	799	1.2000	12.50
38	LGLFTKRSH	588	1.1800	12.29
39	MRLLSAEAK	264	1.1000	11.46
40	LKNQPIRYE	524	1.1000	11.46
41	LRESGCLTA	394	1.0000	10.42
42	WKHSPSRSR	749	1.0000	10.42
43	LISTVPTAA	105	0.9000	9.38
44	FVALEDLLQ	174	0.9000	9.38
45	LLSAEAKIK	266	0.9000	9.38
46	LEVPVVAIS	367	0.9000	9.38
47	LDFMRSCSI	236	0.8000	8.33
48	YYGSTSRRL	638	0.8000	8.33
49	VVEITSIGD	783	0.7800	8.12
50	IKLSDMRSG	273	0.7000	7.29
51	YESRQVEVS	346	0.7000	7.29
52	VVAISQLNR	371	0.6800	7.08
53	IRAKARRLR	316	0.6000	6.25
54	YLQLMTSGK	336	0.6000	6.25
55	VAFGELMRS	415	0.5000	5.21
56	VRFLRHVGV	686	0.5000	5.21
57	LRRIGGAPY	93	0.4800	5.00
58	LLRVGIFSW	654	0.4000	4.17
59	VANGISLHN	806	0.4000	4.17
60	FILAKHRNG	844	0.4000	4.17
61	LRPGDFYRP	51	0.3000	3.12
62	WITHAPKLG	662	0.3000	3.12
63	VGVHGAEAV	692	0.3000	3.12
64	FVANGISLH	805	0.2800	2.92
65	VVQYGYAGA	138	0.2000	2.08
66	INVFPSGRK	444	0.2000	2.08

67	LRVGIFSWI	655	0.2000	2.08
68	VLGGMLLSK	33	0.1000	1.04
69	LLSKDAIAD	38	0.1000	1.04
70	VEATGSHPF	465	0.1000	1.04
71	ILLHRPDAF	824	0.1000	1.04
72	LKLIVVDYL	329	-0.0200	0
73	YGRQPPQDL	19	-0.1000	0
74	MLLSKDAIA	37	-0.1000	0
75	IVVDYLQLM	332	-0.1000	0
76	FRAPNDQVA	605	-0.1000	0
77	VPTAANAGY	109	-0.2000	0
78	IVAEKALLR	121	-0.2000	0
79	LGLDFMRSC	234	-0.2000	0
80	ILRADTGAE	406	-0.2000	0
81	LAAVTVSAA	539	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRWDPTNGQ	626	4.2000	47.73
2	VMRLLSAEA	263	3.8000	43.18
3	LQLMTSGKK	337	3.5000	39.77
4	LRHLWSAGG	616	3.4000	38.64
5	LRHVGVHGA	689	3.4000	38.64
6	MRLLSAEAK	264	3.2000	36.36
7	YLQLMTSGK	336	3.1000	35.23
8	LSRFANMAR	865	2.4000	27.27
9	MVIVAARPG	220	2.2000	25.00
10	VGIFSWITH	657	2.1600	24.55
11	IFSLEMSKS	252	2.1000	23.86
12	LDFMRSCSI	236	2.0000	22.73
13	LHTLISTVP	102	1.9000	21.59
14	LTMMEIRAK	311	1.9000	21.59
15	LKLIVVDYL	329	1.9000	21.59
16	LAAVTVSAA	539	1.9000	21.59
17	FVALEDLLQ	174	1.8000	20.45
18	INVFPSGRK	444	1.8000	20.45

19	VRFLRHVGV	686	1.8000	20.45
20	VRNRLSAKQ	729	1.8000	20.45
21	MINVFPSGR	443	1.6000	18.18
22	IRYEPVDEA	529	1.6000	18.18
23	LRRIGGAPY	93	1.5000	17.05
24	ISLHNSLEQ	810	1.5000	17.05
25	VVEITSIGD	783	1.3800	15.68
26	LRQKANLKL	323	1.3000	14.77
27	FMRSCSIRH	238	1.2600	14.32
28	LVEAGTRVV	131	1.2000	13.64
29	VPSLRPARQ	563	1.2000	13.64
30	IFSWITHAP	659	1.1500	13.07
31	LLRVGIFSW	654	1.0500	11.93
32	VVAISQLNR	371	1.0000	11.36
33	LEVPVVAIS	367	0.9000	10.23
34	MIGDGSCLK	517	0.9000	10.23
35	VFRAPNDQV	604	0.9000	10.23
36	VHGAEAVAA	694	0.9000	10.23
37	FVANGISLH	805	0.8800	10.00
38	LISTVPTAA	105	0.8000	9.09
39	VDYLQLMTS	334	0.8000	9.09
40	ISTVPTAAN	106	0.7000	7.95
41	ILRADTGAE	406	0.7000	7.95
42	VYYGSTSRR	637	0.7000	7.95
43	LRESGCLTA	394	0.6000	6.82
44	WAQVRNRLS	726	0.6000	6.82
45	IQLHEPTMW	741	0.6000	6.82
46	VVILLHRPD	822	0.6000	6.82
47	LARMIGDGS	514	0.5000	5.68
48	LHIHGAKDQ	677	0.5000	5.68
49	MRSCSIRHR	239	0.4000	4.55
50	LEMSKSEIV	255	0.4000	4.55
51	LRMVARPMI	436	0.4000	4.55
52	VFRLRLASG	454	0.4000	4.55
53	IVAEKALLR	121	0.3000	3.41
54	LRRLVEAGT	128	0.3000	3.41
55	IDAIASSGG	188	0.3000	3.41
56	VSGTHNFVA	799	0.2500	2.84
57	LGGMLLSKD	34	0.2000	2.27
58	MLLSKDAIA	37	0.2000	2.27
59	VVQYGYAGA	138	0.2000	2.27

60	IRHRMASVI	244	0.2000	2.27
61	LFIDDSPNL	303	0.2000	2.27
62	LRLASGREV	457	0.1000	1.14
63	MWKHSPSRS	748	0.1000	1.14
64	FEGWTPLAQ	476	0.0500	0.57
65	IVAARPGVG	222	-0.1000	0
66	LIVVDYLQL	331	-0.1000	0
67	VPVVAISQL	369	-0.1000	0
68	VEITSIGDQ	784	-0.1000	0
69	VPTAANAGY	109	-0.2000	0
70	YYASIVAEK	117	-0.2000	0
71	IVVDYLQLM	332	-0.2000	0
72	LAGLGLFTK	585	-0.2500	0
73	YRPAHQNVY	57	-0.3000	0
74	LAQLKVGDR	482	-0.3000	0
75	VAAQEMLRQ	700	-0.3000	0
76	LRQLKGPVR	706	-0.3000	0
77	VILLHRPDA	823	-0.3000	0
78	LERLRPGDF	48	-0.4000	0
79	YASIVAEKA	118	-0.4000	0
80	YGYAGAEGA	141	-0.4000	0
81	LLSAEAKIK	266	-0.4000	0
82	LSDMRSGRM	275	-0.4000	0
83	LISLARMIG	511	-0.4000	0
84	LFTKRSHEK	590	-0.4000	0
85	LHLSRFANM	863	-0.4000	0
86	VSAAHSDRA	544	-0.5000	0

ALLELE: DRB1_0405	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	VRWDPTNGQ	626	4.0000	42.55
2	LRHLWSAGG	616	3.7000	39.36
3	FVALEDLLQ	174	3.6000	38.30
4	FMRSCSIRH	238	3.4800	37.02
5	YLQLMTSGK	336	3.4000	36.17
6	FVANGISLH	805	3.1000	32.98

7	VVEITSIGD	783	3.0800	32.77
8	VMRLLSAEA	263	2.8000	29.79
9	ILRADTGAE	406	2.7000	28.72
10	MVIVAARPG	220	2.5000	26.60
11	LRHVGVHGA	689	2.4000	25.53
12	VGIFSWITH	657	2.3800	25.32
13	VVILLHRPD	822	2.3000	24.47
14	LGGMLLSKD	34	1.9000	20.21
15	LKLIVVDYL	329	1.9000	20.21
16	FEGWTPLAQ	476	1.8500	19.68
17	YRPAHQNVY	57	1.8000	19.15
18	LQLMTSGKK	337	1.8000	19.15
19	ISTVPTAAN	106	1.7000	18.09
20	LRRIGGAPY	93	1.6000	17.02
21	WAQVRNRLS	726	1.6000	17.02
22	VRNRLSAKQ	729	1.6000	17.02
23	MRLLSAEAK	264	1.5000	15.96
24	LSRFANMAR	865	1.4000	14.89
25	LHTLISTVP	102	1.3000	13.83
26	LRQKANLKL	323	1.3000	13.83
27	ISLHNSLEQ	810	1.3000	13.83
28	LDFMRSCSI	236	1.2000	12.77
29	IFSLEMSKS	252	1.1000	11.70
30	VRFLRHVGV	686	1.1000	11.70
31	YGRQPPQDL	19	1.0000	10.64
32	VPSLRPARQ	563	1.0000	10.64
33	LLRVGIFSW	654	0.9500	10.11
34	LKNQPIRYE	524	0.9000	9.57
35	LAAVTVSAA	539	0.9000	9.57
36	YLAARVPSL	558	0.9000	9.57
37	IVMRLLSAE	262	0.8000	8.51
38	VFRLRLASG	454	0.7000	7.45
39	YASIVAEKA	118	0.6000	6.38
40	YGYAGAEGA	141	0.6000	6.38
41	IDAIASSGG	188	0.6000	6.38
42	FSLEMSKSE	253	0.6000	6.38
43	MINVFPSGR	443	0.6000	6.38
44	IRYEPVDEA	529	0.6000	6.38
45	IFSWITHAP	659	0.5500	5.85
46	LVEAGTRVV	131	0.5000	5.32
47	FLRHLWSAG	615	0.5000	5.32

48	YYGSTSRRL	638	0.5000	5.32
49	IQLHEPTMW	741	0.5000	5.32
50	MASVIFSLE	248	0.4000	4.26
51	YLHTLISTV	101	0.3000	3.19
52	LKLLAKELE	360	0.3000	3.19
53	FRLRLASGR	455	0.3000	3.19
54	LHIHGAKDQ	677	0.3000	3.19
55	LRRLVEAGT	128	0.2000	2.13
56	IVAARPGVG	222	0.2000	2.13
57	LFIDDSPNL	303	0.2000	2.13
58	LTMMEIRAK	311	0.2000	2.13
59	VFRAPNDQV	604	0.2000	2.13
60	YYASIVAEK	117	0.1000	1.06
61	INVFPSGRK	444	0.1000	1.06
62	FILAKHRNG	844	0.1000	1.06
63	VPTAANAGY	109	-0.1000	0
64	LIVVDYLQL	331	-0.1000	0
65	IVVDYLQLM	332	-0.1000	0
66	LEVPVVAIS	367	-0.1000	0
67	VPVVAISQL	369	-0.1000	0
68	LISLARMIG	511	-0.1000	0
69	VHGAEAVAA	694	-0.1000	0
70	LISTVPTAA	105	-0.2000	0
71	VDYLQLMTS	334	-0.2000	0
72	LLSKDAIAD	38	-0.2200	0
73	LEMSKSEIV	255	-0.3000	0
74	LSDMRSGRM	275	-0.3000	0
75	VAISQLNRG	372	-0.3000	0
76	FGELMRSGE	417	-0.3000	0
77	WTPLAQLKV	479	-0.3000	0
78	VYYGSTSRR	637	-0.3000	0
79	WKHSPSRSR	749	-0.3000	0
80	VEITSIGDQ	784	-0.3000	0
81	LHLSRFANM	863	-0.3000	0
82	ISLARMIGD	512	-0.3200	0
83	VEVSEFSRH	351	-0.4000	0
84	LRESGCLTA	394	-0.4000	0
85	LRMVARPMI	436	-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	YLQLMTSGK	336	4.1000	46.59
2	VRWDPTNGQ	626	3.2000	36.36
3	FVALEDLLQ	174	2.8000	31.82
4	VMRLLSAEA	263	2.8000	31.82
5	LQLMTSGKK	337	2.5000	28.41
6	LRHLWSAGG	616	2.4000	27.27
7	LRHVGVHGA	689	2.4000	27.27
8	FMRSCSIRH	238	2.2600	25.68
9	MRLLSAEAK	264	2.2000	25.00
10	FVANGISLH	805	1.8800	21.36
11	WAQVRNRLS	726	1.6000	18.18
12	LSRFANMAR	865	1.4000	15.91
13	MVIVAARPG	220	1.2000	13.64
14	VGIFSWITH	657	1.1600	13.18
15	IFSLEMSKS	252	1.1000	12.50
16	FEGWTPLAQ	476	1.0500	11.93
17	LDFMRSCSI	236	1.0000	11.36
18	LHTLISTVP	102	0.9000	10.23
19	LTMMEIRAK	311	0.9000	10.23
20	LKLIVVDYL	329	0.9000	10.23
21	LAAVTVSAA	539	0.9000	10.23
22	YYASIVAEK	117	0.8000	9.09
23	INVFPSGRK	444	0.8000	9.09
24	VRFLRHVGV	686	0.8000	9.09
25	VRNRLSAKQ	729	0.8000	9.09
26	YRPAHQNVY	57	0.7000	7.95
27	YASIVAEKA	118	0.6000	6.82
28	YGYAGAEGA	141	0.6000	6.82
29	MINVFPSGR	443	0.6000	6.82
30	IRYEPVDEA	529	0.6000	6.82
31	LRRIGGAPY	93	0.5000	5.68
32	ISLHNSLEQ	810	0.5000	5.68
33	VVEITSIGD	783	0.3800	4.32
34	LRQKANLKL	323	0.3000	3.41
35	FRLRLASGR	455	0.3000	3.41
36	LVEAGTRVV	131	0.2000	2.27
37	VPSLRPARQ	563	0.2000	2.27

38	IFSWITHAP	659	0.1500	1.70
39	LLRVGIFSW	654	0.0500	0.57
40	LEVPVVAIS	367	-0.1000	0
41	MIGDGSCLK	517	-0.1000	0
42	YLAARVPSL	558	-0.1000	0
43	VFRAPNDQV	604	-0.1000	0
44	VHGAEAVAA	694	-0.1000	0
45	LISTVPTAA	105	-0.2000	0
46	VDYLQLMTS	334	-0.2000	0
47	ISTVPTAAN	106	-0.3000	0
48	ILRADTGAE	406	-0.3000	0
49	VYYGSTSRR	637	-0.3000	0
50	WKHSPSRSR	749	-0.3000	0
51	LRESGCLTA	394	-0.4000	0
52	FRAPNDQVA	605	-0.4000	0
53	IQLHEPTMW	741	-0.4000	0
54	VVILLHRPD	822	-0.4000	0
55	LARMIGDGS	514	-0.5000	0
56	YYGSTSRRL	638	-0.5000	0
57	LHIHGAKDQ	677	-0.5000	0
58	MRSCSIRHR	239	-0.6000	0
59	LEMSKSEIV	255	-0.6000	0
60	LRMVARPMI	436	-0.6000	0
61	VFRLRLASG	454	-0.6000	0
62	WTPLAQLKV	479	-0.6000	0
63	IVAEKALLR	121	-0.7000	0
64	LRRLVEAGT	128	-0.7000	0
65	IDAIASSGG	188	-0.7000	0
66	WRLHIHGAK	675	-0.7000	0
67	VSGTHNFVA	799	-0.7500	0
68	LGGMLLSKD	34	-0.8000	0
69	MLLSKDAIA	37	-0.8000	0
70	VVQYGYAGA	138	-0.8000	0
71	IRHRMASVI	244	-0.8000	0
72	LFIDDSPNL	303	-0.8000	0
73	FLRHLWSAG	615	-0.8000	0
74	WTRLARRMS	288	-0.9000	0
75	LRLASGREV	457	-0.9000	0
76	FSWITHAPK	660	-0.9000	0
77	MWKHSPSRS	748	-0.9000	0
78	IVAARPGVG	222	-1.1000	0

79	LIVVDYLQL	331	-1.1000	0
80	VPVVAISQL	369	-1.1000	0
81	VEITSIGDQ	784	-1.1000	0
82	YGRGEPADA	72	-1.2000	0
83	VPTAANAGY	109	-1.2000	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	VRWDPTNGQ	626	5.0000	53.19
2	LRHLWSAGG	616	4.7000	50.00
3	VVEITSIGD	783	4.0800	43.40
4	VMRLLSAEA	263	3.8000	40.43
5	ILRADTGAE	406	3.7000	39.36
6	MVIVAARPG	220	3.5000	37.23
7	LRHVGVHGA	689	3.4000	36.17
8	VGIFSWITH	657	3.3800	35.96
9	VVILLHRPD	822	3.3000	35.11
10	LGGMLLSKD	34	2.9000	30.85
11	LKLIVVDYL	329	2.9000	30.85
12	LQLMTSGKK	337	2.8000	29.79
13	ISTVPTAAN	106	2.7000	28.72
14	LRRIGGAPY	93	2.6000	27.66
15	FVALEDLLQ	174	2.6000	27.66
16	VRNRLSAKQ	729	2.6000	27.66
17	MRLLSAEAK	264	2.5000	26.60
18	FMRSCSIRH	238	2.4800	26.38
19	YLQLMTSGK	336	2.4000	25.53
20	LSRFANMAR	865	2.4000	25.53
21	LHTLISTVP	102	2.3000	24.47
22	LRQKANLKL	323	2.3000	24.47
23	ISLHNSLEQ	810	2.3000	24.47
24	LDFMRSCSI	236	2.2000	23.40
25	IFSLEMSKS	252	2.1000	22.34
26	VRFLRHVGV	686	2.1000	22.34
27	FVANGISLH	805	2.1000	22.34
28	VPSLRPARQ	563	2.0000	21.28

29	LLRVGIFSW	654	1.9500	20.74
30	LKNQPIRYE	524	1.9000	20.21
31	LAAVTVSAA	539	1.9000	20.21
32	IVMRLLSAE	262	1.8000	19.15
33	VFRLRLASG	454	1.7000	18.09
34	IDAIASSGG	188	1.6000	17.02
35	MINVFPSGR	443	1.6000	17.02
36	IRYEPVDEA	529	1.6000	17.02
37	IFSWITHAP	659	1.5500	16.49
38	LVEAGTRVV	131	1.5000	15.96
39	IQLHEPTMW	741	1.5000	15.96
40	MASVIFSLE	248	1.4000	14.89
41	LKLLAKELE	360	1.3000	13.83
42	LHIHGAKDQ	677	1.3000	13.83
43	LRRLVEAGT	128	1.2000	12.77
44	IVAARPGVG	222	1.2000	12.77
45	LFIDDSPNL	303	1.2000	12.77
46	LTMMEIRAK	311	1.2000	12.77
47	VFRAPNDQV	604	1.2000	12.77
48	INVFPSGRK	444	1.1000	11.70
49	VVAISQLNR	371	1.0000	10.64
50	VPTAANAGY	109	0.9000	9.57
51	LIVVDYLQL	331	0.9000	9.57
52	IVVDYLQLM	332	0.9000	9.57
53	LEVPVVAIS	367	0.9000	9.57
54	VPVVAISQL	369	0.9000	9.57
55	LISLARMIG	511	0.9000	9.57
56	VHGAEAVAA	694	0.9000	9.57
57	FEGWTPLAQ	476	0.8500	9.04
58	YRPAHQNVY	57	0.8000	8.51
59	LISTVPTAA	105	0.8000	8.51
60	VDYLQLMTS	334	0.8000	8.51
61	LLSKDAIAD	38	0.7800	8.30
62	LEMSKSEIV	255	0.7000	7.45
63	LSDMRSGRM	275	0.7000	7.45
64	VAISQLNRG	372	0.7000	7.45
65	VYYGSTSRR	637	0.7000	7.45
66	VEITSIGDQ	784	0.7000	7.45
67	LHLSRFANM	863	0.7000	7.45
68	ISLARMIGD	512	0.6800	7.23
69	VEVSEFSRH	351	0.6000	6.38

70	LRESGCLTA	394	0.6000	6.38
71	LRMVARPMI	436	0.6000	6.38
72	WAQVRNRLS	726	0.6000	6.38
73	LERLRPGDF	48	0.5000	5.32
74	LARMIGDGS	514	0.5000	5.32
75	LGLFTKRSH	588	0.5000	5.32
76	VAAQEMLRQ	700	0.5000	5.32
77	MRSCSIRHR	239	0.4000	4.26
78	IRHRMASVI	244	0.4000	4.26
79	MRSGRMSDD	278	0.4000	4.26
80	LRLASGREV	457	0.4000	4.26
81	VTVSAAHSD	542	0.4000	4.26
82	IGDQHVFDG	789	0.3500	3.72
83	IVAEKALLR	121	0.3000	3.19
84	VSGTHNFVA	799	0.2500	2.66
85	MLLSKDAIA	37	0.2000	2.13
86	VVQYGYAGA	138	0.2000	2.13
87	MKFEGWTPL	474	0.2000	2.13

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	VRWDPTNGQ	626	4.9000	54.44
2	IRYEPVDEA	529	4.1000	45.56
3	IVAEKALLR	121	3.8000	42.22
4	LRHLWSAGG	616	3.6000	40.00
5	YLQLMTSGK	336	3.3000	36.67
6	FMRSCSIRH	238	3.1800	35.33
7	MRLLSAEAK	264	3.0000	33.33
8	IVVDYLQLM	332	3.0000	33.33
9	LFIDDSPNL	303	2.9600	32.89
10	LEMSKSEIV	255	2.8000	31.11
11	ILLHRPDAF	824	2.7000	30.00
12	FSLEMSKSE	253	2.6000	28.89
13	VMRLLSAEA	263	2.6000	28.89
14	MIGDGSCLK	517	2.5000	27.78
15	LKLIVVDYL	329	2.4600	27.33

16	YYASIVAEK	117	2.4000	26.67
17	WKHSPSRSR	749	2.4000	26.67
18	FVALEDLLQ	174	2.3000	25.56
19	WITHAPKLG	662	2.3000	25.56
20	ISLHNSLEQ	810	2.3000	25.56
21	FVANGISLH	805	2.2000	24.44
22	FLRHLWSAG	615	2.0000	22.22
23	LAAEQSVLG	27	1.9800	22.00
24	YGRQPPQDL	19	1.9600	21.78
25	YRPAHQNVY	57	1.9000	21.11
26	YLHTLISTV	101	1.9000	21.11
27	LHIHGAKDQ	677	1.9000	21.11
28	VFRAPNDQV	604	1.8000	20.00
29	VRFLRHVGV	686	1.7800	19.78
30	FLRHVGVHG	688	1.7800	19.78
31	VEATGSHPF	465	1.7000	18.89
32	YYGSTSRRL	638	1.6600	18.44
33	VVDDLAPGM	2	1.6000	17.78
34	LQLMTSGKK	337	1.6000	17.78
35	VVAISQLNR	371	1.6000	17.78
36	FRLRLASGR	455	1.6000	17.78
37	VGVHGAEAV	692	1.6000	17.78
38	LHLSRFANM	863	1.6000	17.78
39	LRRIGGAPY	93	1.5000	16.67
40	YGYAGAEGA	141	1.5000	16.67
41	LRESGCLTA	394	1.5000	16.67
42	WSLDERLRM	430	1.5000	16.67
43	LRQKANLKL	323	1.4600	16.22
44	LRADTGAEV	407	1.4000	15.56
45	WRLHIHGAK	675	1.4000	15.56
46	LRHVGVHGA	689	1.4000	15.56
47	FIDDSPNLT	304	1.3000	14.44
48	VYYGSTSRR	637	1.3000	14.44
49	MKFEGWTPL	474	1.2600	14.00
50	LHTLISTVP	102	1.2000	13.33
51	YASIVAEKA	118	1.2000	13.33
52	VAISQLNRG	372	1.2000	13.33
53	IQLHEPTMW	741	1.2000	13.33
54	VVEITSIGD	783	1.1800	13.11
55	YLAARVPSL	558	1.1600	12.89
56	LSRFANMAR	865	1.1000	12.22

57	LDFMRSCSI	236	1.0000	11.11
58	ILRADTGAE	406	1.0000	11.11
59	MVWSLDERL	428	0.9600	10.67
60	LISTVPTAA	105	0.9000	10.00
61	LVEAGTRVV	131	0.9000	10.00
62	MVIVAARPG	220	0.9000	10.00
63	MWKHSPSRS	748	0.9000	10.00
64	VALEDLLQP	175	0.8000	8.89
65	MLLSKDAIA	37	0.7000	7.78
66	IRDDYLAAR	554	0.7000	7.78
67	MRSCSIRHR	239	0.6000	6.67
68	IFSLEMSKS	252	0.6000	6.67
69	YESRQVEVS	346	0.6000	6.67
70	VFRLRLASG	454	0.6000	6.67
71	WTPLAQLKV	479	0.6000	6.67
72	VRNRLSAKQ	729	0.6000	6.67
73	IFSWITHAP	659	0.4000	4.44
74	LGGHDSWRL	669	0.3600	4.00
75	LSKDAIADV	39	0.3000	3.33
76	LLRRLVEAG	127	0.3000	3.33
77	IDDSPNLTM	305	0.3000	3.33
78	LRQLKGPVR	706	0.3000	3.33
79	WAQVRNRLS	726	0.3000	3.33
80	LERLRPGDF	48	0.2000	2.22
81	IVAARPGVG	222	0.2000	2.22
82	VVILLHRPD	822	0.2000	2.22
83	LIDDVAQLL	646	0.1600	1.78
84	VPTAANAGY	109	0.1000	1.11
85	LARRMSEIS	291	0.1000	1.11
86	VDYLQLMTS	334	0.1000	1.11
87	VHGAEAVAA	694	0.0800	0.89

ALLELE: DRB1_0423	Threshold for 3 % with score: 1.68	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRWDPTNGQ	626	4.2000	47.73
2	VMRLLSAEA	263	3.8000	43.18

3	LQLMTSGKK	337	3.5000	39.77
4	LRHLWSAGG	616	3.4000	38.64
5	LRHVGVHGA	689	3.4000	38.64
6	MRLLSAEAK	264	3.2000	36.36
7	YLQLMTSGK	336	3.1000	35.23
8	LSRFANMAR	865	2.4000	27.27
9	MVIVAARPG	220	2.2000	25.00
10	VGIFSWITH	657	2.1600	24.55
11	IFSLEMSKS	252	2.1000	23.86
12	LDFMRSCSI	236	2.0000	22.73
13	LHTLISTVP	102	1.9000	21.59
14	LTMMEIRAK	311	1.9000	21.59
15	LKLIVVDYL	329	1.9000	21.59
16	LAAVTVSAA	539	1.9000	21.59
17	FVALEDLLQ	174	1.8000	20.45
18	INVFPSGRK	444	1.8000	20.45
19	VRFLRHVGV	686	1.8000	20.45
20	VRNRLSAKQ	729	1.8000	20.45
21	MINVFPSGR	443	1.6000	18.18
22	IRYEPVDEA	529	1.6000	18.18
23	LRRIGGAPY	93	1.5000	17.05
24	ISLHNSLEQ	810	1.5000	17.05
25	VVEITSIGD	783	1.3800	15.68
26	LRQKANLKL	323	1.3000	14.77
27	FMRSCSIRH	238	1.2600	14.32
28	LVEAGTRVV	131	1.2000	13.64
29	VPSLRPARQ	563	1.2000	13.64
30	IFSWITHAP	659	1.1500	13.07
31	LLRVGIFSW	654	1.0500	11.93
32	VVAISQLNR	371	1.0000	11.36
33	LEVPVVAIS	367	0.9000	10.23
34	MIGDGSCLK	517	0.9000	10.23
35	VFRAPNDQV	604	0.9000	10.23
36	VHGAEAVAA	694	0.9000	10.23
37	FVANGISLH	805	0.8800	10.00
38	LISTVPTAA	105	0.8000	9.09
39	VDYLQLMTS	334	0.8000	9.09
40	ISTVPTAAN	106	0.7000	7.95
41	ILRADTGAE	406	0.7000	7.95
42	VYYGSTSRR	637	0.7000	7.95
43	LRESGCLTA	394	0.6000	6.82

44	WAQVRNRLS	726	0.6000	6.82
45	IQLHEPTMW	741	0.6000	6.82
46	VVILLHRPD	822	0.6000	6.82
47	LARMIGDGS	514	0.5000	5.68
48	LHIHGAKDQ	677	0.5000	5.68
49	MRSCSIRHR	239	0.4000	4.55
50	LEMSKSEIV	255	0.4000	4.55
51	LRMVARPMI	436	0.4000	4.55
52	VFRLRLASG	454	0.4000	4.55
53	IVAEKALLR	121	0.3000	3.41
54	LRRLVEAGT	128	0.3000	3.41
55	IDAIASSGG	188	0.3000	3.41
56	VSGTHNFVA	799	0.2500	2.84
57	LGGMLLSKD	34	0.2000	2.27
58	MLLSKDAIA	37	0.2000	2.27
59	VVQYGYAGA	138	0.2000	2.27
60	IRHRMASVI	244	0.2000	2.27
61	LFIDDSPNL	303	0.2000	2.27
62	LRLASGREV	457	0.1000	1.14
63	MWKHSPSRS	748	0.1000	1.14
64	FEGWTPLAQ	476	0.0500	0.57
65	IVAARPGVG	222	-0.1000	0
66	LIVVDYLQL	331	-0.1000	0
67	VPVVAISQL	369	-0.1000	0
68	VEITSIGDQ	784	-0.1000	0
69	VPTAANAGY	109	-0.2000	0
70	YYASIVAEK	117	-0.2000	0
71	IVVDYLQLM	332	-0.2000	0
72	LAGLGLFTK	585	-0.2500	0
73	YRPAHQNVY	57	-0.3000	0
74	LAQLKVGDR	482	-0.3000	0
75	VAAQEMLRQ	700	-0.3000	0
76	LRQLKGPVR	706	-0.3000	0
77	VILLHRPDA	823	-0.3000	0
78	LERLRPGDF	48	-0.4000	0
79	YASIVAEKA	118	-0.4000	0
80	YGYAGAEGA	141	-0.4000	0
81	LLSAEAKIK	266	-0.4000	0
82	LSDMRSGRM	275	-0.4000	0
83	LISLARMIG	511	-0.4000	0
84	LFTKRSHEK	590	-0.4000	0

85	LHLSRFANM	863	-0.4000	0
86	VSAAHSDRA	544	-0.5000	0

ALLELE: DRB1_0426	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRWDPTNGQ	626	5.6000	65.12
2	IRYEPVDEA	529	4.1000	47.67
3	FMRSCSIRH	238	3.7600	43.72
4	YLQLMTSGK	336	3.2000	37.21
5	FVALEDLLQ	174	3.0000	34.88
6	ISLHNSLEQ	810	3.0000	34.88
7	MRLLSAEAK	264	2.9000	33.72
8	FVANGISLH	805	2.7800	32.33
9	VMRLLSAEA	263	2.6000	30.23
10	LHIHGAKDQ	677	2.6000	30.23
11	MIGDGSCLK	517	2.4000	27.91
12	YYASIVAEK	117	2.3000	26.74
13	IVAEKALLR	121	2.3000	26.74
14	LRHLWSAGG	616	2.2000	25.58
15	LFIDDSPNL	303	2.0000	23.26
16	LEMSKSEIV	255	1.8000	20.93
17	YGYAGAEGA	141	1.5000	17.44
18	LKLIVVDYL	329	1.5000	17.44
19	IVVDYLQLM	332	1.5000	17.44
20	LQLMTSGKK	337	1.5000	17.44
21	LRESGCLTA	394	1.5000	17.44
22	LRHVGVHGA	689	1.4000	16.28
23	WRLHIHGAK	675	1.3000	15.12
24	VRNRLSAKQ	729	1.3000	15.12
25	YASIVAEKA	118	1.2000	13.95
26	FSLEMSKSE	253	1.2000	13.95
27	IQLHEPTMW	741	1.2000	13.95
28	YGRQPPQDL	19	1.0000	11.63
29	YLHTLISTV	101	0.9000	10.47
30	LISTVPTAA	105	0.9000	10.47
31	WITHAPKLG	662	0.9000	10.47

32	WKHSPSRSR	749	0.9000	10.47
33	VFRAPNDQV	604	0.8000	9.30
34	ILLHRPDAF	824	0.8000	9.30
35	VRFLRHVGV	686	0.7800	9.07
36	MLLSKDAIA	37	0.7000	8.14
37	YYGSTSRRL	638	0.7000	8.14
38	YRPAHQNVY	57	0.6000	6.98
39	FIDDSPNLT	304	0.6000	6.98
40	FLRHLWSAG	615	0.6000	6.98
41	VGVHGAEAV	692	0.6000	6.98
42	LAAEQSVLG	27	0.5800	6.74
43	LRQKANLKL	323	0.5000	5.81
44	MWKHSPSRS	748	0.5000	5.81
45	LRADTGAEV	407	0.4000	4.65
46	VEITSIGDQ	784	0.4000	4.65
47	FLRHVGVHG	688	0.3800	4.42
48	MKFEGWTPL	474	0.3000	3.49
49	FEGWTPLAQ	476	0.3000	3.49
50	LRRIGGAPY	93	0.2000	2.33
51	LHTLISTVP	102	0.2000	2.33
52	IFSLEMSKS	252	0.2000	2.33
53	YESRQVEVS	346	0.2000	2.33
54	YLAARVPSL	558	0.2000	2.33
55	VVDDLAPGM	2	0.1000	1.16
56	LDFMRSCSI	236	0.1000	1.16
57	VVAISQLNR	371	0.1000	1.16
58	FRLRLASGR	455	0.1000	1.16
59	LHLSRFANM	863	0.1000	1.16
60	VHGAEAVAA	694	0.0800	0.93
61	VVEITSIGD	783	0.0800	0.93
62	LVEAGTRVV	131	-0.1000	0
63	VAAQEMLRQ	700	-0.1000	0
64	WAQVRNRLS	726	-0.1000	0
65	VSGTHNFVA	799	-0.1000	0
66	VALEDLLQP	175	-0.2000	0
67	VIFSLEMSK	251	-0.2000	0
68	FSRHLKLLA	356	-0.2000	0
69	VAISQLNRG	372	-0.2000	0
70	VEATGSHPF	465	-0.2000	0
71	VYYGSTSRR	637	-0.2000	0
72	LARRMSEIS	291	-0.3000	0

73	LTMMEIRAK	311	-0.3000	0
74	VDYLQLMTS	334	-0.3000	0
75	YGRGEPADA	72	-0.4000	0
76	LGLDFMRSC	234	-0.4000	0
77	LLSAEAKIK	266	-0.4000	0
78	LEVPVVAIS	367	-0.4000	0
79	ILRADTGAE	406	-0.4000	0
80	WTPLAQLKV	479	-0.4000	0
81	LSRFANMAR	865	-0.4000	0
82	MVIVAARPG	220	-0.5000	0
83	LARMIGDGS	514	-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	YYGSTSRRL	638	7.3000	62.93
2	FMRSCSIRH	238	6.1000	52.59
3	LIVVDYLQL	331	6.1000	52.59
4	LRMVARPMI	436	5.6000	48.28
5	LEMSKSEIV	255	5.5000	47.41
6	LGGHDSWRL	669	5.2000	44.83
7	YGSTSRRLI	639	5.1000	43.97
8	LRQKANLKL	323	4.9000	42.24
9	YLHTLISTV	101	4.5000	38.79
10	LKLIVVDYL	329	4.4000	37.93
11	MVWSLDERL	428	4.4000	37.93
12	LRLASGREV	457	4.3000	37.07
13	YLAARVPSL	558	4.3000	37.07
14	IRHRMASVI	244	4.1000	35.34
15	VEATGSHPF	465	4.1000	35.34
16	LLRVGIFSW	654	4.0000	34.48
17	VRFLRHVGV	686	4.0000	34.48
18	VTVAHQLHL	857	4.0000	34.48
19	YRPAHQNVY	57	3.9000	33.62
20	YGRQPPQDL	19	3.7000	31.90
21	LRESGCLTA	394	3.7000	31.90
22	MPESELISL	506	3.7000	31.90

23	MVIVAARPG	220	3.6000	31.03
24	MVARPMINV	438	3.6000	31.03
25	LRVGIFSWI	655	3.6000	31.03
26	LRRIGGAPY	93	3.5000	30.17
27	LFIDDSPNL	303	3.5000	30.17
28	LHLSRFANM	863	3.5000	30.17
29	LRHVGVHGA	689	3.3000	28.45
30	WKHSPSRSR	749	3.3000	28.45
31	VPVVAISQL	369	3.2000	27.59
32	VFPSGRKEV	446	3.0000	25.86
33	VGVHGAEAV	692	3.0000	25.86
34	MKFEGWTPL	474	2.9000	25.00
35	VVEITSIGD	783	2.8000	24.14
36	FYRPAHQNV	56	2.7000	23.28
37	WTPLAQLKV	479	2.6000	22.41
38	LVEAGTRVV	131	2.5200	21.72
39	VVAISQLNR	371	2.5000	21.55
40	LMRSGERPM	420	2.5000	21.55
41	VGIFSWITH	657	2.5000	21.55
42	IQLHEPTMW	741	2.5000	21.55
43	LPRGRCTPI	573	2.4000	20.69
44	YASIVAEKA	118	2.2000	18.97
45	YGYAGAEGA	141	2.2000	18.97
46	IVVDYLQLM	332	2.2000	18.97
47	WSLDERLRM	430	2.2000	18.97
48	YEPVDEANL	531	2.2000	18.97
49	FLRHVGVHG	688	2.2000	18.97
50	LISTVPTAA	105	2.1000	18.10
51	LDFMRSCSI	236	2.1000	18.10
52	LSAEAKIKL	267	2.0000	17.24
53	IKLSDMRSG	273	1.9000	16.38
54	VAISQLNRG	372	1.9000	16.38
55	WLAGLGLFT	584	1.9000	16.38
56	LHPGQMVIV	215	1.8000	15.52
57	IDDVAQLLL	647	1.8000	15.52
58	LSAKQMMDI	733	1.8000	15.52
59	VSGTHNFVA	799	1.8000	15.52
60	FRLRLASGR	455	1.7000	14.66
61	LIDDVAQLL	646	1.7000	14.66
62	ISLHNSLEQ	810	1.7000	14.66
63	YAGAEGADV	143	1.6000	13.79

64	LARGVATGF	197	1.6000	13.79
65	FSRHLKLLA	356	1.6000	13.79
66	WSAGGSVRW	620	1.6000	13.79
67	VHGAEAVAA	694	1.6000	13.79
68	IASSGGLAR	191	1.5000	12.93
69	IDDSPNLTM	305	1.5000	12.93
70	VARPMINVF	439	1.5000	12.93
71	FMKFEGWTP	473	1.5000	12.93
72	YYASIVAEK	117	1.4000	12.07
73	LLLRVGIFS	653	1.4000	12.07
74	WRLHIHGAK	675	1.4000	12.07
75	YWDTVVEIT	779	1.4000	12.07
76	ILLHRPDAF	824	1.4000	12.07
77	FILAKHRNG	844	1.4000	12.07
78	IGGAPYLHT	96	1.3000	11.21
79	VIVAARPGV	221	1.3000	11.21
80	MRLLSAEAK	264	1.2000	10.34
81	IVAEKALLR	121	1.1000	9.48
82	IYDVADRRL	162	1.1000	9.48
83	VWAQVRNRL	725	1.1000	9.48
84	VVDRAQAEI	154	1.0000	8.62
85	LTASTRILR	400	1.0000	8.62
86	LRADTGAEV	407	1.0000	8.62
87	MRSGERPMV	421	1.0000	8.62

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	YYGSTSRRL	638	7.3000	62.93
2	FMRSCSIRH	238	6.1000	52.59
3	LIVVDYLQL	331	6.1000	52.59
4	LRMVARPMI	436	5.6000	48.28
5	LEMSKSEIV	255	5.5000	47.41
6	LGGHDSWRL	669	5.2000	44.83
7	YGSTSRRLI	639	5.1000	43.97
8	LRQKANLKL	323	4.9000	42.24
9	YLHTLISTV	101	4.5000	38.79

10	LKLIVVDYL	329	4.4000	37.93
11	MVWSLDERL	428	4.4000	37.93
12	LRLASGREV	457	4.3000	37.07
13	YLAARVPSL	558	4.3000	37.07
14	IRHRMASVI	244	4.1000	35.34
15	VEATGSHPF	465	4.1000	35.34
16	LLRVGIFSW	654	4.0000	34.48
17	VRFLRHVGV	686	4.0000	34.48
18	VTVAHQLHL	857	4.0000	34.48
19	YRPAHQNVY	57	3.9000	33.62
20	YGRQPPQDL	19	3.7000	31.90
21	LRESGCLTA	394	3.7000	31.90
22	MPESELISL	506	3.7000	31.90
23	MVIVAARPG	220	3.6000	31.03
24	MVARPMINV	438	3.6000	31.03
25	LRVGIFSWI	655	3.6000	31.03
26	LRRIGGAPY	93	3.5000	30.17
27	LFIDDSPNL	303	3.5000	30.17
28	LHLSRFANM	863	3.5000	30.17
29	LRHVGVHGA	689	3.3000	28.45
30	WKHSPSRSR	749	3.3000	28.45
31	VPVVAISQL	369	3.2000	27.59
32	VFPSGRKEV	446	3.0000	25.86
33	VGVHGAEAV	692	3.0000	25.86
34	MKFEGWTPL	474	2.9000	25.00
35	VVEITSIGD	783	2.8000	24.14
36	FYRPAHQNV	56	2.7000	23.28
37	WTPLAQLKV	479	2.6000	22.41
38	LVEAGTRVV	131	2.5200	21.72
39	VVAISQLNR	371	2.5000	21.55
40	LMRSGERPM	420	2.5000	21.55
41	VGIFSWITH	657	2.5000	21.55
42	IQLHEPTMW	741	2.5000	21.55
43	LPRGRCTPI	573	2.4000	20.69
44	YASIVAEKA	118	2.2000	18.97
45	YGYAGAEGA	141	2.2000	18.97
46	IVVDYLQLM	332	2.2000	18.97
47	WSLDERLRM	430	2.2000	18.97
48	YEPVDEANL	531	2.2000	18.97
49	FLRHVGVHG	688	2.2000	18.97
50	LISTVPTAA	105	2.1000	18.10

51	LDFMRSCSI	236	2.1000	18.10
52	LSAEAKIKL	267	2.0000	17.24
53	IKLSDMRSG	273	1.9000	16.38
54	VAISQLNRG	372	1.9000	16.38
55	WLAGLGLFT	584	1.9000	16.38
56	LHPGQMVIV	215	1.8000	15.52
57	IDDVAQLLL	647	1.8000	15.52
58	LSAKQMMDI	733	1.8000	15.52
59	VSGTHNFVA	799	1.8000	15.52
60	FRLRLASGR	455	1.7000	14.66
61	LIDDVAQLL	646	1.7000	14.66
62	ISLHNSLEQ	810	1.7000	14.66
63	YAGAEGADV	143	1.6000	13.79
64	LARGVATGF	197	1.6000	13.79
65	FSRHLKLLA	356	1.6000	13.79
66	WSAGGSVRW	620	1.6000	13.79
67	VHGAEAVAA	694	1.6000	13.79
68	IASSGGLAR	191	1.5000	12.93
69	IDDSPNLTM	305	1.5000	12.93
70	VARPMINVF	439	1.5000	12.93
71	FMKFEGWTP	473	1.5000	12.93
72	YYASIVAEK	117	1.4000	12.07
73	LLLRVGIFS	653	1.4000	12.07
74	WRLHIHGAK	675	1.4000	12.07
75	YWDTVVEIT	779	1.4000	12.07
76	ILLHRPDAF	824	1.4000	12.07
77	FILAKHRNG	844	1.4000	12.07
78	IGGAPYLHT	96	1.3000	11.21
79	VIVAARPGV	221	1.3000	11.21
80	MRLLSAEAK	264	1.2000	10.34
81	IVAEKALLR	121	1.1000	9.48
82	IYDVADRRL	162	1.1000	9.48
83	VWAQVRNRL	725	1.1000	9.48
84	VVDRAQAEI	154	1.0000	8.62
85	LTASTRILR	400	1.0000	8.62
86	LRADTGAEV	407	1.0000	8.62
87	MRSGERPMV	421	1.0000	8.62

ALLELE: DRB1_0801	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNRLSAKQ	729	5.2000	60.47
2	IVMRLLSAE	262	5.0000	58.14
3	VVILLHRPD	822	3.6000	41.86
4	MEIRAKARR	314	3.2000	37.21
5	FRLRLASGR	455	3.2000	37.21
6	LGLFTKRSH	588	3.0000	34.88
7	IRAKARRLR	316	2.9000	33.72
8	FVANGISLH	805	2.8000	32.56
9	LLSKDAIAD	38	2.7000	31.40
10	MVIVAARPG	220	2.6000	30.23
11	LRQKANLKL	323	2.6000	30.23
12	LRMVARPMI	436	2.6000	30.23
13	WTRLARRMS	288	2.5000	29.07
14	LLLRVGIFS	653	2.5000	29.07
15	IRHRMASVI	244	2.3000	26.74
16	ILRADTGAE	406	2.3000	26.74
17	LRHLWSAGG	616	2.3000	26.74
18	LLRRLVEAG	127	2.1000	24.42
19	YESRQVEVS	346	2.1000	24.42
20	LFLRHLWSA	614	2.1000	24.42
21	LKLLAKELE	360	2.0000	23.26
22	LISLARMIG	511	2.0000	23.26
23	LRHVGVHGA	689	2.0000	23.26
24	VLERLRPGD	47	1.9000	22.09
25	VVQYGYAGA	138	1.9000	22.09
26	FEGWTPLAQ	476	1.8000	20.93
27	VVDRAQAEI	154	1.7000	19.77
28	VFRLRLASG	454	1.7000	19.77
29	FILAKHRNG	844	1.7000	19.77
30	LRRIGGAPY	93	1.6000	18.60
31	VILLHRPDA	823	1.6000	18.60
32	FVALEDLLQ	174	1.4000	16.28
33	IVAARPGVG	222	1.4000	16.28
34	VMRLLSAEA	263	1.4000	16.28
35	MVARPMINV	438	1.3000	15.12
36	FMRSCSIRH	238	1.2000	13.95
37	ISQLNRGPE	374	1.2000	13.95

38	VPSLRPARQ	563	1.2000	13.95
39	VVDYLQLMT	333	1.1000	12.79
40	WSLDERLRM	430	1.1000	12.79
41	VRFLRHVGV	686	1.1000	12.79
42	VEITSIGDQ	784	1.1000	12.79
43	LLHRPDAFD	825	1.1000	12.79
44	ILAKHRNGP	845	1.1000	12.79
45	LGGMLLSKD	34	1.0000	11.63
46	YRPAHQNVY	57	1.0000	11.63
47	LQLMTSGKK	337	1.0000	11.63
48	FGELMRSGE	417	1.0000	11.63
49	LKNQPIRYE	524	1.0000	11.63
50	YLAARVPSL	558	1.0000	11.63
51	VRWDPTNGQ	626	1.0000	11.63
52	LLRRIGGAP	92	0.9000	10.47
53	LRRLVEAGT	128	0.9000	10.47
54	LTMMEIRAK	311	0.9000	10.47
55	LMTSGKKYE	339	0.9000	10.47
56	LYGRGEPAD	71	0.8000	9.30
57	VQYGYAGAE	139	0.8000	9.30
58	LHIHGAKDQ	677	0.8000	9.30
59	YGRGEPADA	72	0.7000	8.14
60	LLRVGIFSW	654	0.7000	8.14
61	VGIFSWITH	657	0.6000	6.98
62	WRLHIHGAK	675	0.6000	6.98
63	LDLYGRGEP	69	0.5000	5.81
64	MRSCSIRHR	239	0.5000	5.81
65	LEVPVVAIS	367	0.5000	5.81
66	LRLASGREV	457	0.5000	5.81
67	VALFLRHLW	612	0.5000	5.81
68	ITHAPKLGG	663	0.5000	5.81
69	LERLRPGDF	48	0.4000	4.65
70	ISTVPTAAN	106	0.4000	4.65
71	FSRHLKLLA	356	0.4000	4.65
72	YDVADRRLS	163	0.3000	3.49
73	IVVDYLQLM	332	0.3000	3.49
74	VVEITSIGD	783	0.3000	3.49
75	LARRMSEIS	291	0.2000	2.33
76	LKLIVVDYL	329	0.2000	2.33
77	YLQLMTSGK	336	0.2000	2.33
78	YYASIVAEK	117	0.1000	1.16

79	FSLEMSKSE	253	0.1000	1.16
80	LFTKRSHEK	590	0.1000	1.16
81	WITHAPKLG	662	0.1000	1.16
82	MLRQLKGPV	705	0.1000	1.16
83	VADRRLSED	165	-0.1000	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	VRNRLSAKQ	729	4.4000	55.00
2	MEIRAKARR	314	3.2000	40.00
3	FRLRLASGR	455	3.2000	40.00
4	IRAKARRLR	316	2.9000	36.25
5	WTRLARRMS	288	2.5000	31.25
6	LLLRVGIFS	653	2.5000	31.25
7	LRMVARPMI	436	2.4000	30.00
8	IRHRMASVI	244	2.1000	26.25
9	YESRQVEVS	346	2.1000	26.25
10	LFLRHLWSA	614	2.1000	26.25
11	IVMRLLSAE	262	2.0000	25.00
12	LRHVGVHGA	689	2.0000	25.00
13	VVQYGYAGA	138	1.9000	23.75
14	LGLFTKRSH	588	1.7800	22.25
15	LQLMTSGKK	337	1.7000	21.25
16	LTMMEIRAK	311	1.6000	20.00
17	LRQKANLKL	323	1.6000	20.00
18	VILLHRPDA	823	1.6000	20.00
19	FVANGISLH	805	1.5800	19.75
20	VVDRAQAEI	154	1.5000	18.75
21	VMRLLSAEA	263	1.4000	17.50
22	MVIVAARPG	220	1.3000	16.25
23	WRLHIHGAK	675	1.3000	16.25
24	MVARPMINV	438	1.0000	12.50
25	FEGWTPLAQ	476	1.0000	12.50
26	LRHLWSAGG	616	1.0000	12.50
27	YLQLMTSGK	336	0.9000	11.25
28	VVILLHRPD	822	0.9000	11.25

29	YYASIVAEK	117	0.8000	10.00
30	LLRRLVEAG	127	0.8000	10.00
31	LFTKRSHEK	590	0.8000	10.00
32	VRFLRHVGV	686	0.8000	10.00
33	YGRGEPADA	72	0.7000	8.75
34	LISLARMIG	511	0.7000	8.75
35	ILAKHRNGP	845	0.7000	8.75
36	FVALEDLLQ	174	0.6000	7.50
37	LLRRIGGAP	92	0.5000	6.25
38	LRRIGGAPY	93	0.5000	6.25
39	MRSCSIRHR	239	0.5000	6.25
40	LEVPVVAIS	367	0.5000	6.25
41	FSRHLKLLA	356	0.4000	5.00
42	VFRLRLASG	454	0.4000	5.00
43	VPSLRPARQ	563	0.4000	5.00
44	FILAKHRNG	844	0.4000	5.00
45	YDVADRRLS	163	0.3000	3.75
46	VEITSIGDQ	784	0.3000	3.75
47	MRLLSAEAK	264	0.2000	2.50
48	LARRMSEIS	291	0.2000	2.50
49	VVDYLQLMT	333	0.2000	2.50
50	LRLASGREV	457	0.2000	2.50
51	VRWDPTNGQ	626	0.2000	2.50
52	LDLYGRGEP	69	0.1000	1.25
53	IVAARPGVG	222	0.1000	1.25
54	FMRSCSIRH	238	-0.0200	0
55	YRPAHQNVY	57	-0.1000	0
56	INVFPSGRK	444	-0.1000	0
57	VDYLQLMTS	334	-0.2000	0
58	VVAISQLNR	371	-0.2000	0
59	LKVGDRIAA	485	-0.2000	0
60	IRYEPVDEA	529	-0.2000	0
61	FTKRSHEKC	591	-0.2000	0
62	YGSTSRRLI	639	-0.2000	0
63	LLRVGIFSW	654	-0.2000	0
64	MLRQLKGPV	705	-0.2000	0
65	WAQVRNRLS	726	-0.2000	0
66	IHELARGDA	770	-0.2000	0
67	VIVAARPGV	221	-0.3000	0
68	WTPLAQLKV	479	-0.3000	0
69	LDRRGLLRR	87	-0.4000	0

70	VALFLRHLW	612	-0.4000	0
71	FSWITHAPK	660	-0.4000	0
72	LERLRPGDF	48	-0.5000	0
73	LDFMRSCSI	236	-0.5000	0
74	MRSGERPMV	421	-0.5000	0
75	LDERLRMVA	432	-0.5000	0
76	VGDRIAAPR	487	-0.5000	0
77	LAARVPSLR	559	-0.5000	0
78	LSAKQMMDI	733	-0.5000	0
79	LVEAGTRVV	131	-0.6000	0
80	VAFGELMRS	415	-0.6000	0
81	LAQLKVGDR	482	-0.6000	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	VRNRLSAKQ	729	5.4000	67.50
2	MEIRAKARR	314	4.2000	52.50
3	IRAKARRLR	316	3.9000	48.75
4	LLLRVGIFS	653	3.5000	43.75
5	LRMVARPMI	436	3.4000	42.50
6	IRHRMASVI	244	3.1000	38.75
7	LFLRHLWSA	614	3.1000	38.75
8	IVMRLLSAE	262	3.0000	37.50
9	LRHVGVHGA	689	3.0000	37.50
10	VVQYGYAGA	138	2.9000	36.25
11	LGLFTKRSH	588	2.7800	34.75
12	LQLMTSGKK	337	2.7000	33.75
13	LTMMEIRAK	311	2.6000	32.50
14	LRQKANLKL	323	2.6000	32.50
15	VILLHRPDA	823	2.6000	32.50
16	VVDRAQAEI	154	2.5000	31.25
17	VMRLLSAEA	263	2.4000	30.00
18	MVIVAARPG	220	2.3000	28.75
19	FRLRLASGR	455	2.2000	27.50
20	MVARPMINV	438	2.0000	25.00
21	LRHLWSAGG	616	2.0000	25.00

22	VVILLHRPD	822	1.9000	23.75
23	LLRRLVEAG	127	1.8000	22.50
24	LFTKRSHEK	590	1.8000	22.50
25	VRFLRHVGV	686	1.8000	22.50
26	LISLARMIG	511	1.7000	21.25
27	ILAKHRNGP	845	1.7000	21.25
28	LLRRIGGAP	92	1.5000	18.75
29	LRRIGGAPY	93	1.5000	18.75
30	MRSCSIRHR	239	1.5000	18.75
31	WTRLARRMS	288	1.5000	18.75
32	LEVPVVAIS	367	1.5000	18.75
33	VFRLRLASG	454	1.4000	17.50
34	VPSLRPARQ	563	1.4000	17.50
35	VEITSIGDQ	784	1.3000	16.25
36	MRLLSAEAK	264	1.2000	15.00
37	LARRMSEIS	291	1.2000	15.00
38	VVDYLQLMT	333	1.2000	15.00
39	LRLASGREV	457	1.2000	15.00
40	VRWDPTNGQ	626	1.2000	15.00
41	LDLYGRGEP	69	1.1000	13.75
42	IVAARPGVG	222	1.1000	13.75
43	YESRQVEVS	346	1.1000	13.75
44	LLSKDAIAD	38	1.0000	12.50
45	LRRLVEAGT	128	1.0000	12.50
46	LHIHGAKDQ	677	1.0000	12.50
47	INVFPSGRK	444	0.9000	11.25
48	VDYLQLMTS	334	0.8000	10.00
49	VVAISQLNR	371	0.8000	10.00
50	LKVGDRIAA	485	0.8000	10.00
51	IRYEPVDEA	529	0.8000	10.00
52	LLRVGIFSW	654	0.8000	10.00
53	MLRQLKGPV	705	0.8000	10.00
54	IHELARGDA	770	0.8000	10.00
55	VIVAARPGV	221	0.7000	8.75
56	LDRRGLLRR	87	0.6000	7.50
57	VALFLRHLW	612	0.6000	7.50
58	FVANGISLH	805	0.5800	7.25
59	LERLRPGDF	48	0.5000	6.25
60	LDFMRSCSI	236	0.5000	6.25
61	MRSGERPMV	421	0.5000	6.25
62	LDERLRMVA	432	0.5000	6.25

63	VGDRIAAPR	487	0.5000	6.25
64	LAARVPSLR	559	0.5000	6.25
65	LSAKQMMDI	733	0.5000	6.25
66	LVEAGTRVV	131	0.4000	5.00
67	VAFGELMRS	415	0.4000	5.00
68	LAQLKVGDR	482	0.4000	5.00
69	VGIFSWITH	657	0.3800	4.75
70	ILRADTGAE	406	0.3000	3.75
71	LRPARQRLP	566	0.3000	3.75
72	WRLHIHGAK	675	0.3000	3.75
73	VLERLRPGD	47	0.2000	2.50
74	VAARPGVGK	223	0.2000	2.50
75	IFSLEMSKS	252	0.2000	2.50
76	LKLIVVDYL	329	0.2000	2.50
77	IVVDYLQLM	332	0.2000	2.50
78	LAAVTVSAA	539	0.2000	2.50
79	ITHAPKLGG	663	0.2000	2.50
80	LLSAEAKIK	266	0.1000	1.25
81	MTSGKKYES	340	0.1000	1.25
82	MINVFPSGR	443	0.1000	1.25

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	VRNRLSAKQ	729	6.2000	72.09
2	IVMRLLSAE	262	6.0000	69.77
3	VVILLHRPD	822	4.6000	53.49
4	MEIRAKARR	314	4.2000	48.84
5	LGLFTKRSH	588	4.0000	46.51
6	IRAKARRLR	316	3.9000	45.35
7	LLSKDAIAD	38	3.7000	43.02
8	MVIVAARPG	220	3.6000	41.86
9	LRQKANLKL	323	3.6000	41.86
10	LRMVARPMI	436	3.6000	41.86
11	LLLRVGIFS	653	3.5000	40.70
12	IRHRMASVI	244	3.3000	38.37
13	ILRADTGAE	406	3.3000	38.37

14	LRHLWSAGG	616	3.3000	38.37
15	LLRRLVEAG	127	3.1000	36.05
16	LFLRHLWSA	614	3.1000	36.05
17	LKLLAKELE	360	3.0000	34.88
18	LISLARMIG	511	3.0000	34.88
19	LRHVGVHGA	689	3.0000	34.88
20	VLERLRPGD	47	2.9000	33.72
21	VVQYGYAGA	138	2.9000	33.72
22	VVDRAQAEI	154	2.7000	31.40
23	VFRLRLASG	454	2.7000	31.40
24	LRRIGGAPY	93	2.6000	30.23
25	VILLHRPDA	823	2.6000	30.23
26	IVAARPGVG	222	2.4000	27.91
27	VMRLLSAEA	263	2.4000	27.91
28	MVARPMINV	438	2.3000	26.74
29	ISQLNRGPE	374	2.2000	25.58
30	FRLRLASGR	455	2.2000	25.58
31	VPSLRPARQ	563	2.2000	25.58
32	VVDYLQLMT	333	2.1000	24.42
33	VRFLRHVGV	686	2.1000	24.42
34	VEITSIGDQ	784	2.1000	24.42
35	LLHRPDAFD	825	2.1000	24.42
36	ILAKHRNGP	845	2.1000	24.42
37	LGGMLLSKD	34	2.0000	23.26
38	LQLMTSGKK	337	2.0000	23.26
39	LKNQPIRYE	524	2.0000	23.26
40	VRWDPTNGQ	626	2.0000	23.26
41	LLRRIGGAP	92	1.9000	22.09
42	LRRLVEAGT	128	1.9000	22.09
43	LTMMEIRAK	311	1.9000	22.09
44	LMTSGKKYE	339	1.9000	22.09
45	LYGRGEPAD	71	1.8000	20.93
46	VQYGYAGAE	139	1.8000	20.93
47	LHIHGAKDQ	677	1.8000	20.93
48	FVANGISLH	805	1.8000	20.93
49	LLRVGIFSW	654	1.7000	19.77
50	VGIFSWITH	657	1.6000	18.60
51	LDLYGRGEP	69	1.5000	17.44
52	MRSCSIRHR	239	1.5000	17.44
53	WTRLARRMS	288	1.5000	17.44
54	LEVPVVAIS	367	1.5000	17.44

55	LRLASGREV	457	1.5000	17.44
56	VALFLRHLW	612	1.5000	17.44
57	ITHAPKLGG	663	1.5000	17.44
58	LERLRPGDF	48	1.4000	16.28
59	ISTVPTAAN	106	1.4000	16.28
60	IVVDYLQLM	332	1.3000	15.12
61	VVEITSIGD	783	1.3000	15.12
62	LARRMSEIS	291	1.2000	13.95
63	LKLIVVDYL	329	1.2000	13.95
64	YESRQVEVS	346	1.1000	12.79
65	LFTKRSHEK	590	1.1000	12.79
66	MLRQLKGPV	705	1.1000	12.79
67	VIVAARPGV	221	1.0000	11.63
68	VADRRLSED	165	0.9000	10.47
69	IEDRAIHEL	765	0.9000	10.47
70	VDYLQLMTS	334	0.8000	9.30
71	VVAISQLNR	371	0.8000	9.30
72	MRSGERPMV	421	0.8000	9.30
73	FEGWTPLAQ	476	0.8000	9.30
74	LKVGDRIAA	485	0.8000	9.30
75	IRYEPVDEA	529	0.8000	9.30
76	IHELARGDA	770	0.8000	9.30
77	LVEAGTRVV	131	0.7000	8.14
78	LDFMRSCSI	236	0.7000	8.14
79	LRPARQRLP	566	0.7000	8.14
80	LSAKQMMDI	733	0.7000	8.14
81	FILAKHRNG	844	0.7000	8.14
82	LDRRGLLRR	87	0.6000	6.98
83	VAQLLLRVG	650	0.6000	6.98
84	LKGPVRNPN	709	0.6000	6.98
85	ISLHNSLEQ	810	0.6000	6.98
86	MRLLSAEAK	264	0.5000	5.81
87	LDERLMVA	432	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	FRLRLASGR	455	5.0000	57.47
2	VRNRLSAKQ	729	4.4000	50.57
3	IRHRMASVI	244	3.9000	44.83
4	IVMRLLSAE	262	3.8000	43.68
5	YESRQVEVS	346	3.8000	43.68
6	LLLRVGIFS	653	3.3800	38.85
7	FVANGISLH	805	3.3800	38.85
8	MEIRAKARR	314	3.2000	36.78
9	YLQLMTSGK	336	2.7000	31.03
10	ILAKHRNGP	845	2.7000	31.03
11	IRAKARRLR	316	2.6000	29.89
12	LRMVARPMI	436	2.6000	29.89
13	LFLRHLWSA	614	2.6000	29.89
14	LLRRLVEAG	127	2.5000	28.74
15	LRHVGVHGA	689	2.5000	28.74
16	WTRLARRMS	288	2.2000	25.29
17	LRQKANLKL	323	2.2000	25.29
18	VRWDPTNGQ	626	2.2000	25.29
19	YRPAHQNVY	57	1.9000	21.84
20	VVQYGYAGA	138	1.9000	21.84
21	MRLLSAEAK	264	1.9000	21.84
22	LARRMSEIS	291	1.9000	21.84
23	MVARPMINV	438	1.8800	21.61
24	VRFLRHVGV	686	1.8000	20.69
25	VILLHRPDA	823	1.8000	20.69
26	LISLARMIG	511	1.7000	19.54
27	FEGWTPLAQ	476	1.6000	18.39
28	VVDRAQAEI	154	1.5000	17.24
29	FTKRSHEKC	591	1.5000	17.24
30	LGLFTKRSH	588	1.4800	17.01
31	VMRLLSAEA	263	1.4000	16.09
32	LTMMEIRAK	311	1.3000	14.94
33	LAARVPSLR	559	1.3000	14.94
34	LFTKRSHEK	590	1.3000	14.94
35	FVALEDLLQ	174	1.2000	13.79
36	MVIVAARPG	220	1.0000	11.49
37	IFSLEMSKS	252	1.0000	11.49
38	LQLMTSGKK	337	1.0000	11.49
39	FSRHLKLLA	356	1.0000	11.49
40	IRYEPVDEA	529	1.0000	11.49
41	LAAVTVSAA	539	1.0000	11.49

42	LRHLWSAGG	616	1.0000	11.49
43	MINVFPSGR	443	0.9000	10.34
44	LLSKDAIAD	38	0.8800	10.11
45	FMRSCSIRH	238	0.8600	9.89
46	YYASIVAEK	117	0.8000	9.20
47	VVDYLQLMT	333	0.8000	9.20
48	VDYLQLMTS	334	0.8000	9.20
49	YGRGEPADA	72	0.7000	8.05
50	YLHTLISTV	101	0.7000	8.05
51	LKLLAKELE	360	0.7000	8.05
52	LKVGDRIAA	485	0.6800	7.82
53	LLRVGIFSW	654	0.6500	7.47
54	YGYAGAEGA	141	0.6000	6.90
55	WSLDERLRM	430	0.6000	6.90
56	WRLHIHGAK	675	0.6000	6.90
57	VVILLHRPD	822	0.6000	6.90
58	LRRIGGAPY	93	0.5000	5.75
59	LLAKELEVP	362	0.5000	5.75
60	LEVPVVAIS	367	0.5000	5.75
61	LDERLRMVA	432	0.5000	5.75
62	LSAKQMMDI	733	0.5000	5.75
63	LKLIVVDYL	329	0.4000	4.60
64	VVAISQLNR	371	0.4000	4.60
65	VAFGELMRS	415	0.4000	4.60
66	VFRLRLASG	454	0.4000	4.60
67	VPSLRPARQ	563	0.4000	4.60
68	WTPLAQLKV	479	0.3000	3.45
69	VGIFSWITH	657	0.2600	2.99
70	LDRRGLLRR	87	0.2000	2.30
71	LISTVPTAA	105	0.2000	2.30
72	VAARPGVGK	223	0.2000	2.30
73	MRSCSIRHR	239	0.2000	2.30
74	IVVDYLQLM	332	0.2000	2.30
75	YLAARVPSL	558	0.2000	2.30
76	LGGMLLSKD	34	0.1000	1.15
77	VALFLRHLW	612	0.1000	1.15
78	IQLHEPTMW	741	0.1000	1.15
79	FILAKHRNG	844	0.1000	1.15
80	VIVAARPGV	221	-0.1000	0
81	LRLASGREV	457	-0.1000	0
82	LARMIGDGS	514	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRNRLSAKQ	729	5.2000	51.49
2	IVMRLLSAE	262	5.0000	49.50
3	LRQKANLKL	323	4.4000	43.56
4	LLSKDAIAD	38	4.3000	42.57
5	LLLRVGIFS	653	4.1000	40.59
6	VVILLHRPD	822	3.8000	37.62
7	LRMVARPMI	436	3.7500	37.13
8	FEGWTPLAQ	476	3.6000	35.64
9	LISLARMIG	511	3.6000	35.64
10	LLRRLVEAG	127	3.2000	31.68
11	FVALEDLLQ	174	3.2000	31.68
12	MEIRAKARR	314	3.2000	31.68
13	YESRQVEVS	346	3.2000	31.68
14	FRLRLASGR	455	3.2000	31.68
15	LGLFTKRSH	588	3.2000	31.68
16	IRAKARRLR	316	3.1000	30.69
17	LKLLAKELE	360	3.1000	30.69
18	VLERLRPGD	47	3.0500	30.20
19	VVDYLQLMT	333	2.9000	28.71
20	WSLDERLRM	430	2.9000	28.71
21	MVARPMINV	438	2.9000	28.71
22	LFLRHLWSA	614	2.9000	28.71
23	MVIVAARPG	220	2.8000	27.72
24	FMRSCSIRH	238	2.8000	27.72
25	FVANGISLH	805	2.8000	27.72
26	VILLHRPDA	823	2.7500	27.23
27	WTRLARRMS	288	2.7000	26.73
28	LRHVGVHGA	689	2.7000	26.73
29	ILRADTGAE	406	2.4000	23.76
30	IRHRMASVI	244	2.3000	22.77
31	LRHLWSAGG	616	2.3000	22.77
32	ITHAPKLGG	663	2.3000	22.77
33	FSRHLKLLA	356	2.2000	21.78
34	VGIFSWITH	657	2.2000	21.78

35	YLAARVPSL	558	2.1500	21.29
36	LYGRGEPAD	71	1.9500	19.31
37	VVQYGYAGA	138	1.9000	18.81
38	VVEITSIGD	783	1.9000	18.81
39	FILAKHRNG	844	1.9000	18.81
40	WTPLAQLKV	479	1.8000	17.82
41	VVDRAQAEI	154	1.7000	16.83
42	VFRLRLASG	454	1.7000	16.83
43	LRRIGGAPY	93	1.6000	15.84
44	VVAISQLNR	371	1.6000	15.84
45	VRFLRHVGV	686	1.6000	15.84
46	IVAARPGVG	222	1.5000	14.85
47	LMTSGKKYE	339	1.5000	14.85
48	LDRRGLLRR	87	1.4000	13.86
49	VMRLLSAEA	263	1.4000	13.86
50	VDYLQLMTS	334	1.4000	13.86
51	LKVGDRIAA	485	1.4000	13.86
52	LHIHGAKDQ	677	1.4000	13.86
53	ISLHNSLEQ	810	1.4000	13.86
54	ILAKHRNGP	845	1.4000	13.86
55	YRPAHQNVY	57	1.3000	12.87
56	LARRMSEIS	291	1.3000	12.87
57	ISQLNRGPE	374	1.3000	12.87
58	VRWDPTNGQ	626	1.3000	12.87
59	LSAKQMMDI	733	1.3000	12.87
60	LKNQPIRYE	524	1.2000	11.88
61	VPSLRPARQ	563	1.2000	11.88
62	VALFLRHLW	612	1.2000	11.88
63	LLRVGIFSW	654	1.2000	11.88
64	VEITSIGDQ	784	1.2000	11.88
65	VIVAARPGV	221	1.1500	11.39
66	LTMMEIRAK	311	1.1000	10.89
67	LQLMTSGKK	337	1.1000	10.89
68	LDERLRMVA	432	1.1000	10.89
69	LLHRPDAFD	825	1.1000	10.89
70	LGGMLLSKD	34	1.0000	9.90
71	LLRRIGGAP	92	1.0000	9.90
72	LIVVDYLQL	331	1.0000	9.90
73	VAFGELMRS	415	1.0000	9.90
74	FGELMRSGE	417	1.0000	9.90
75	MRSGERPMV	421	0.9500	9.41

76	LRRLVEAGT	128	0.9000	8.91
77	VQYGYAGAE	139	0.9000	8.91
78	FTKRSHEKC	591	0.9000	8.91
79	VAEKALLRR	122	0.8000	7.92
80	LFTKRSHEK	590	0.8000	7.92
81	YGRGEPADA	72	0.7000	6.93
82	MRSCSIRHR	239	0.7000	6.93
83	FSLEMSKSE	253	0.7000	6.93
84	LRLASGREV	457	0.7000	6.93
85	WITHAPKLG	662	0.7000	6.93
86	WRLHIHGAK	675	0.7000	6.93
87	VTVAHQLHL	857	0.7000	6.93

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	LRMVARPMI	436	3.6500	43.98
2	VILLHRPDA	823	3.1500	37.95
3	WTRLARRMS	288	3.1000	37.35
4	FVALEDLLQ	174	2.8000	33.73
5	LRHVGVHGA	689	2.8000	33.73
6	FEGWTPLAQ	476	2.7000	32.53
7	LISLARMIG	511	2.7000	32.53
8	FSRHLKLLA	356	2.6000	31.33
9	VVAISQLNR	371	2.2000	26.51
10	WTPLAQLKV	479	1.9000	22.89
11	FMRSCSIRH	238	1.8800	22.65
12	LGLFTKRSH	588	1.8800	22.65
13	VMRLLSAEA	263	1.8000	21.69
14	VDYLQLMTS	334	1.8000	21.69
15	WRLHIHGAK	675	1.8000	21.69
16	MRLLSAEAK	264	1.7000	20.48
17	VRFLRHVGV	686	1.7000	20.48
18	MVIVAARPG	220	1.6000	19.28
19	FVANGISLH	805	1.5800	19.04
20	VVILLHRPD	822	1.5000	18.07
21	LTMMEIRAK	311	1.4000	16.87

22	LQLMTSGKK	337	1.4000	16.87
23	LRHLWSAGG	616	1.4000	16.87
24	VRNRLSAKQ	729	1.4000	16.87
25	YLQLMTSGK	336	1.3000	15.66
26	YLAARVPSL	558	1.1500	13.86
27	LRRIGGAPY	93	1.1000	13.25
28	YYASIVAEK	117	1.1000	13.25
29	WSLDERLRM	430	1.1000	13.25
30	LLLRVGIFS	653	1.1000	13.25
31	ITHAPKLGG	663	1.0000	12.05
32	LHIHGAKDQ	677	1.0000	12.05
33	ISLHNSLEQ	810	1.0000	12.05
34	VGIFSWITH	657	0.8800	10.60
35	VIVAARPGV	221	0.8500	10.24
36	LRESGCLTA	394	0.8000	9.64
37	VFRLRLASG	454	0.8000	9.64
38	VPSLRPARQ	563	0.8000	9.64
39	VEITSIGDQ	784	0.8000	9.64
40	MRSCSIRHR	239	0.7000	8.43
41	LKVGDRIAA	485	0.7000	8.43
42	LRQKANLKL	323	0.6000	7.23
43	FILAKHRNG	844	0.6000	7.23
44	LRQLKGPVR	706	0.5500	6.63
45	YDVADRRLS	163	0.5000	6.02
46	LKLLAKELE	360	0.5000	6.02
47	MLRQLKGPV	705	0.5000	6.02
48	LRRLVEAGT	128	0.4000	4.82
49	LRLASGREV	457	0.4000	4.82
50	YGSTSRRLI	639	0.4000	4.82
51	LLRVGIFSW	654	0.4000	4.82
52	IRAKARRLR	316	0.3000	3.61
53	VAFGELMRS	415	0.3000	3.61
54	IHELARGDA	770	0.3000	3.61
55	YRPAHQNVY	57	0.2000	2.41
56	IVAARPGVG	222	0.2000	2.41
57	MEIRAKARR	314	0.2000	2.41
58	YESRQVEVS	346	0.2000	2.41
59	FRLRLASGR	455	0.2000	2.41
60	VALFLRHLW	612	0.2000	2.41
61	FSWITHAPK	660	0.2000	2.41
62	LIVVDYLQL	331	0.1000	1.20

63	WAQVRNRLS	726	0.1000	1.20
64	MRSGERPMV	421	-0.0500	0
65	VLGGMLLSK	33	-0.1000	0
66	IVAEKALLR	121	-0.1000	0
67	INVFPSGRK	444	-0.1000	0
68	LAQLKVGDR	482	-0.1000	0
69	LFLRHLWSA	614	-0.1000	0
70	YASIVAEKA	118	-0.2000	0
71	VIFSLEMSK	251	-0.2000	0
72	LEVPVVAIS	367	-0.2000	0
73	LAGLGLFTK	585	-0.2000	0
74	VRWDPTNGQ	626	-0.2000	0
75	WITHAPKLG	662	-0.2000	0
76	VVEITSIGD	783	-0.2000	0
77	LLSAEAKIK	266	-0.3000	0
78	VAAQEMLRQ	700	-0.3000	0
79	VTVAHQLHL	857	-0.3000	0
80	LVEAGTRVV	131	-0.4000	0
81	IFSLEMSKS	252	-0.4000	0
82	MVARPMINV	438	-0.4000	0
83	LKLIVVDYL	329	-0.5000	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	LGLFTKRSH	588	4.8800	58.10
2	LHIHGAKDQ	677	4.3000	51.19
3	IRAKARRLR	316	4.2000	50.00
4	LTMMEIRAK	311	3.8000	45.24
5	VVILLHRPD	822	3.4000	40.48
6	MRSCSIRHR	239	3.3000	39.29
7	VRNRLSAKQ	729	3.3000	39.29
8	WTRLARRMS	288	3.0000	35.71
9	LRLASGREV	457	3.0000	35.71
10	LRHVGVHGA	689	3.0000	35.71
11	ISLHNSLEQ	810	3.0000	35.71
12	VILLHRPDA	823	3.0000	35.71

13	MVIVAARPG	220	2.9000	34.52
14	LRMVARPMI	436	2.9000	34.52
15	FSRHLKLLA	356	2.6000	30.95
16	LFLRHLWSA	614	2.6000	30.95
17	VRFLRHVGV	686	2.5000	29.76
18	LKNQPIRYE	524	2.4000	28.57
19	MRLLSAEAK	264	2.3000	27.38
20	IQLHEPTMW	741	2.3000	27.38
21	LVEAGTRVV	131	2.2000	26.19
22	VRWDPTNGQ	626	2.2000	26.19
23	VMRLLSAEA	263	2.1000	25.00
24	MEIRAKARR	314	2.1000	25.00
25	LRPARQRLP	566	2.1000	25.00
26	VALFLRHLW	612	2.1000	25.00
27	LRQKANLKL	323	1.8000	21.43
28	WRLHIHGAK	675	1.8000	21.43
29	LISLARMIG	511	1.7000	20.24
30	LRHLWSAGG	616	1.7000	20.24
31	LLLRVGIFS	653	1.7000	20.24
32	MWKHSPSRS	748	1.7000	20.24
33	IRYEPVDEA	529	1.6000	19.05
34	ILAKHRNGP	845	1.6000	19.05
35	LFTKRSHEK	590	1.5000	17.86
36	IFSWITHAP	659	1.5000	17.86
37	LGGHDSWRL	669	1.5000	17.86
38	ILLHRPDAF	824	1.5000	17.86
39	VIVAARPGV	221	1.4000	16.67
40	IRHRMASVI	244	1.4000	16.67
41	FEGWTPLAQ	476	1.4000	16.67
42	MLRQLKGPV	705	1.4000	16.67
43	IVMRLLSAE	262	1.3000	15.48
44	FILAKHRNG	844	1.2000	14.29
45	LLRRLVEAG	127	1.1000	13.10
46	VVQYGYAGA	138	1.1000	13.10
47	YDVADRRLS	163	1.1000	13.10
48	LQLMTSGKK	337	1.1000	13.10
49	LKLLAKELE	360	1.1000	13.10
50	VFRLRLASG	454	1.1000	13.10
51	VPSLRPARQ	563	1.1000	13.10
52	LAGLGLFTK	585	1.1000	13.10
53	LLRVGIFSW	654	1.1000	13.10

54	WITHAPKLG	662	1.1000	13.10
55	FVANGISLH	805	1.0800	12.86
56	LEVPVVAIS	367	1.0000	11.90
57	VGIFSWITH	657	0.9800	11.67
58	LLSAEAKIK	266	0.9000	10.71
59	ITHAPKLGG	663	0.9000	10.71
60	VHGAEAVAA	694	0.9000	10.71
61	IKLSDMRSG	273	0.8000	9.52
62	VDYLQLMTS	334	0.8000	9.52
63	LRESGCLTA	394	0.8000	9.52
64	VFPSGRKEV	446	0.8000	9.52
65	VAQLLLRVG	650	0.8000	9.52
66	VGVHGAEAV	692	0.8000	9.52
67	LRRLVEAGT	128	0.7000	8.33
68	MRSGERPMV	421	0.7000	8.33
69	LRRIGGAPY	93	0.6000	7.14
70	IVVDYLQLM	332	0.6000	7.14
71	VVAISQLNR	371	0.6000	7.14
72	LMRSGERPM	420	0.6000	7.14
73	LKVGDRIAA	485	0.6000	7.14
74	VAAQEMLRQ	700	0.6000	7.14
75	VWAQVRNRL	725	0.6000	7.14
76	IGDQHVFDG	789	0.6000	7.14
77	LARRMSEIS	291	0.5000	5.95
78	MTSGKKYES	340	0.5000	5.95
79	FRLRLASGR	455	0.5000	5.95
80	YGSTSRRLI	639	0.5000	5.95
81	IVAEKALLR	121	0.4000	4.76
82	VVDRAQAEI	154	0.4000	4.76
83	LGLDFMRSC	234	0.4000	4.76
84	YESRQVEVS	346	0.4000	4.76
85	FLRHVGVHG	688	0.4000	4.76
86	LRQLKGPVR	706	0.4000	4.76
87	YRPAHQNVY	57	0.3000	3.57

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	LRMVARPMI	436	4.6500	56.02
2	VILLHRPDA	823	4.1500	50.00
3	LRHVGVHGA	689	3.8000	45.78
4	LISLARMIG	511	3.7000	44.58
5	VVAISQLNR	371	3.2000	38.55
6	LGLFTKRSH	588	2.8800	34.70
7	VMRLLSAEA	263	2.8000	33.73
8	VDYLQLMTS	334	2.8000	33.73
9	MRLLSAEAK	264	2.7000	32.53
10	VRFLRHVGV	686	2.7000	32.53
11	MVIVAARPG	220	2.6000	31.33
12	VVILLHRPD	822	2.5000	30.12
13	LTMMEIRAK	311	2.4000	28.92
14	LQLMTSGKK	337	2.4000	28.92
15	LRHLWSAGG	616	2.4000	28.92
16	VRNRLSAKQ	729	2.4000	28.92
17	LRRIGGAPY	93	2.1000	25.30
18	WTRLARRMS	288	2.1000	25.30
19	LLLRVGIFS	653	2.1000	25.30
20	ITHAPKLGG	663	2.0000	24.10
21	LHIHGAKDQ	677	2.0000	24.10
22	ISLHNSLEQ	810	2.0000	24.10
23	VGIFSWITH	657	1.8800	22.65
24	VIVAARPGV	221	1.8500	22.29
25	FVALEDLLQ	174	1.8000	21.69
26	LRESGCLTA	394	1.8000	21.69
27	VFRLRLASG	454	1.8000	21.69
28	VPSLRPARQ	563	1.8000	21.69
29	VEITSIGDQ	784	1.8000	21.69
30	MRSCSIRHR	239	1.7000	20.48
31	FEGWTPLAQ	476	1.7000	20.48
32	LKVGDRIAA	485	1.7000	20.48
33	LRQKANLKL	323	1.6000	19.28
34	FSRHLKLLA	356	1.6000	19.28
35	LRQLKGPVR	706	1.5500	18.67
36	LKLLAKELE	360	1.5000	18.07
37	MLRQLKGPV	705	1.5000	18.07
38	LRRLVEAGT	128	1.4000	16.87
39	LRLASGREV	457	1.4000	16.87
40	LLRVGIFSW	654	1.4000	16.87

41	IRAKARRLR	316	1.3000	15.66
42	VAFGELMRS	415	1.3000	15.66
43	IHELARGDA	770	1.3000	15.66
44	IVAARPGVG	222	1.2000	14.46
45	MEIRAKARR	314	1.2000	14.46
46	VALFLRHLW	612	1.2000	14.46
47	LIVVDYLQL	331	1.1000	13.25
48	LERLRPGDF	48	1.0000	12.05
49	MRSGERPMV	421	0.9500	11.45
50	VLGGMLLSK	33	0.9000	10.84
51	IVAEKALLR	121	0.9000	10.84
52	INVFPSGRK	444	0.9000	10.84
53	WTPLAQLKV	479	0.9000	10.84
54	LAQLKVGDR	482	0.9000	10.84
55	LFLRHLWSA	614	0.9000	10.84
56	FMRSCSIRH	238	0.8800	10.60
57	VIFSLEMSK	251	0.8000	9.64
58	LEVPVVAIS	367	0.8000	9.64
59	LAGLGLFTK	585	0.8000	9.64
60	VRWDPTNGQ	626	0.8000	9.64
61	WRLHIHGAK	675	0.8000	9.64
62	VVEITSIGD	783	0.8000	9.64
63	LLSAEAKIK	266	0.7000	8.43
64	VAAQEMLRQ	700	0.7000	8.43
65	VTVAHQLHL	857	0.7000	8.43
66	LVEAGTRVV	131	0.6000	7.23
67	IFSLEMSKS	252	0.6000	7.23
68	MVARPMINV	438	0.6000	7.23
69	FVANGISLH	805	0.5800	6.99
70	LKLIVVDYL	329	0.5000	6.02
71	VFPSGRKEV	446	0.5000	6.02
72	LRPARQRLP	566	0.5000	6.02
73	LSRFANMAR	865	0.5000	6.02
74	ILRADTGAE	406	0.4000	4.82
75	VHGAEAVAA	694	0.4000	4.82
76	YLQLMTSGK	336	0.3000	3.61
77	LAAVTVSAA	539	0.3000	3.61
78	MINVFPSGR	443	0.2000	2.41
79	IFSWITHAP	659	0.2000	2.41
80	VAHQLHLSR	859	0.2000	2.41
81	YLAARVPSL	558	0.1500	1.81

82	YYASIVAEK	117	0.1000	1.20
83	LDFMRSCSI	236	0.1000	1.20
84	IRHRMASVI	244	0.1000	1.20
85	VVDYLQLMT	333	0.1000	1.20
86	MTSGKKYES	340	0.1000	1.20
87	LTASTRILR	400	0.1000	1.20

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	LRMVARPMI	436	4.6500	56.02
2	VILLHRPDA	823	4.1500	50.00
3	LRHVGVHGA	689	3.8000	45.78
4	LISLARMIG	511	3.7000	44.58
5	VVAISQLNR	371	3.2000	38.55
6	LGLFTKRSH	588	2.8800	34.70
7	VMRLLSAEA	263	2.8000	33.73
8	VDYLQLMTS	334	2.8000	33.73
9	MRLLSAEAK	264	2.7000	32.53
10	VRFLRHVGV	686	2.7000	32.53
11	MVIVAARPG	220	2.6000	31.33
12	VVILLHRPD	822	2.5000	30.12
13	LTMMEIRAK	311	2.4000	28.92
14	LQLMTSGKK	337	2.4000	28.92
15	LRHLWSAGG	616	2.4000	28.92
16	VRNRLSAKQ	729	2.4000	28.92
17	LRRIGGAPY	93	2.1000	25.30
18	WTRLARRMS	288	2.1000	25.30
19	LLLRVGIFS	653	2.1000	25.30
20	ITHAPKLGG	663	2.0000	24.10
21	LHIHGAKDQ	677	2.0000	24.10
22	ISLHNSLEQ	810	2.0000	24.10
23	VGIFSWITH	657	1.8800	22.65
24	VIVAARPGV	221	1.8500	22.29
25	FVALEDLLQ	174	1.8000	21.69
26	LRESGCLTA	394	1.8000	21.69
27	VFRLRLASG	454	1.8000	21.69

28	VPSLRPARQ	563	1.8000	21.69
29	VEITSIGDQ	784	1.8000	21.69
30	MRSCSIRHR	239	1.7000	20.48
31	FEGWTPLAQ	476	1.7000	20.48
32	LKVGDRIAA	485	1.7000	20.48
33	LRQKANLKL	323	1.6000	19.28
34	FSRHLKLLA	356	1.6000	19.28
35	LRQLKGPVR	706	1.5500	18.67
36	LKLLAKELE	360	1.5000	18.07
37	MLRQLKGPV	705	1.5000	18.07
38	LRRLVEAGT	128	1.4000	16.87
39	LRLASGREV	457	1.4000	16.87
40	LLRVGIFSW	654	1.4000	16.87
41	IRAKARRLR	316	1.3000	15.66
42	VAFGELMRS	415	1.3000	15.66
43	IHELARGDA	770	1.3000	15.66
44	IVAARPGVG	222	1.2000	14.46
45	MEIRAKARR	314	1.2000	14.46
46	VALFLRHLW	612	1.2000	14.46
47	LIVVDYLQL	331	1.1000	13.25
48	LERLRPGDF	48	1.0000	12.05
49	MRSGERPMV	421	0.9500	11.45
50	VLGGMLLSK	33	0.9000	10.84
51	IVAEKALLR	121	0.9000	10.84
52	INVFPSGRK	444	0.9000	10.84
53	WTPLAQLKV	479	0.9000	10.84
54	LAQLKVGDR	482	0.9000	10.84
55	LFLRHLWSA	614	0.9000	10.84
56	FMRSCSIRH	238	0.8800	10.60
57	VIFSLEMSK	251	0.8000	9.64
58	LEVPVVAIS	367	0.8000	9.64
59	LAGLGLFTK	585	0.8000	9.64
60	VRWDPTNGQ	626	0.8000	9.64
61	WRLHIHGAK	675	0.8000	9.64
62	VVEITSIGD	783	0.8000	9.64
63	LLSAEAKIK	266	0.7000	8.43
64	VAAQEMLRQ	700	0.7000	8.43
65	VTVAHQLHL	857	0.7000	8.43
66	LVEAGTRVV	131	0.6000	7.23
67	IFSLEMSKS	252	0.6000	7.23
68	MVARPMINV	438	0.6000	7.23

69	FVANGISLH	805	0.5800	6.99
70	LKLIVVDYL	329	0.5000	6.02
71	VFPSGRKEV	446	0.5000	6.02
72	LRPARQRLP	566	0.5000	6.02
73	LSRFANMAR	865	0.5000	6.02
74	ILRADTGAE	406	0.4000	4.82
75	VHGAEAVAA	694	0.4000	4.82
76	YLQLMTSGK	336	0.3000	3.61
77	LAAVTVSAA	539	0.3000	3.61
78	MINVFPSGR	443	0.2000	2.41
79	IFSWITHAP	659	0.2000	2.41
80	VAHQLHLSR	859	0.2000	2.41
81	YLAARVPSL	558	0.1500	1.81
82	YYASIVAEK	117	0.1000	1.20
83	LDFMRSCSI	236	0.1000	1.20
84	IRHRMASVI	244	0.1000	1.20
85	VVDYLQLMT	333	0.1000	1.20
86	MTSGKKYES	340	0.1000	1.20
87	LTASTRILR	400	0.1000	1.20

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	VRWDPTNGQ	626	5.7100	62.75
2	LRMVARPMI	436	5.0000	54.95
3	IVVDYLQLM	332	4.6000	50.55
4	LFIDDSPNL	303	4.2000	46.15
5	MRSGERPMV	421	3.9000	42.86
6	VILLHRPDA	823	3.8000	41.76
7	LKVGDRIAA	485	3.5000	38.46
8	VVDDLAPGM	2	3.4000	37.36
9	VAFGELMRS	415	3.3000	36.26
10	MIGDGSCLK	517	3.2000	35.16
11	MLADLRESG	390	3.1000	34.07
12	LRADTGAEV	407	3.1000	34.07
13	WSLDERLRM	430	2.8000	30.77
14	LRHVGVHGA	689	2.8000	30.77

15	MRLLSAEAK	264	2.7000	29.67
16	MTSGKKYES	340	2.6500	29.12
17	VIVAARPGV	221	2.6000	28.57
18	IRYEPVDEA	529	2.6000	28.57
19	LISLARMIG	511	2.4000	26.37
20	IRDDYLAAR	554	2.4000	26.37
21	VRFLRHVGV	686	2.4000	26.37
22	MLRQLKGPV	705	2.4000	26.37
23	VEAGTRVVQ	132	2.3000	25.27
24	LKLIVVDYL	329	2.2000	24.18
25	FVANGISLH	805	2.1500	23.63
26	VTNGLHPGQ	211	2.1000	23.08
27	VRNRLSAKQ	729	2.1000	23.08
28	VYYGSTSRR	637	2.0700	22.75
29	LSKDAIADV	39	2.0000	21.98
30	LGLDFMRSC	234	2.0000	21.98
31	VIFSLEMSK	251	2.0000	21.98
32	LQLMTSGKK	337	1.9000	20.88
33	LRESGCLTA	394	1.9000	20.88
34	LLRVGIFSW	654	1.9000	20.88
35	WRLHIHGAK	675	1.9000	20.88
36	LHIHGAKDQ	677	1.9000	20.88
37	VEITSIGDQ	784	1.9000	20.88
38	FMRSCSIRH	238	1.8800	20.66
39	VLGGMLLSK	33	1.8000	19.78
40	LRRIGGAPY	93	1.7000	18.68
41	MVIVAARPG	220	1.7000	18.68
42	IVAARPGVG	222	1.7000	18.68
43	VMRLLSAEA	263	1.7000	18.68
44	IQLHEPTMW	741	1.6000	17.58
45	LRVGIFSWI	655	1.5700	17.25
46	YYASIVAEK	117	1.5000	16.48
47	VDYLQLMTS	334	1.5000	16.48
48	LKLLAKELE	360	1.5000	16.48
49	LEVPVVAIS	367	1.5000	16.48
50	VVAISQLNR	371	1.5000	16.48
51	LLLRVGIFS	653	1.4000	15.38
52	VAISQLNRG	372	1.3100	14.40
53	LRHLWSAGG	616	1.3000	14.29
54	VRNPNLDSA	713	1.3000	14.29
55	ISLHNSLEQ	810	1.3000	14.29

56	LAAVTVSAA	539	1.2700	13.96
57	YGRGEPADA	72	1.2000	13.19
58	MRSCSIRHR	239	1.2000	13.19
59	LEMSKSEIV	255	1.2000	13.19
60	VFPSGRKEV	446	1.2000	13.19
61	VHGAEAVAA	694	1.2000	13.19
62	LRQLKGPVR	706	1.2000	13.19
63	IRHRMASVI	244	1.1700	12.86
64	MINVFPSGR	443	1.1700	12.86
65	MWKHSPSRS	748	1.1700	12.86
66	LTASTRILR	400	1.1000	12.09
67	IVMRLLSAE	262	1.0700	11.76
68	LIDDVAQLL	646	1.0000	10.99
69	LGLFTKRSH	588	0.9800	10.77
70	VQYGYAGAE	139	0.9000	9.89
71	LTMMEIRAK	311	0.9000	9.89
72	MEIRAKARR	314	0.9000	9.89
73	FSRHLKLLA	356	0.9000	9.89
74	ILRADTGAE	406	0.9000	9.89
75	LRLASGREV	457	0.9000	9.89
76	YLAARVPSL	558	0.9000	9.89
77	VVILLHRPD	822	0.9000	9.89
78	ILLHRPDAF	824	0.9000	9.89
79	IFSLEMSKS	252	0.8700	9.56
80	LISTVPTAA	105	0.7000	7.69
81	LLRRLVEAG	127	0.7000	7.69
82	VFRLRLASG	454	0.7000	7.69
83	VPSLRPARQ	563	0.7000	7.69
84	ITHAPKLGG	663	0.7000	7.69
85	IHELARGDA	770	0.7000	7.69
86	LHLSRFANM	863	0.7000	7.69
87	LAGLGLFTK	585	0.6000	6.59

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	WTRLARRMS	288	4.0000	47.62

2	LGLFTKRSH	588	3.8800	46.19
3	FSRHLKLLA	356	3.6000	42.86
4	LHIHGAKDQ	677	3.3000	39.29
5	IRAKARRLR	316	3.2000	38.10
6	LTMMEIRAK	311	2.8000	33.33
7	WRLHIHGAK	675	2.8000	33.33
8	FEGWTPLAQ	476	2.4000	28.57
9	VVILLHRPD	822	2.4000	28.57
10	MRSCSIRHR	239	2.3000	27.38
11	VRNRLSAKQ	729	2.3000	27.38
12	FILAKHRNG	844	2.2000	26.19
13	YDVADRRLS	163	2.1000	25.00
14	WITHAPKLG	662	2.1000	25.00
15	FVANGISLH	805	2.0800	24.76
16	LRLASGREV	457	2.0000	23.81
17	LRHVGVHGA	689	2.0000	23.81
18	ISLHNSLEQ	810	2.0000	23.81
19	VILLHRPDA	823	2.0000	23.81
20	MVIVAARPG	220	1.9000	22.62
21	LRMVARPMI	436	1.9000	22.62
22	LFLRHLWSA	614	1.6000	19.05
23	FRLRLASGR	455	1.5000	17.86
24	YGSTSRRLI	639	1.5000	17.86
25	VRFLRHVGV	686	1.5000	17.86
26	YESRQVEVS	346	1.4000	16.67
27	LKNQPIRYE	524	1.4000	16.67
28	FLRHVGVHG	688	1.4000	16.67
29	YRPAHQNVY	57	1.3000	15.48
30	MRLLSAEAK	264	1.3000	15.48
31	IQLHEPTMW	741	1.3000	15.48
32	YYASIVAEK	117	1.2000	14.29
33	LVEAGTRVV	131	1.2000	14.29
34	VRWDPTNGQ	626	1.2000	14.29
35	VMRLLSAEA	263	1.1000	13.10
36	MEIRAKARR	314	1.1000	13.10
37	LRPARQRLP	566	1.1000	13.10
38	VALFLRHLW	612	1.1000	13.10
39	FVALEDLLQ	174	1.0000	11.90
40	YLQLMTSGK	336	1.0000	11.90
41	YGRQPPQDL	19	0.9000	10.71
42	LRQKANLKL	323	0.8000	9.52

43	WKHSPSRSR	749	0.8000	9.52
44	LISLARMIG	511	0.7000	8.33
45	YLAARVPSL	558	0.7000	8.33
46	LRHLWSAGG	616	0.7000	8.33
47	LLLRVGIFS	653	0.7000	8.33
48	MWKHSPSRS	748	0.7000	8.33
49	FMRSCSIRH	238	0.6800	8.10
50	IRYEPVDEA	529	0.6000	7.14
51	YYGSTSRRL	638	0.6000	7.14
52	ILAKHRNGP	845	0.6000	7.14
53	LFTKRSHEK	590	0.5000	5.95
54	IFSWITHAP	659	0.5000	5.95
55	LGGHDSWRL	669	0.5000	5.95
56	ILLHRPDAF	824	0.5000	5.95
57	VIVAARPGV	221	0.4000	4.76
58	IRHRMASVI	244	0.4000	4.76
59	MLRQLKGPV	705	0.4000	4.76
60	WAQVRNRLS	726	0.4000	4.76
61	YGYAGAEGA	141	0.3000	3.57
62	IVMRLLSAE	262	0.3000	3.57
63	WSLDERLRM	430	0.3000	3.57
64	FMKFEGWTP	473	0.3000	3.57
65	YGRGEPADA	72	0.2000	2.38
66	LLRRLVEAG	127	0.1000	1.19
67	VVQYGYAGA	138	0.1000	1.19
68	LQLMTSGKK	337	0.1000	1.19
69	LKLLAKELE	360	0.1000	1.19
70	VFRLRLASG	454	0.1000	1.19
71	WTPLAQLKV	479	0.1000	1.19
72	VPSLRPARQ	563	0.1000	1.19
73	LAGLGLFTK	585	0.1000	1.19
74	LLRVGIFSW	654	0.1000	1.19
75	VGIFSWITH	657	-0.0200	0
76	LLSAEAKIK	266	-0.1000	0
77	FLRHLWSAG	615	-0.1000	0
78	ITHAPKLGG	663	-0.1000	0
79	VHGAEAVAA	694	-0.1000	0
80	IKLSDMRSG	273	-0.2000	0
81	VDYLQLMTS	334	-0.2000	0
82	LRESGCLTA	394	-0.2000	0
83	VFPSGRKEV	446	-0.2000	0

84	VAQLLLRVG	650	-0.2000	0
85	VGVHGAEAV	692	-0.2000	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	IRAKARRLR	316	4.7000	53.41
2	WTRLARRMS	288	4.4000	50.00
3	MRSCSIRHR	239	3.8000	43.18
4	FSRHLKLLA	356	3.6000	40.91
5	FILAKHRNG	844	3.6000	40.91
6	WITHAPKLG	662	3.5000	39.77
7	VVILLHRPD	822	3.5000	39.77
8	MVIVAARPG	220	3.3000	37.50
9	LGLFTKRSH	588	3.3000	37.50
10	FRLRLASGR	455	3.0000	34.09
11	LRLASGREV	457	3.0000	34.09
12	LTMMEIRAK	311	2.9000	32.95
13	WRLHIHGAK	675	2.9000	32.95
14	LRMVARPMI	436	2.8000	31.82
15	LKNQPIRYE	524	2.8000	31.82
16	FLRHVGVHG	688	2.8000	31.82
17	YRPAHQNVY	57	2.6000	29.55
18	MEIRAKARR	314	2.6000	29.55
19	LHIHGAKDQ	677	2.6000	29.55
20	YDVADRRLS	163	2.5000	28.41
21	VRFLRHVGV	686	2.5000	28.41
22	YGSTSRRLI	639	2.4000	27.27
23	ILLHRPDAF	824	2.4000	27.27
24	WKHSPSRSR	749	2.3000	26.14
25	LVEAGTRVV	131	2.2000	25.00
26	LISLARMIG	511	2.1000	23.86
27	LRPARQRLP	566	2.1000	23.86
28	LRHLWSAGG	616	2.1000	23.86
29	LRHVGVHGA	689	2.0000	22.73
30	VILLHRPDA	823	2.0000	22.73
31	YGRQPPQDL	19	1.8600	21.14

32	YESRQVEVS	346	1.8000	20.45
33	WSLDERLRM	430	1.8000	20.45
34	LRQKANLKL	323	1.7600	20.00
35	IVMRLLSAE	262	1.7000	19.32
36	FEGWTPLAQ	476	1.7000	19.32
37	YLAARVPSL	558	1.6600	18.86
38	LFLRHLWSA	614	1.6000	18.18
39	VRNRLSAKQ	729	1.6000	18.18
40	ILAKHRNGP	845	1.6000	18.18
41	YYGSTSRRL	638	1.5600	17.73
42	LLRRLVEAG	127	1.5000	17.05
43	LKLLAKELE	360	1.5000	17.05
44	VFRLRLASG	454	1.5000	17.05
45	IFSWITHAP	659	1.5000	17.05
46	FVANGISLH	805	1.5000	17.05
47	LGGHDSWRL	669	1.4600	16.59
48	VIVAARPGV	221	1.4000	15.91
49	MRLLSAEAK	264	1.4000	15.91
50	MLRQLKGPV	705	1.4000	15.91
51	YYASIVAEK	117	1.3000	14.77
52	IRHRMASVI	244	1.3000	14.77
53	FMKFEGWTP	473	1.3000	14.77
54	FLRHLWSAG	615	1.3000	14.77
55	ITHAPKLGG	663	1.3000	14.77
56	IQLHEPTMW	741	1.3000	14.77
57	ISLHNSLEQ	810	1.3000	14.77
58	IKLSDMRSG	273	1.2000	13.64
59	VAQLLLRVG	650	1.2000	13.64
60	VMRLLSAEA	263	1.1000	12.50
61	IVVDYLQLM	332	1.1000	12.50
62	YLQLMTSGK	336	1.1000	12.50
63	VVAISQLNR	371	1.1000	12.50
64	LMRSGERPM	420	1.1000	12.50
65	WTPLAQLKV	479	1.1000	12.50
66	VALFLRHLW	612	1.1000	12.50
67	LLLRVGIFS	653	1.1000	12.50
68	MWKHSPSRS	748	1.1000	12.50
69	IGDQHVFDG	789	1.0000	11.36
70	LRRIGGAPY	93	0.9000	10.23
71	IVAEKALLR	121	0.9000	10.23
72	LRQLKGPVR	706	0.9000	10.23

73	VFPSGRKEV	446	0.8000	9.09
74	VGVHGAEAV	692	0.8000	9.09
75	WAQVRNRLS	726	0.8000	9.09
76	MRSGERPMV	421	0.7000	7.95
77	VAISQLNRG	372	0.6000	6.82
78	IRYEPVDEA	529	0.6000	6.82
79	LFTKRSHEK	590	0.6000	6.82
80	VAHQLHLSR	859	0.6000	6.82
81	VWAQVRNRL	725	0.5600	6.36
82	IVAARPGVG	222	0.5000	5.68
83	LMTSGKKYE	339	0.5000	5.68
84	VRWDPTNGQ	626	0.5000	5.68
85	LRRLVEAGT	128	0.4000	4.55
86	LEVPVVAIS	367	0.4000	4.55
87	YGYAGAEGA	141	0.3000	3.41

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	LGLFTKRSH	588	4.8800	58.10
2	LHIHGAKDQ	677	4.3000	51.19
3	IRAKARRLR	316	4.2000	50.00
4	LTMMEIRAK	311	3.8000	45.24
5	VVILLHRPD	822	3.4000	40.48
6	MRSCSIRHR	239	3.3000	39.29
7	VRNRLSAKQ	729	3.3000	39.29
8	WTRLARRMS	288	3.0000	35.71
9	LRLASGREV	457	3.0000	35.71
10	LRHVGVHGA	689	3.0000	35.71
11	ISLHNSLEQ	810	3.0000	35.71
12	VILLHRPDA	823	3.0000	35.71
13	MVIVAARPG	220	2.9000	34.52
14	LRMVARPMI	436	2.9000	34.52
15	FSRHLKLLA	356	2.6000	30.95
16	LFLRHLWSA	614	2.6000	30.95
17	VRFLRHVGV	686	2.5000	29.76
18	LKNQPIRYE	524	2.4000	28.57

19	MRLLSAEAK	264	2.3000	27.38
20	IQLHEPTMW	741	2.3000	27.38
21	LVEAGTRVV	131	2.2000	26.19
22	VRWDPTNGQ	626	2.2000	26.19
23	VMRLLSAEA	263	2.1000	25.00
24	MEIRAKARR	314	2.1000	25.00
25	LRPARQRLP	566	2.1000	25.00
26	VALFLRHLW	612	2.1000	25.00
27	LRQKANLKL	323	1.8000	21.43
28	WRLHIHGAK	675	1.8000	21.43
29	LISLARMIG	511	1.7000	20.24
30	LRHLWSAGG	616	1.7000	20.24
31	LLLRVGIFS	653	1.7000	20.24
32	MWKHSPSRS	748	1.7000	20.24
33	IRYEPVDEA	529	1.6000	19.05
34	ILAKHRNGP	845	1.6000	19.05
35	LFTKRSHEK	590	1.5000	17.86
36	IFSWITHAP	659	1.5000	17.86
37	LGGHDSWRL	669	1.5000	17.86
38	ILLHRPDAF	824	1.5000	17.86
39	VIVAARPGV	221	1.4000	16.67
40	IRHRMASVI	244	1.4000	16.67
41	FEGWTPLAQ	476	1.4000	16.67
42	MLRQLKGPV	705	1.4000	16.67
43	IVMRLLSAE	262	1.3000	15.48
44	FILAKHRNG	844	1.2000	14.29
45	LLRRLVEAG	127	1.1000	13.10
46	VVQYGYAGA	138	1.1000	13.10
47	YDVADRRLS	163	1.1000	13.10
48	LQLMTSGKK	337	1.1000	13.10
49	LKLLAKELE	360	1.1000	13.10
50	VFRLRLASG	454	1.1000	13.10
51	VPSLRPARQ	563	1.1000	13.10
52	LAGLGLFTK	585	1.1000	13.10
53	LLRVGIFSW	654	1.1000	13.10
54	WITHAPKLG	662	1.1000	13.10
55	FVANGISLH	805	1.0800	12.86
56	LEVPVVAIS	367	1.0000	11.90
57	VGIFSWITH	657	0.9800	11.67
58	LLSAEAKIK	266	0.9000	10.71
59	ITHAPKLGG	663	0.9000	10.71

60	VHGAEAVAA	694	0.9000	10.71
61	IKLSDMRSG	273	0.8000	9.52
62	VDYLQLMTS	334	0.8000	9.52
63	LRESGCLTA	394	0.8000	9.52
64	VFPSGRKEV	446	0.8000	9.52
65	VAQLLLRVG	650	0.8000	9.52
66	VGVHGAEAV	692	0.8000	9.52
67	LRRLVEAGT	128	0.7000	8.33
68	MRSGERPMV	421	0.7000	8.33
69	LRRIGGAPY	93	0.6000	7.14
70	IVVDYLQLM	332	0.6000	7.14
71	VVAISQLNR	371	0.6000	7.14
72	LMRSGERPM	420	0.6000	7.14
73	LKVGDRIAA	485	0.6000	7.14
74	VAAQEMLRQ	700	0.6000	7.14
75	VWAQVRNRL	725	0.6000	7.14
76	IGDQHVFDG	789	0.6000	7.14
77	LARRMSEIS	291	0.5000	5.95
78	MTSGKKYES	340	0.5000	5.95
79	FRLRLASGR	455	0.5000	5.95
80	YGSTSRRLI	639	0.5000	5.95
81	IVAEKALLR	121	0.4000	4.76
82	VVDRAQAEI	154	0.4000	4.76
83	LGLDFMRSC	234	0.4000	4.76
84	YESRQVEVS	346	0.4000	4.76
85	FLRHVGVHG	688	0.4000	4.76
86	LRQLKGPVR	706	0.4000	4.76
87	YRPAHQNVY	57	0.3000	3.57

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	LRMVARPMI	436	4.5500	52.30
2	LISLARMIG	511	4.1000	47.13
3	VVAISQLNR	371	3.7000	42.53
4	WTRLARRMS	288	3.5000	40.23
5	VILLHRPDA	823	3.1500	36.21

6	MVIVAARPG	220	3.0000	34.48
7	WTPLAQLKV	479	2.9000	33.33
8	LRHLWSAGG	616	2.8000	32.18
9	LRHVGVHGA	689	2.8000	32.18
10	VRFLRHVGV	686	2.7000	31.03
11	FSRHLKLLA	356	2.6000	29.89
12	WSLDERLRM	430	2.6000	29.89
13	VVILLHRPD	822	2.6000	29.89
14	LRRIGGAPY	93	2.4000	27.59
15	ITHAPKLGG	663	2.4000	27.59
16	MRSCSIRHR	239	2.2000	25.29
17	VDYLQLMTS	334	2.2000	25.29
18	VFRLRLASG	454	2.2000	25.29
19	YLAARVPSL	558	2.1100	24.25
20	FVALEDLLQ	174	2.1000	24.14
21	LRQLKGPVR	706	2.0500	23.56
22	FEGWTPLAQ	476	2.0000	22.99
23	FILAKHRNG	844	2.0000	22.99
24	LERLRPGDF	48	1.9000	21.84
25	LKLLAKELE	360	1.9000	21.84
26	WRLHIHGAK	675	1.9000	21.84
27	VIVAARPGV	221	1.8500	21.26
28	VMRLLSAEA	263	1.8000	20.69
29	MRLLSAEAK	264	1.8000	20.69
30	IRAKARRLR	316	1.8000	20.69
31	MEIRAKARR	314	1.7000	19.54
32	FRLRLASGR	455	1.7000	19.54
33	IVAARPGVG	222	1.6000	18.39
34	LRQKANLKL	323	1.5600	17.93
35	YRPAHQNVY	57	1.5000	17.24
36	LTMMEIRAK	311	1.5000	17.24
37	LQLMTSGKK	337	1.5000	17.24
38	LLLRVGIFS	653	1.5000	17.24
39	MLRQLKGPV	705	1.5000	17.24
40	IVAEKALLR	121	1.4000	16.09
41	YLQLMTSGK	336	1.4000	16.09
42	LRLASGREV	457	1.4000	16.09
43	LAQLKVGDR	482	1.4000	16.09
44	FMRSCSIRH	238	1.3000	14.94
45	LGLFTKRSH	588	1.3000	14.94
46	YGSTSRRLI	639	1.3000	14.94

47	YYASIVAEK	117	1.2000	13.79
48	WITHAPKLG	662	1.2000	13.79
49	LRRLVEAGT	128	1.1000	12.64
50	LIVVDYLQL	331	1.0600	12.18
51	FVANGISLH	805	1.0000	11.49
52	LSRFANMAR	865	1.0000	11.49
53	MRSGERPMV	421	0.9500	10.92
54	YDVADRRLS	163	0.9000	10.34
55	VVEITSIGD	783	0.9000	10.34
56	LRESGCLTA	394	0.8000	9.20
57	ILRADTGAE	406	0.8000	9.20
58	VAFGELMRS	415	0.7000	8.05
59	MINVFPSGR	443	0.7000	8.05
60	LKVGDRIAA	485	0.7000	8.05
61	VRNRLSAKQ	729	0.7000	8.05
62	VAHQLHLSR	859	0.7000	8.05
63	VTVAHQLHL	857	0.6600	7.59
64	LVEAGTRVV	131	0.6000	6.90
65	YESRQVEVS	346	0.6000	6.90
66	LTASTRILR	400	0.6000	6.90
67	MVARPMINV	438	0.6000	6.90
68	WKHSPSRSR	749	0.6000	6.90
69	VFPSGRKEV	446	0.5000	5.75
70	LRPARQRLP	566	0.5000	5.75
71	WAQVRNRLS	726	0.5000	5.75
72	LKLIVVDYL	329	0.4600	5.29
73	IVMRLLSAE	262	0.4000	4.60
74	LLRVGIFSW	654	0.4000	4.60
75	YLHTLISTV	101	0.3000	3.45
76	LLRRLVEAG	127	0.3000	3.45
77	VAQLLLRVG	650	0.3000	3.45
78	VGIFSWITH	657	0.3000	3.45
79	FSWITHAPK	660	0.3000	3.45
80	LHIHGAKDQ	677	0.3000	3.45
81	IHELARGDA	770	0.3000	3.45
82	ISLHNSLEQ	810	0.3000	3.45
83	LMTSGKKYE	339	0.2000	2.30
84	LEVPVVAIS	367	0.2000	2.30
85	LKNQPIRYE	524	0.2000	2.30
86	VALFLRHLW	612	0.2000	2.30
87	IFSWITHAP	659	0.2000	2.30

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	IRAKARRLR	316	5.7000	64.77
2	MRSCSIRHR	239	4.8000	54.55
3	VVILLHRPD	822	4.5000	51.14
4	MVIVAARPG	220	4.3000	48.86
5	LGLFTKRSH	588	4.3000	48.86
6	LRLASGREV	457	4.0000	45.45
7	LTMMEIRAK	311	3.9000	44.32
8	LRMVARPMI	436	3.8000	43.18
9	LKNQPIRYE	524	3.8000	43.18
10	MEIRAKARR	314	3.6000	40.91
11	LHIHGAKDQ	677	3.6000	40.91
12	VRFLRHVGV	686	3.5000	39.77
13	WTRLARRMS	288	3.4000	38.64
14	ILLHRPDAF	824	3.4000	38.64
15	LVEAGTRVV	131	3.2000	36.36
16	LISLARMIG	511	3.1000	35.23
17	LRPARQRLP	566	3.1000	35.23
18	LRHLWSAGG	616	3.1000	35.23
19	LRHVGVHGA	689	3.0000	34.09
20	VILLHRPDA	823	3.0000	34.09
21	LRQKANLKL	323	2.7600	31.36
22	IVMRLLSAE	262	2.7000	30.68
23	FSRHLKLLA	356	2.6000	29.55
24	LFLRHLWSA	614	2.6000	29.55
25	VRNRLSAKQ	729	2.6000	29.55
26	FILAKHRNG	844	2.6000	29.55
27	ILAKHRNGP	845	2.6000	29.55
28	LLRRLVEAG	127	2.5000	28.41
29	LKLLAKELE	360	2.5000	28.41
30	VFRLRLASG	454	2.5000	28.41
31	IFSWITHAP	659	2.5000	28.41
32	WITHAPKLG	662	2.5000	28.41
33	LGGHDSWRL	669	2.4600	27.95
34	VIVAARPGV	221	2.4000	27.27

35	MRLLSAEAK	264	2.4000	27.27
36	MLRQLKGPV	705	2.4000	27.27
37	IRHRMASVI	244	2.3000	26.14
38	ITHAPKLGG	663	2.3000	26.14
39	IQLHEPTMW	741	2.3000	26.14
40	ISLHNSLEQ	810	2.3000	26.14
41	IKLSDMRSG	273	2.2000	25.00
42	VAQLLLRVG	650	2.2000	25.00
43	VMRLLSAEA	263	2.1000	23.86
44	IVVDYLQLM	332	2.1000	23.86
45	VVAISQLNR	371	2.1000	23.86
46	LMRSGERPM	420	2.1000	23.86
47	VALFLRHLW	612	2.1000	23.86
48	LLLRVGIFS	653	2.1000	23.86
49	MWKHSPSRS	748	2.1000	23.86
50	FRLRLASGR	455	2.0000	22.73
51	IGDQHVFDG	789	2.0000	22.73
52	LRRIGGAPY	93	1.9000	21.59
53	IVAEKALLR	121	1.9000	21.59
54	WRLHIHGAK	675	1.9000	21.59
55	LRQLKGPVR	706	1.9000	21.59
56	VFPSGRKEV	446	1.8000	20.45
57	FLRHVGVHG	688	1.8000	20.45
58	VGVHGAEAV	692	1.8000	20.45
59	MRSGERPMV	421	1.7000	19.32
60	YRPAHQNVY	57	1.6000	18.18
61	VAISQLNRG	372	1.6000	18.18
62	IRYEPVDEA	529	1.6000	18.18
63	LFTKRSHEK	590	1.6000	18.18
64	VAHQLHLSR	859	1.6000	18.18
65	VWAQVRNRL	725	1.5600	17.73
66	YDVADRRLS	163	1.5000	17.05
67	IVAARPGVG	222	1.5000	17.05
68	LMTSGKKYE	339	1.5000	17.05
69	VRWDPTNGQ	626	1.5000	17.05
70	LRRLVEAGT	128	1.4000	15.91
71	LEVPVVAIS	367	1.4000	15.91
72	YGSTSRRLI	639	1.4000	15.91
73	VVDRAQAEI	154	1.3000	14.77
74	WKHSPSRSR	749	1.3000	14.77
75	VDYLQLMTS	334	1.2000	13.64

76	LQLMTSGKK	337	1.2000	13.64
77	MVARPMINV	438	1.2000	13.64
78	LAGLGLFTK	585	1.2000	13.64
79	LKLIVVDYL	329	1.1600	13.18
80	LERLRPGDF	48	1.1000	12.50
81	VVQYGYAGA	138	1.1000	12.50
82	LLRVGIFSW	654	1.1000	12.50
83	LHRPDAFDR	826	1.1000	12.50
84	LSRFANMAR	865	1.1000	12.50
85	LLSAEAKIK	266	1.0000	11.36
86	LLSKDAIAD	38	0.9000	10.23
87	LARRMSEIS	291	0.9000	10.23

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	IRAKARRLR	316	4.7000	53.41
2	WTRLARRMS	288	4.4000	50.00
3	MRSCSIRHR	239	3.8000	43.18
4	FSRHLKLLA	356	3.6000	40.91
5	FILAKHRNG	844	3.6000	40.91
6	WITHAPKLG	662	3.5000	39.77
7	VVILLHRPD	822	3.5000	39.77
8	MVIVAARPG	220	3.3000	37.50
9	LGLFTKRSH	588	3.3000	37.50
10	FRLRLASGR	455	3.0000	34.09
11	LRLASGREV	457	3.0000	34.09
12	LTMMEIRAK	311	2.9000	32.95
13	WRLHIHGAK	675	2.9000	32.95
14	LRMVARPMI	436	2.8000	31.82
15	LKNQPIRYE	524	2.8000	31.82
16	FLRHVGVHG	688	2.8000	31.82
17	YRPAHQNVY	57	2.6000	29.55
18	MEIRAKARR	314	2.6000	29.55
19	LHIHGAKDQ	677	2.6000	29.55
20	YDVADRRLS	163	2.5000	28.41
21	VRFLRHVGV	686	2.5000	28.41

22	YGSTSRRLI	639	2.4000	27.27
23	ILLHRPDAF	824	2.4000	27.27
24	WKHSPSRSR	749	2.3000	26.14
25	LVEAGTRVV	131	2.2000	25.00
26	LISLARMIG	511	2.1000	23.86
27	LRPARQRLP	566	2.1000	23.86
28	LRHLWSAGG	616	2.1000	23.86
29	LRHVGVHGA	689	2.0000	22.73
30	VILLHRPDA	823	2.0000	22.73
31	YGRQPPQDL	19	1.8600	21.14
32	YESRQVEVS	346	1.8000	20.45
33	WSLDERLRM	430	1.8000	20.45
34	LRQKANLKL	323	1.7600	20.00
35	IVMRLLSAE	262	1.7000	19.32
36	FEGWTPLAQ	476	1.7000	19.32
37	YLAARVPSL	558	1.6600	18.86
38	LFLRHLWSA	614	1.6000	18.18
39	VRNRLSAKQ	729	1.6000	18.18
40	ILAKHRNGP	845	1.6000	18.18
41	YYGSTSRRL	638	1.5600	17.73
42	LLRRLVEAG	127	1.5000	17.05
43	LKLLAKELE	360	1.5000	17.05
44	VFRLRLASG	454	1.5000	17.05
45	IFSWITHAP	659	1.5000	17.05
46	FVANGISLH	805	1.5000	17.05
47	LGGHDSWRL	669	1.4600	16.59
48	VIVAARPGV	221	1.4000	15.91
49	MRLLSAEAK	264	1.4000	15.91
50	MLRQLKGPV	705	1.4000	15.91
51	YYASIVAEK	117	1.3000	14.77
52	IRHRMASVI	244	1.3000	14.77
53	FMKFEGWTP	473	1.3000	14.77
54	FLRHLWSAG	615	1.3000	14.77
55	ITHAPKLGG	663	1.3000	14.77
56	IQLHEPTMW	741	1.3000	14.77
57	ISLHNSLEQ	810	1.3000	14.77
58	IKLSDMRSG	273	1.2000	13.64
59	VAQLLLRVG	650	1.2000	13.64
60	VMRLLSAEA	263	1.1000	12.50
61	IVVDYLQLM	332	1.1000	12.50
62	YLQLMTSGK	336	1.1000	12.50

63	VVAISQLNR	371	1.1000	12.50
64	LMRSGERPM	420	1.1000	12.50
65	WTPLAQLKV	479	1.1000	12.50
66	VALFLRHLW	612	1.1000	12.50
67	LLLRVGIFS	653	1.1000	12.50
68	MWKHSPSRS	748	1.1000	12.50
69	IGDQHVFDG	789	1.0000	11.36
70	LRRIGGAPY	93	0.9000	10.23
71	IVAEKALLR	121	0.9000	10.23
72	LRQLKGPVR	706	0.9000	10.23
73	VFPSGRKEV	446	0.8000	9.09
74	VGVHGAEAV	692	0.8000	9.09
75	WAQVRNRLS	726	0.8000	9.09
76	MRSGERPMV	421	0.7000	7.95
77	VAISQLNRG	372	0.6000	6.82
78	IRYEPVDEA	529	0.6000	6.82
79	LFTKRSHEK	590	0.6000	6.82
80	VAHQLHLSR	859	0.6000	6.82
81	VWAQVRNRL	725	0.5600	6.36
82	IVAARPGVG	222	0.5000	5.68
83	LMTSGKKYE	339	0.5000	5.68
84	VRWDPTNGQ	626	0.5000	5.68
85	LRRLVEAGT	128	0.4000	4.55
86	LEVPVVAIS	367	0.4000	4.55
87	YGYAGAEGA	141	0.3000	3.41

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	LGLFTKRSH	588	6.1000	67.78
2	VVILLHRPD	822	6.1000	67.78
3	LKNQPIRYE	524	5.4000	60.00
4	LHIHGAKDQ	677	5.1000	56.67
5	IVMRLLSAE	262	4.3000	47.78
6	MVIVAARPG	220	4.2000	46.67
7	IRAKARRLR	316	4.2000	46.67
8	LKLLAKELE	360	4.1000	45.56

9	VRNRLSAKQ	729	4.1000	45.56
10	ISLHNSLEQ	810	3.8000	42.22
11	MRSCSIRHR	239	3.3000	36.67
12	LRLASGREV	457	3.3000	36.67
13	IQLHEPTMW	741	3.2000	35.56
14	LTMMEIRAK	311	3.1000	34.44
15	LMTSGKKYE	339	3.1000	34.44
16	LRMVARPMI	436	3.1000	34.44
17	WTRLARRMS	288	3.0000	33.33
18	LISLARMIG	511	3.0000	33.33
19	VALFLRHLW	612	3.0000	33.33
20	LRHLWSAGG	616	3.0000	33.33
21	VRWDPTNGQ	626	3.0000	33.33
22	LRHVGVHGA	689	3.0000	33.33
23	VILLHRPDA	823	3.0000	33.33
24	LRQKANLKL	323	2.8000	31.11
25	VRFLRHVGV	686	2.8000	31.11
26	FSRHLKLLA	356	2.6000	28.89
27	LFLRHLWSA	614	2.6000	28.89
28	LLSKDAIAD	38	2.5000	27.78
29	LVEAGTRVV	131	2.5000	27.78
30	LRPARQRLP	566	2.5000	27.78
31	LGGHDSWRL	669	2.5000	27.78
32	FILAKHRNG	844	2.5000	27.78
33	LLRRLVEAG	127	2.4000	26.67
34	VFRLRLASG	454	2.4000	26.67
35	WITHAPKLG	662	2.4000	26.67
36	ILLHRPDAF	824	2.4000	26.67
37	ILRADTGAE	406	2.3000	25.56
38	FVANGISLH	805	2.3000	25.56
39	FEGWTPLAQ	476	2.2000	24.44
40	VGIFSWITH	657	2.2000	24.44
41	ITHAPKLGG	663	2.2000	24.44
42	VMRLLSAEA	263	2.1000	23.33
43	IKLSDMRSG	273	2.1000	23.33
44	MEIRAKARR	314	2.1000	23.33
45	VAQLLLRVG	650	2.1000	23.33
46	LLRVGIFSW	654	2.0000	22.22
47	ILAKHRNGP	845	2.0000	22.22
48	ILDLYGRGE	68	1.9000	21.11
49	VPSLRPARQ	563	1.9000	21.11

50	IFSWITHAP	659	1.9000	21.11
51	IGDQHVFDG	789	1.9000	21.11
52	LGGMLLSKD	34	1.8000	20.00
53	LRRIGGAPY	93	1.7000	18.89
54	VIVAARPGV	221	1.7000	18.89
55	IVVDYLQLM	332	1.7000	18.89
56	LMRSGERPM	420	1.7000	18.89
57	LLLRVGIFS	653	1.7000	18.89
58	FLRHVGVHG	688	1.7000	18.89
59	MLRQLKGPV	705	1.7000	18.89
60	MWKHSPSRS	748	1.7000	18.89
61	LRRLVEAGT	128	1.6000	17.78
62	IRHRMASVI	244	1.6000	17.78
63	MRLLSAEAK	264	1.6000	17.78
64	IRYEPVDEA	529	1.6000	17.78
65	VWAQVRNRL	725	1.6000	17.78
66	VLERLRPGD	47	1.5000	16.67
67	VAISQLNRG	372	1.5000	16.67
68	LKGPVRNPN	709	1.5000	16.67
69	YRPAHQNVY	57	1.4000	15.56
70	IVAARPGVG	222	1.4000	15.56
71	VAAQEMLRQ	700	1.4000	15.56
72	LKLIVVDYL	329	1.2000	13.33
73	VTVSAAHSD	542	1.2000	13.33
74	VVQYGYAGA	138	1.1000	12.22
75	YDVADRRLS	163	1.1000	12.22
76	VFPSGRKEV	446	1.1000	12.22
77	WRLHIHGAK	675	1.1000	12.22
78	VGVHGAEAV	692	1.1000	12.22
79	VVDYLQLMT	333	1.0000	11.11
80	LEVPVVAIS	367	1.0000	11.11
81	MRSGERPMV	421	1.0000	11.11
82	VEITSIGDQ	784	1.0000	11.11
83	YGRQPPQDL	19	0.9000	10.00
84	FMRSCSIRH	238	0.9000	10.00
85	ISQLNRGPE	374	0.9000	10.00
86	VHGAEAVAA	694	0.9000	10.00
87	VEAGTRVVQ	132	0.8000	8.89

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	LRMVARPMI	436	4.5500	52.30
2	LISLARMIG	511	4.1000	47.13
3	VVAISQLNR	371	3.7000	42.53
4	WTRLARRMS	288	3.5000	40.23
5	VILLHRPDA	823	3.1500	36.21
6	MVIVAARPG	220	3.0000	34.48
7	WTPLAQLKV	479	2.9000	33.33
8	LRHLWSAGG	616	2.8000	32.18
9	LRHVGVHGA	689	2.8000	32.18
10	VRFLRHVGV	686	2.7000	31.03
11	FSRHLKLLA	356	2.6000	29.89
12	WSLDERLRM	430	2.6000	29.89
13	VVILLHRPD	822	2.6000	29.89
14	LRRIGGAPY	93	2.4000	27.59
15	ITHAPKLGG	663	2.4000	27.59
16	MRSCSIRHR	239	2.2000	25.29
17	VDYLQLMTS	334	2.2000	25.29
18	VFRLRLASG	454	2.2000	25.29
19	YLAARVPSL	558	2.1100	24.25
20	FVALEDLLQ	174	2.1000	24.14
21	LRQLKGPVR	706	2.0500	23.56
22	FEGWTPLAQ	476	2.0000	22.99
23	FILAKHRNG	844	2.0000	22.99
24	LERLRPGDF	48	1.9000	21.84
25	LKLLAKELE	360	1.9000	21.84
26	WRLHIHGAK	675	1.9000	21.84
27	VIVAARPGV	221	1.8500	21.26
28	VMRLLSAEA	263	1.8000	20.69
29	MRLLSAEAK	264	1.8000	20.69
30	IRAKARRLR	316	1.8000	20.69
31	MEIRAKARR	314	1.7000	19.54
32	FRLRLASGR	455	1.7000	19.54
33	IVAARPGVG	222	1.6000	18.39
34	LRQKANLKL	323	1.5600	17.93
35	YRPAHQNVY	57	1.5000	17.24
36	LTMMEIRAK	311	1.5000	17.24
37	LQLMTSGKK	337	1.5000	17.24

38	LLLRVGIFS	653	1.5000	17.24
39	MLRQLKGPV	705	1.5000	17.24
40	IVAEKALLR	121	1.4000	16.09
41	YLQLMTSGK	336	1.4000	16.09
42	LRLASGREV	457	1.4000	16.09
43	LAQLKVGDR	482	1.4000	16.09
44	FMRSCSIRH	238	1.3000	14.94
45	LGLFTKRSH	588	1.3000	14.94
46	YGSTSRRLI	639	1.3000	14.94
47	YYASIVAEK	117	1.2000	13.79
48	WITHAPKLG	662	1.2000	13.79
49	LRRLVEAGT	128	1.1000	12.64
50	LIVVDYLQL	331	1.0600	12.18
51	FVANGISLH	805	1.0000	11.49
52	LSRFANMAR	865	1.0000	11.49
53	MRSGERPMV	421	0.9500	10.92
54	YDVADRRLS	163	0.9000	10.34
55	VVEITSIGD	783	0.9000	10.34
56	LRESGCLTA	394	0.8000	9.20
57	ILRADTGAE	406	0.8000	9.20
58	VAFGELMRS	415	0.7000	8.05
59	MINVFPSGR	443	0.7000	8.05
60	LKVGDRIAA	485	0.7000	8.05
61	VRNRLSAKQ	729	0.7000	8.05
62	VAHQLHLSR	859	0.7000	8.05
63	VTVAHQLHL	857	0.6600	7.59
64	LVEAGTRVV	131	0.6000	6.90
65	YESRQVEVS	346	0.6000	6.90
66	LTASTRILR	400	0.6000	6.90
67	MVARPMINV	438	0.6000	6.90
68	WKHSPSRSR	749	0.6000	6.90
69	VFPSGRKEV	446	0.5000	5.75
70	LRPARQRLP	566	0.5000	5.75
71	WAQVRNRLS	726	0.5000	5.75
72	LKLIVVDYL	329	0.4600	5.29
73	IVMRLLSAE	262	0.4000	4.60
74	LLRVGIFSW	654	0.4000	4.60
75	YLHTLISTV	101	0.3000	3.45
76	LLRRLVEAG	127	0.3000	3.45
77	VAQLLLRVG	650	0.3000	3.45
78	VGIFSWITH	657	0.3000	3.45

79	FSWITHAPK	660	0.3000	3.45
80	LHIHGAKDQ	677	0.3000	3.45
81	IHELARGDA	770	0.3000	3.45
82	ISLHNSLEQ	810	0.3000	3.45
83	LMTSGKKYE	339	0.2000	2.30
84	LEVPVVAIS	367	0.2000	2.30
85	LKNQPIRYE	524	0.2000	2.30
86	VALFLRHLW	612	0.2000	2.30
87	IFSWITHAP	659	0.2000	2.30

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	WTRLARRMS	288	2.9000	42.65
2	LRMVARPMI	436	2.5000	36.76
3	LRHVGVHGA	689	2.1000	30.88
4	VILLHRPDA	823	2.0000	29.41
5	VMRLLSAEA	263	1.8000	26.47
6	WRLHIHGAK	675	1.7000	25.00
7	LGLFTKRSH	588	1.6800	24.71
8	FVANGISLH	805	1.5800	23.24
9	MVIVAARPG	220	1.4000	20.59
10	LRHLWSAGG	616	1.4000	20.59
11	VRNRLSAKQ	729	1.4000	20.59
12	YLQLMTSGK	336	1.3000	19.12
13	LQLMTSGKK	337	1.3000	19.12
14	VVILLHRPD	822	1.3000	19.12
15	LTMMEIRAK	311	1.2000	17.65
16	VRFLRHVGV	686	1.2000	17.65
17	LRRIGGAPY	93	1.1000	16.18
18	YYASIVAEK	117	1.1000	16.18
19	LISLARMIG	511	1.1000	16.18
20	FVALEDLLQ	174	1.0000	14.71
21	FEGWTPLAQ	476	0.9000	13.24
22	FSRHLKLLA	356	0.8000	11.76
23	VFRLRLASG	454	0.8000	11.76
24	VPSLRPARQ	563	0.8000	11.76

25	VEITSIGDQ	784	0.7000	10.29
26	MRLLSAEAK	264	0.6000	8.82
27	MRSCSIRHR	239	0.5000	7.35
28	LRRLVEAGT	128	0.4000	5.88
29	VVAISQLNR	371	0.4000	5.88
30	LHIHGAKDQ	677	0.4000	5.88
31	MLRQLKGPV	705	0.4000	5.88
32	FILAKHRNG	844	0.4000	5.88
33	YDVADRRLS	163	0.3000	4.41
34	FMRSCSIRH	238	0.2800	4.12
35	MEIRAKARR	314	0.2000	2.94
36	VDYLQLMTS	334	0.2000	2.94
37	FRLRLASGR	455	0.2000	2.94
38	LRLASGREV	457	0.2000	2.94
39	YGSTSRRLI	639	0.2000	2.94
40	FSWITHAPK	660	0.2000	2.94
41	IHELARGDA	770	0.2000	2.94
42	IVAARPGVG	222	0.1000	1.47
43	IRAKARRLR	316	0.1000	1.47
44	WTPLAQLKV	479	0.1000	1.47
45	LERLRPGDF	48	-0.1000	0
46	YRPAHQNVY	57	-0.1000	0
47	LLRVGIFSW	654	-0.1000	0
48	WAQVRNRLS	726	-0.1000	0
49	LKLIVVDYL	329	-0.2000	0
50	LEVPVVAIS	367	-0.2000	0
51	INVFPSGRK	444	-0.2000	0
52	LAQLKVGDR	482	-0.2000	0
53	VIVAARPGV	221	-0.3000	0
54	IFSLEMSKS	252	-0.4000	0
55	VALFLRHLW	612	-0.5000	0
56	VRWDPTNGQ	626	-0.5000	0
57	LLLRVGIFS	653	-0.5000	0
58	LVEAGTRVV	131	-0.6000	0
59	LKLLAKELE	360	-0.6000	0
60	LRQLKGPVR	706	-0.6000	0
61	YLHTLISTV	101	-0.7000	0
62	ILRADTGAE	406	-0.7000	0
63	WSLDERLRM	430	-0.7000	0
64	LAAVTVSAA	539	-0.7000	0
65	LRPARQRLP	566	-0.7000	0

66	LAGLGLFTK	585	-0.7000	0
67	VGIFSWITH	657	-0.7200	0
68	MINVFPSGR	443	-0.8000	0
69	WITHAPKLG	662	-0.8000	0
70	ITHAPKLGG	663	-0.8000	0
71	ISLHNSLEQ	810	-0.8000	0
72	YGRQPPQDL	19	-0.9000	0
73	LDFMRSCSI	236	-0.9000	0
74	IRHRMASVI	244	-0.9000	0
75	LLSAEAKIK	266	-0.9000	0
76	YESRQVEVS	346	-0.9000	0
77	LKVGDRIAA	485	-0.9000	0
78	IRYEPVDEA	529	-0.9000	0
79	LFLRHLWSA	614	-0.9000	0
80	VVQYGYAGA	138	-1.0000	0
81	IVMRLLSAE	262	-1.0000	0
82	LRESGCLTA	394	-1.0000	0
83	YGYAGAEGA	141	-1.1000	0
84	VFPSGRKEV	446	-1.1000	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	LRMVARPMI	436	4.6500	56.02
2	VILLHRPDA	823	4.1500	50.00
3	LRHVGVHGA	689	3.8000	45.78
4	LISLARMIG	511	3.7000	44.58
5	VVAISQLNR	371	3.2000	38.55
6	LGLFTKRSH	588	2.8800	34.70
7	VMRLLSAEA	263	2.8000	33.73
8	VDYLQLMTS	334	2.8000	33.73
9	MRLLSAEAK	264	2.7000	32.53
10	VRFLRHVGV	686	2.7000	32.53
11	MVIVAARPG	220	2.6000	31.33
12	VVILLHRPD	822	2.5000	30.12
13	LTMMEIRAK	311	2.4000	28.92
14	LQLMTSGKK	337	2.4000	28.92

15	LRHLWSAGG	616	2.4000	28.92
16	VRNRLSAKQ	729	2.4000	28.92
17	LRRIGGAPY	93	2.1000	25.30
18	WTRLARRMS	288	2.1000	25.30
19	LLLRVGIFS	653	2.1000	25.30
20	ITHAPKLGG	663	2.0000	24.10
21	LHIHGAKDQ	677	2.0000	24.10
22	ISLHNSLEQ	810	2.0000	24.10
23	VGIFSWITH	657	1.8800	22.65
24	VIVAARPGV	221	1.8500	22.29
25	FVALEDLLQ	174	1.8000	21.69
26	LRESGCLTA	394	1.8000	21.69
27	VFRLRLASG	454	1.8000	21.69
28	VPSLRPARQ	563	1.8000	21.69
29	VEITSIGDQ	784	1.8000	21.69
30	MRSCSIRHR	239	1.7000	20.48
31	FEGWTPLAQ	476	1.7000	20.48
32	LKVGDRIAA	485	1.7000	20.48
33	LRQKANLKL	323	1.6000	19.28
34	FSRHLKLLA	356	1.6000	19.28
35	LRQLKGPVR	706	1.5500	18.67
36	LKLLAKELE	360	1.5000	18.07
37	MLRQLKGPV	705	1.5000	18.07
38	LRRLVEAGT	128	1.4000	16.87
39	LRLASGREV	457	1.4000	16.87
40	LLRVGIFSW	654	1.4000	16.87
41	IRAKARRLR	316	1.3000	15.66
42	VAFGELMRS	415	1.3000	15.66
43	IHELARGDA	770	1.3000	15.66
44	IVAARPGVG	222	1.2000	14.46
45	MEIRAKARR	314	1.2000	14.46
46	VALFLRHLW	612	1.2000	14.46
47	LIVVDYLQL	331	1.1000	13.25
48	LERLRPGDF	48	1.0000	12.05
49	MRSGERPMV	421	0.9500	11.45
50	VLGGMLLSK	33	0.9000	10.84
51	IVAEKALLR	121	0.9000	10.84
52	INVFPSGRK	444	0.9000	10.84
53	WTPLAQLKV	479	0.9000	10.84
54	LAQLKVGDR	482	0.9000	10.84
55	LFLRHLWSA	614	0.9000	10.84

56	FMRSCSIRH	238	0.8800	10.60
57	VIFSLEMSK	251	0.8000	9.64
58	LEVPVVAIS	367	0.8000	9.64
59	LAGLGLFTK	585	0.8000	9.64
60	VRWDPTNGQ	626	0.8000	9.64
61	WRLHIHGAK	675	0.8000	9.64
62	VVEITSIGD	783	0.8000	9.64
63	LLSAEAKIK	266	0.7000	8.43
64	VAAQEMLRQ	700	0.7000	8.43
65	VTVAHQLHL	857	0.7000	8.43
66	LVEAGTRVV	131	0.6000	7.23
67	IFSLEMSKS	252	0.6000	7.23
68	MVARPMINV	438	0.6000	7.23
69	FVANGISLH	805	0.5800	6.99
70	LKLIVVDYL	329	0.5000	6.02
71	VFPSGRKEV	446	0.5000	6.02
72	LRPARQRLP	566	0.5000	6.02
73	LSRFANMAR	865	0.5000	6.02
74	ILRADTGAE	406	0.4000	4.82
75	VHGAEAVAA	694	0.4000	4.82
76	YLQLMTSGK	336	0.3000	3.61
77	LAAVTVSAA	539	0.3000	3.61
78	MINVFPSGR	443	0.2000	2.41
79	IFSWITHAP	659	0.2000	2.41
80	VAHQLHLSR	859	0.2000	2.41
81	YLAARVPSL	558	0.1500	1.81
82	YYASIVAEK	117	0.1000	1.20
83	LDFMRSCSI	236	0.1000	1.20
84	IRHRMASVI	244	0.1000	1.20
85	VVDYLQLMT	333	0.1000	1.20
86	MTSGKKYES	340	0.1000	1.20
87	LTASTRILR	400	0.1000	1.20

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	VVILLHRPD	822	4.2000	47.19

2	LISLARMIG	511	4.0000	44.94
3	LRMVARPMI	436	3.8500	43.26
4	FVALEDLLQ	174	3.6000	40.45
5	LKLLAKELE	360	3.5000	39.33
6	FEGWTPLAQ	476	3.5000	39.33
7	VILLHRPDA	823	3.1500	35.39
8	FMRSCSIRH	238	3.1000	34.83
9	WTRLARRMS	288	3.1000	34.83
10	LGLFTKRSH	588	3.1000	34.83
11	MVIVAARPG	220	2.9000	32.58
12	LRHVGVHGA	689	2.8000	31.46
13	FVANGISLH	805	2.8000	31.46
14	LRHLWSAGG	616	2.7000	30.34
15	FSRHLKLLA	356	2.6000	29.21
16	VVEITSIGD	783	2.5000	28.09
17	ILRADTGAE	406	2.4000	26.97
18	ITHAPKLGG	663	2.3000	25.84
19	LRRIGGAPY	93	2.2000	24.72
20	VVAISQLNR	371	2.2000	24.72
21	WSLDERLRM	430	2.2000	24.72
22	WTPLAQLKV	479	2.2000	24.72
23	VRNRLSAKQ	729	2.2000	24.72
24	YLAARVPSL	558	2.1500	24.16
25	VFRLRLASG	454	2.1000	23.60
26	VGIFSWITH	657	2.1000	23.60
27	IVMRLLSAE	262	2.0000	22.47
28	VRFLRHVGV	686	2.0000	22.47
29	FILAKHRNG	844	1.9000	21.35
30	VMRLLSAEA	263	1.8000	20.22
31	VDYLQLMTS	334	1.8000	20.22
32	LMTSGKKYE	339	1.8000	20.22
33	LKNQPIRYE	524	1.8000	20.22
34	LHIHGAKDQ	677	1.8000	20.22
35	ISLHNSLEQ	810	1.8000	20.22
36	ISQLNRGPE	374	1.7000	19.10
37	LRQKANLKL	323	1.6000	17.98
38	VPSLRPARQ	563	1.6000	17.98
39	VEITSIGDQ	784	1.6000	17.98
40	LLSKDAIAD	38	1.5000	16.85
41	IVAARPGVG	222	1.5000	16.85
42	FGELMRSGE	417	1.4000	15.73

43	YRPAHQNVY	57	1.3000	14.61
44	LRRLVEAGT	128	1.3000	14.61
45	LLRVGIFSW	654	1.3000	14.61
46	VIVAARPGV	221	1.1500	12.92
47	LIVVDYLQL	331	1.1000	12.36
48	VALFLRHLW	612	1.1000	12.36
49	LLLRVGIFS	653	1.1000	12.36
50	WITHAPKLG	662	1.1000	12.36
51	WRLHIHGAK	675	1.1000	12.36
52	MRLLSAEAK	264	1.0000	11.24
53	LERLRPGDF	48	0.9000	10.11
54	LRESGCLTA	394	0.8000	8.99
55	MLRQLKGPV	705	0.8000	8.99
56	MRSCSIRHR	239	0.7000	7.87
57	LTMMEIRAK	311	0.7000	7.87
58	LQLMTSGKK	337	0.7000	7.87
59	LRLASGREV	457	0.7000	7.87
60	LKVGDRIAA	485	0.7000	7.87
61	VTVAHQLHL	857	0.7000	7.87
62	LGGMLLSKD	34	0.6000	6.74
63	YLQLMTSGK	336	0.6000	6.74
64	ISLARMIGD	512	0.6000	6.74
65	VRWDPTNGQ	626	0.6000	6.74
66	YGSTSRRLI	639	0.6000	6.74
67	LRQLKGPVR	706	0.5500	6.18
68	ISTVPTAAN	106	0.5000	5.62
69	YDVADRRLS	163	0.5000	5.62
70	LKLIVVDYL	329	0.5000	5.62
71	VAAQEMLRQ	700	0.5000	5.62
72	YYASIVAEK	117	0.4000	4.49
73	IRAKARRLR	316	0.3000	3.37
74	VAFGELMRS	415	0.3000	3.37
75	IHELARGDA	770	0.3000	3.37
76	MRSGERPMV	421	0.2500	2.81
77	YGRQPPQDL	19	0.2000	2.25
78	LLRRLVEAG	127	0.2000	2.25
79	VQYGYAGAE	139	0.2000	2.25
80	MEIRAKARR	314	0.2000	2.25
81	YESRQVEVS	346	0.2000	2.25
82	FRLRLASGR	455	0.2000	2.25
83	VAQLLLRVG	650	0.2000	2.25

84	FLRHVGVHG	688	0.1000	1.12
85	WAQVRNRLS	726	0.1000	1.12
86	VLERLRPGD	47	0.0500	0.56

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	LGLFTKRSH	588	4.8800	58.10
2	LHIHGAKDQ	677	4.3000	51.19
3	IRAKARRLR	316	4.2000	50.00
4	LTMMEIRAK	311	3.8000	45.24
5	VVILLHRPD	822	3.4000	40.48
6	MRSCSIRHR	239	3.3000	39.29
7	VRNRLSAKQ	729	3.3000	39.29
8	WTRLARRMS	288	3.0000	35.71
9	LRLASGREV	457	3.0000	35.71
10	LRHVGVHGA	689	3.0000	35.71
11	ISLHNSLEQ	810	3.0000	35.71
12	VILLHRPDA	823	3.0000	35.71
13	MVIVAARPG	220	2.9000	34.52
14	LRMVARPMI	436	2.9000	34.52
15	FSRHLKLLA	356	2.6000	30.95
16	LFLRHLWSA	614	2.6000	30.95
17	VRFLRHVGV	686	2.5000	29.76
18	LKNQPIRYE	524	2.4000	28.57
19	MRLLSAEAK	264	2.3000	27.38
20	IQLHEPTMW	741	2.3000	27.38
21	LVEAGTRVV	131	2.2000	26.19
22	VRWDPTNGQ	626	2.2000	26.19
23	VMRLLSAEA	263	2.1000	25.00
24	MEIRAKARR	314	2.1000	25.00
25	LRPARQRLP	566	2.1000	25.00
26	VALFLRHLW	612	2.1000	25.00
27	LRQKANLKL	323	1.8000	21.43
28	WRLHIHGAK	675	1.8000	21.43
29	LISLARMIG	511	1.7000	20.24
30	LRHLWSAGG	616	1.7000	20.24

31	LLLRVGIFS	653	1.7000	20.24
32	MWKHSPSRS	748	1.7000	20.24
33	IRYEPVDEA	529	1.6000	19.05
34	ILAKHRNGP	845	1.6000	19.05
35	LFTKRSHEK	590	1.5000	17.86
36	IFSWITHAP	659	1.5000	17.86
37	LGGHDSWRL	669	1.5000	17.86
38	ILLHRPDAF	824	1.5000	17.86
39	VIVAARPGV	221	1.4000	16.67
40	IRHRMASVI	244	1.4000	16.67
41	FEGWTPLAQ	476	1.4000	16.67
42	MLRQLKGPV	705	1.4000	16.67
43	IVMRLLSAE	262	1.3000	15.48
44	FILAKHRNG	844	1.2000	14.29
45	LLRRLVEAG	127	1.1000	13.10
46	VVQYGYAGA	138	1.1000	13.10
47	YDVADRRLS	163	1.1000	13.10
48	LQLMTSGKK	337	1.1000	13.10
49	LKLLAKELE	360	1.1000	13.10
50	VFRLRLASG	454	1.1000	13.10
51	VPSLRPARQ	563	1.1000	13.10
52	LAGLGLFTK	585	1.1000	13.10
53	LLRVGIFSW	654	1.1000	13.10
54	WITHAPKLG	662	1.1000	13.10
55	FVANGISLH	805	1.0800	12.86
56	LEVPVVAIS	367	1.0000	11.90
57	VGIFSWITH	657	0.9800	11.67
58	LLSAEAKIK	266	0.9000	10.71
59	ITHAPKLGG	663	0.9000	10.71
60	VHGAEAVAA	694	0.9000	10.71
61	IKLSDMRSG	273	0.8000	9.52
62	VDYLQLMTS	334	0.8000	9.52
63	LRESGCLTA	394	0.8000	9.52
64	VFPSGRKEV	446	0.8000	9.52
65	VAQLLLRVG	650	0.8000	9.52
66	VGVHGAEAV	692	0.8000	9.52
67	LRRLVEAGT	128	0.7000	8.33
68	MRSGERPMV	421	0.7000	8.33
69	LRRIGGAPY	93	0.6000	7.14
70	IVVDYLQLM	332	0.6000	7.14
71	VVAISQLNR	371	0.6000	7.14

72	LMRSGERPM	420	0.6000	7.14
73	LKVGDRIAA	485	0.6000	7.14
74	VAAQEMLRQ	700	0.6000	7.14
75	VWAQVRNRL	725	0.6000	7.14
76	IGDQHVFDG	789	0.6000	7.14
77	LARRMSEIS	291	0.5000	5.95
78	MTSGKKYES	340	0.5000	5.95
79	FRLRLASGR	455	0.5000	5.95
80	YGSTSRRLI	639	0.5000	5.95
81	IVAEKALLR	121	0.4000	4.76
82	VVDRAQAEI	154	0.4000	4.76
83	LGLDFMRSC	234	0.4000	4.76
84	YESRQVEVS	346	0.4000	4.76
85	FLRHVGVHG	688	0.4000	4.76
86	LRQLKGPVR	706	0.4000	4.76
87	YRPAHQNVY	57	0.3000	3.57

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	WTRLARRMS	288	4.0000	47.62
2	LGLFTKRSH	588	3.8800	46.19
3	FSRHLKLLA	356	3.6000	42.86
4	LHIHGAKDQ	677	3.3000	39.29
5	IRAKARRLR	316	3.2000	38.10
6	LTMMEIRAK	311	2.8000	33.33
7	WRLHIHGAK	675	2.8000	33.33
8	FEGWTPLAQ	476	2.4000	28.57
9	VVILLHRPD	822	2.4000	28.57
10	MRSCSIRHR	239	2.3000	27.38
11	VRNRLSAKQ	729	2.3000	27.38
12	FILAKHRNG	844	2.2000	26.19
13	YDVADRRLS	163	2.1000	25.00
14	WITHAPKLG	662	2.1000	25.00
15	FVANGISLH	805	2.0800	24.76
16	LRLASGREV	457	2.0000	23.81
17	LRHVGVHGA	689	2.0000	23.81

18	ISLHNSLEQ	810	2.0000	23.81
19	VILLHRPDA	823	2.0000	23.81
20	MVIVAARPG	220	1.9000	22.62
21	LRMVARPMI	436	1.9000	22.62
22	LFLRHLWSA	614	1.6000	19.05
23	FRLRLASGR	455	1.5000	17.86
24	YGSTSRRLI	639	1.5000	17.86
25	VRFLRHVGV	686	1.5000	17.86
26	YESRQVEVS	346	1.4000	16.67
27	LKNQPIRYE	524	1.4000	16.67
28	FLRHVGVHG	688	1.4000	16.67
29	YRPAHQNVY	57	1.3000	15.48
30	MRLLSAEAK	264	1.3000	15.48
31	IQLHEPTMW	741	1.3000	15.48
32	YYASIVAEK	117	1.2000	14.29
33	LVEAGTRVV	131	1.2000	14.29
34	VRWDPTNGQ	626	1.2000	14.29
35	VMRLLSAEA	263	1.1000	13.10
36	MEIRAKARR	314	1.1000	13.10
37	LRPARQRLP	566	1.1000	13.10
38	VALFLRHLW	612	1.1000	13.10
39	FVALEDLLQ	174	1.0000	11.90
40	YLQLMTSGK	336	1.0000	11.90
41	YGRQPPQDL	19	0.9000	10.71
42	LRQKANLKL	323	0.8000	9.52
43	WKHSPSRSR	749	0.8000	9.52
44	LISLARMIG	511	0.7000	8.33
45	YLAARVPSL	558	0.7000	8.33
46	LRHLWSAGG	616	0.7000	8.33
47	LLLRVGIFS	653	0.7000	8.33
48	MWKHSPSRS	748	0.7000	8.33
49	FMRSCSIRH	238	0.6800	8.10
50	IRYEPVDEA	529	0.6000	7.14
51	YYGSTSRRL	638	0.6000	7.14
52	ILAKHRNGP	845	0.6000	7.14
53	LFTKRSHEK	590	0.5000	5.95
54	IFSWITHAP	659	0.5000	5.95
55	LGGHDSWRL	669	0.5000	5.95
56	ILLHRPDAF	824	0.5000	5.95
57	VIVAARPGV	221	0.4000	4.76
58	IRHRMASVI	244	0.4000	4.76

59	MLRQLKGPV	705	0.4000	4.76
60	WAQVRNRLS	726	0.4000	4.76
61	YGYAGAEGA	141	0.3000	3.57
62	IVMRLLSAE	262	0.3000	3.57
63	WSLDERLRM	430	0.3000	3.57
64	FMKFEGWTP	473	0.3000	3.57
65	YGRGEPADA	72	0.2000	2.38
66	LLRRLVEAG	127	0.1000	1.19
67	VVQYGYAGA	138	0.1000	1.19
68	LQLMTSGKK	337	0.1000	1.19
69	LKLLAKELE	360	0.1000	1.19
70	VFRLRLASG	454	0.1000	1.19
71	WTPLAQLKV	479	0.1000	1.19
72	VPSLRPARQ	563	0.1000	1.19
73	LAGLGLFTK	585	0.1000	1.19
74	LLRVGIFSW	654	0.1000	1.19
75	VGIFSWITH	657	-0.0200	0
76	LLSAEAKIK	266	-0.1000	0
77	FLRHLWSAG	615	-0.1000	0
78	ITHAPKLGG	663	-0.1000	0
79	VHGAEAVAA	694	-0.1000	0
80	IKLSDMRSG	273	-0.2000	0
81	VDYLQLMTS	334	-0.2000	0
82	LRESGCLTA	394	-0.2000	0
83	VFPSGRKEV	446	-0.2000	0
84	VAQLLLRVG	650	-0.2000	0
85	VGVHGAEAV	692	-0.2000	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	IRAKARRLR	316	5.7000	64.77
2	MRSCSIRHR	239	4.8000	54.55
3	VVILLHRPD	822	4.5000	51.14
4	MVIVAARPG	220	4.3000	48.86
5	LGLFTKRSH	588	4.3000	48.86
6	LRLASGREV	457	4.0000	45.45

7	LTMMEIRAK	311	3.9000	44.32
8	LRMVARPMI	436	3.8000	43.18
9	LKNQPIRYE	524	3.8000	43.18
10	MEIRAKARR	314	3.6000	40.91
11	LHIHGAKDQ	677	3.6000	40.91
12	VRFLRHVGV	686	3.5000	39.77
13	WTRLARRMS	288	3.4000	38.64
14	ILLHRPDAF	824	3.4000	38.64
15	LVEAGTRVV	131	3.2000	36.36
16	LISLARMIG	511	3.1000	35.23
17	LRPARQRLP	566	3.1000	35.23
18	LRHLWSAGG	616	3.1000	35.23
19	LRHVGVHGA	689	3.0000	34.09
20	VILLHRPDA	823	3.0000	34.09
21	LRQKANLKL	323	2.7600	31.36
22	IVMRLLSAE	262	2.7000	30.68
23	FSRHLKLLA	356	2.6000	29.55
24	LFLRHLWSA	614	2.6000	29.55
25	VRNRLSAKQ	729	2.6000	29.55
26	FILAKHRNG	844	2.6000	29.55
27	ILAKHRNGP	845	2.6000	29.55
28	LLRRLVEAG	127	2.5000	28.41
29	LKLLAKELE	360	2.5000	28.41
30	VFRLRLASG	454	2.5000	28.41
31	IFSWITHAP	659	2.5000	28.41
32	WITHAPKLG	662	2.5000	28.41
33	LGGHDSWRL	669	2.4600	27.95
34	VIVAARPGV	221	2.4000	27.27
35	MRLLSAEAK	264	2.4000	27.27
36	MLRQLKGPV	705	2.4000	27.27
37	IRHRMASVI	244	2.3000	26.14
38	ITHAPKLGG	663	2.3000	26.14
39	IQLHEPTMW	741	2.3000	26.14
40	ISLHNSLEQ	810	2.3000	26.14
41	IKLSDMRSG	273	2.2000	25.00
42	VAQLLLRVG	650	2.2000	25.00
43	VMRLLSAEA	263	2.1000	23.86
44	IVVDYLQLM	332	2.1000	23.86
45	VVAISQLNR	371	2.1000	23.86
46	LMRSGERPM	420	2.1000	23.86
47	VALFLRHLW	612	2.1000	23.86

48	LLLRVGIFS	653	2.1000	23.86
49	MWKHSPSRS	748	2.1000	23.86
50	FRLRLASGR	455	2.0000	22.73
51	IGDQHVFDG	789	2.0000	22.73
52	LRRIGGAPY	93	1.9000	21.59
53	IVAEKALLR	121	1.9000	21.59
54	WRLHIHGAK	675	1.9000	21.59
55	LRQLKGPVR	706	1.9000	21.59
56	VFPSGRKEV	446	1.8000	20.45
57	FLRHVGVHG	688	1.8000	20.45
58	VGVHGAEAV	692	1.8000	20.45
59	MRSGERPMV	421	1.7000	19.32
60	YRPAHQNVY	57	1.6000	18.18
61	VAISQLNRG	372	1.6000	18.18
62	IRYEPVDEA	529	1.6000	18.18
63	LFTKRSHEK	590	1.6000	18.18
64	VAHQLHLSR	859	1.6000	18.18
65	VWAQVRNRL	725	1.5600	17.73
66	YDVADRRLS	163	1.5000	17.05
67	IVAARPGVG	222	1.5000	17.05
68	LMTSGKKYE	339	1.5000	17.05
69	VRWDPTNGQ	626	1.5000	17.05
70	LRRLVEAGT	128	1.4000	15.91
71	LEVPVVAIS	367	1.4000	15.91
72	YGSTSRRLI	639	1.4000	15.91
73	VVDRAQAEI	154	1.3000	14.77
74	WKHSPSRSR	749	1.3000	14.77
75	VDYLQLMTS	334	1.2000	13.64
76	LQLMTSGKK	337	1.2000	13.64
77	MVARPMINV	438	1.2000	13.64
78	LAGLGLFTK	585	1.2000	13.64
79	LKLIVVDYL	329	1.1600	13.18
80	LERLRPGDF	48	1.1000	12.50
81	VVQYGYAGA	138	1.1000	12.50
82	LLRVGIFSW	654	1.1000	12.50
83	LHRPDAFDR	826	1.1000	12.50
84	LSRFANMAR	865	1.1000	12.50
85	LLSAEAKIK	266	1.0000	11.36
86	LLSKDAIAD	38	0.9000	10.23
87	LARRMSEIS	291	0.9000	10.23

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	IRAKARRLR	316	5.7000	64.77
2	MRSCSIRHR	239	4.8000	54.55
3	VVILLHRPD	822	4.5000	51.14
4	MVIVAARPG	220	4.3000	48.86
5	LGLFTKRSH	588	4.3000	48.86
6	LRLASGREV	457	4.0000	45.45
7	LTMMEIRAK	311	3.9000	44.32
8	LRMVARPMI	436	3.8000	43.18
9	LKNQPIRYE	524	3.8000	43.18
10	MEIRAKARR	314	3.6000	40.91
11	LHIHGAKDQ	677	3.6000	40.91
12	VRFLRHVGV	686	3.5000	39.77
13	WTRLARRMS	288	3.4000	38.64
14	ILLHRPDAF	824	3.4000	38.64
15	LVEAGTRVV	131	3.2000	36.36
16	LISLARMIG	511	3.1000	35.23
17	LRPARQRLP	566	3.1000	35.23
18	LRHLWSAGG	616	3.1000	35.23
19	LRHVGVHGA	689	3.0000	34.09
20	VILLHRPDA	823	3.0000	34.09
21	LRQKANLKL	323	2.7600	31.36
22	IVMRLLSAE	262	2.7000	30.68
23	FSRHLKLLA	356	2.6000	29.55
24	LFLRHLWSA	614	2.6000	29.55
25	VRNRLSAKQ	729	2.6000	29.55
26	FILAKHRNG	844	2.6000	29.55
27	ILAKHRNGP	845	2.6000	29.55
28	LLRRLVEAG	127	2.5000	28.41
29	LKLLAKELE	360	2.5000	28.41
30	VFRLRLASG	454	2.5000	28.41
31	IFSWITHAP	659	2.5000	28.41
32	WITHAPKLG	662	2.5000	28.41
33	LGGHDSWRL	669	2.4600	27.95
34	VIVAARPGV	221	2.4000	27.27
35	MRLLSAEAK	264	2.4000	27.27

36	MLRQLKGPV	705	2.4000	27.27
37	IRHRMASVI	244	2.3000	26.14
38	ITHAPKLGG	663	2.3000	26.14
39	IQLHEPTMW	741	2.3000	26.14
40	ISLHNSLEQ	810	2.3000	26.14
41	IKLSDMRSG	273	2.2000	25.00
42	VAQLLLRVG	650	2.2000	25.00
43	VMRLLSAEA	263	2.1000	23.86
44	IVVDYLQLM	332	2.1000	23.86
45	VVAISQLNR	371	2.1000	23.86
46	LMRSGERPM	420	2.1000	23.86
47	VALFLRHLW	612	2.1000	23.86
48	LLLRVGIFS	653	2.1000	23.86
49	MWKHSPSRS	748	2.1000	23.86
50	FRLRLASGR	455	2.0000	22.73
51	IGDQHVFDG	789	2.0000	22.73
52	LRRIGGAPY	93	1.9000	21.59
53	IVAEKALLR	121	1.9000	21.59
54	WRLHIHGAK	675	1.9000	21.59
55	LRQLKGPVR	706	1.9000	21.59
56	VFPSGRKEV	446	1.8000	20.45
57	FLRHVGVHG	688	1.8000	20.45
58	VGVHGAEAV	692	1.8000	20.45
59	MRSGERPMV	421	1.7000	19.32
60	YRPAHQNVY	57	1.6000	18.18
61	VAISQLNRG	372	1.6000	18.18
62	IRYEPVDEA	529	1.6000	18.18
63	LFTKRSHEK	590	1.6000	18.18
64	VAHQLHLSR	859	1.6000	18.18
65	VWAQVRNRL	725	1.5600	17.73
66	YDVADRRLS	163	1.5000	17.05
67	IVAARPGVG	222	1.5000	17.05
68	LMTSGKKYE	339	1.5000	17.05
69	VRWDPTNGQ	626	1.5000	17.05
70	LRRLVEAGT	128	1.4000	15.91
71	LEVPVVAIS	367	1.4000	15.91
72	YGSTSRRLI	639	1.4000	15.91
73	VVDRAQAEI	154	1.3000	14.77
74	WKHSPSRSR	749	1.3000	14.77
75	VDYLQLMTS	334	1.2000	13.64
76	LQLMTSGKK	337	1.2000	13.64

77	MVARPMINV	438	1.2000	13.64
78	LAGLGLFTK	585	1.2000	13.64
79	LKLIVVDYL	329	1.1600	13.18
80	LERLRPGDF	48	1.1000	12.50
81	VVQYGYAGA	138	1.1000	12.50
82	LLRVGIFSW	654	1.1000	12.50
83	LHRPDAFDR	826	1.1000	12.50
84	LSRFANMAR	865	1.1000	12.50
85	LLSAEAKIK	266	1.0000	11.36
86	LLSKDAIAD	38	0.9000	10.23
87	LARRMSEIS	291	0.9000	10.23

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	LRMVARPMI	436	5.8000	59.18
2	VVQYGYAGA	138	5.0000	51.02
3	LRQKANLKL	323	4.6000	46.94
4	LIVVDYLQL	331	4.6000	46.94
5	VGIFSWITH	657	4.4000	44.90
6	VVDYLQLMT	333	4.2000	42.86
7	MVARPMINV	438	4.2000	42.86
8	LSRFANMAR	865	4.2000	42.86
9	LKVGDRIAA	485	4.1000	41.84
10	MRSGERPMV	421	4.0000	40.82
11	LLLRVGIFS	653	3.9000	39.80
12	VILLHRPDA	823	3.9000	39.80
13	LISLARMIG	511	3.7000	37.76
14	IRHRMASVI	244	3.6000	36.73
15	VALFLRHLW	612	3.6000	36.73
16	VRFLRHVGV	686	3.6000	36.73
17	LRLASGREV	457	3.5000	35.71
18	LGGHDSWRL	669	3.5000	35.71
19	LRVGIFSWI	655	3.4000	34.69
20	LFIDDSPNL	303	3.3000	33.67
21	VIVAARPGV	221	3.2000	32.65
22	LRRIGGAPY	93	3.1000	31.63

23	VMRLLSAEA	263	2.9000	29.59
24	LRHVGVHGA	689	2.9000	29.59
25	IGGAPYLHT	96	2.8000	28.57
26	VVAISQLNR	371	2.8000	28.57
27	LFLRHLWSA	614	2.8000	28.57
28	LRHLWSAGG	616	2.7000	27.55
29	ISLHNSLEQ	810	2.7000	27.55
30	LRESGCLTA	394	2.6000	26.53
31	LRADTGAEV	407	2.6000	26.53
32	INVFPSGRK	444	2.6000	26.53
33	MVIVAARPG	220	2.5000	25.51
34	FMKFEGWTP	473	2.5000	25.51
35	LRQLKGPVR	706	2.5000	25.51
36	IVAEKALLR	121	2.4000	24.49
37	VAFGELMRS	415	2.4000	24.49
38	IVMRLLSAE	262	2.3000	23.47
39	WSLDERLRM	430	2.2800	23.27
40	LRRLVEAGT	128	2.2000	22.45
41	LKLIVVDYL	329	2.2000	22.45
42	WLAGLGLFT	584	2.2000	22.45
43	IVVDYLQLM	332	2.1800	22.24
44	LDLYGRGEP	69	2.1000	21.43
45	LQLMTSGKK	337	2.1000	21.43
46	FSRHLKLLA	356	2.1000	21.43
47	VTVAHQLHL	857	2.1000	21.43
48	LGLFTKRSH	588	2.0000	20.41
49	LLRVGIFSW	654	1.9500	19.90
50	VRNPNLDSA	713	1.9000	19.39
51	VRNRLSAKQ	729	1.9000	19.39
52	IQLHEPTMW	741	1.9000	19.39
53	LRPGDFYRP	51	1.8000	18.37
54	LHPGQMVIV	215	1.8000	18.37
55	LDFMRSCSI	236	1.8000	18.37
56	VFPSGRKEV	446	1.8000	18.37
57	VFRAPNDQV	604	1.8000	18.37
58	FLRHVGVHG	688	1.8000	18.37
59	VANGISLHN	806	1.8000	18.37
60	ILLHRPDAF	824	1.8000	18.37
61	FRLRLASGR	455	1.7000	17.35
62	VGVHGAEAV	692	1.7000	17.35
63	VVEITSIGD	783	1.7000	17.35

64	VSGTHNFVA	799	1.7000	17.35
65	VLGGMLLSK	33	1.6000	16.33
66	IFSLEMSKS	252	1.6000	16.33
67	VDYLQLMTS	334	1.6000	16.33
68	MKFEGWTPL	474	1.6000	16.33
69	LHRPDAFDR	826	1.6000	16.33
70	LAKHRNGPT	846	1.6000	16.33
71	FVALEDLLQ	174	1.5000	15.31
72	FMRSCSIRH	238	1.5000	15.31
73	LHIHGAKDQ	677	1.5000	15.31
74	LKGPVRNPN	709	1.5000	15.31
75	LSAKQMMDI	733	1.5000	15.31
76	VALEDLLQP	175	1.4000	14.29
77	LEMSKSEIV	255	1.4000	14.29
78	VFRLRLASG	454	1.4000	14.29
79	IRYEPVDEA	529	1.4000	14.29
80	MLLSKDAIA	37	1.3000	13.27
81	LLRRIGGAP	92	1.3000	13.27
82	IASSGGLAR	191	1.3000	13.27
83	MRLLSAEAK	264	1.3000	13.27
84	VAISQLNRG	372	1.3000	13.27
85	VHGAEAVAA	694	1.3000	13.27
86	VWAQVRNRL	725	1.3000	13.27
87	LHLSRFANM	863	1.2800	13.06

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	LRMVARPMI	436	4.8000	48.98
2	VVQYGYAGA	138	4.0000	40.82
3	LRQKANLKL	323	3.6000	36.73
4	LIVVDYLQL	331	3.6000	36.73
5	FMKFEGWTP	473	3.5000	35.71
6	VGIFSWITH	657	3.4000	34.69
7	WSLDERLRM	430	3.2800	33.47
8	VVDYLQLMT	333	3.2000	32.65
9	MVARPMINV	438	3.2000	32.65

10	WLAGLGLFT	584	3.2000	32.65
11	LSRFANMAR	865	3.2000	32.65
12	FSRHLKLLA	356	3.1000	31.63
13	LKVGDRIAA	485	3.1000	31.63
14	MRSGERPMV	421	3.0000	30.61
15	LLLRVGIFS	653	2.9000	29.59
16	VILLHRPDA	823	2.9000	29.59
17	FLRHVGVHG	688	2.8000	28.57
18	FRLRLASGR	455	2.7000	27.55
19	LISLARMIG	511	2.7000	27.55
20	IRHRMASVI	244	2.6000	26.53
21	VALFLRHLW	612	2.6000	26.53
22	VRFLRHVGV	686	2.6000	26.53
23	FVALEDLLQ	174	2.5000	25.51
24	FMRSCSIRH	238	2.5000	25.51
25	LRLASGREV	457	2.5000	25.51
26	LGGHDSWRL	669	2.5000	25.51
27	LRVGIFSWI	655	2.4000	24.49
28	LFIDDSPNL	303	2.3000	23.47
29	VIVAARPGV	221	2.2000	22.45
30	WTPLAQLKV	479	2.2000	22.45
31	LRRIGGAPY	93	2.1000	21.43
32	WRLHIHGAK	675	2.1000	21.43
33	VMRLLSAEA	263	1.9000	19.39
34	FLRHLWSAG	615	1.9000	19.39
35	LRHVGVHGA	689	1.9000	19.39
36	IGGAPYLHT	96	1.8000	18.37
37	VVAISQLNR	371	1.8000	18.37
38	LFLRHLWSA	614	1.8000	18.37
39	LRHLWSAGG	616	1.7000	17.35
40	ISLHNSLEQ	810	1.7000	17.35
41	LRESGCLTA	394	1.6000	16.33
42	LRADTGAEV	407	1.6000	16.33
43	INVFPSGRK	444	1.6000	16.33
44	YGSTSRRLI	639	1.6000	16.33
45	YLHTLISTV	101	1.5500	15.82
46	YRPAHQNVY	57	1.5000	15.31
47	MVIVAARPG	220	1.5000	15.31
48	YLAARVPSL	558	1.5000	15.31
49	LRQLKGPVR	706	1.5000	15.31
50	IVAEKALLR	121	1.4000	14.29

51	WTRLARRMS	288	1.4000	14.29
52	VAFGELMRS	415	1.4000	14.29
53	YYGSTSRRL	638	1.4000	14.29
54	IVMRLLSAE	262	1.3000	13.27
55	LRRLVEAGT	128	1.2000	12.24
56	LKLIVVDYL	329	1.2000	12.24
57	FRAPNDQVA	605	1.2000	12.24
58	IVVDYLQLM	332	1.1800	12.04
59	FVANGISLH	805	1.1500	11.73
60	LDLYGRGEP	69	1.1000	11.22
61	LQLMTSGKK	337	1.1000	11.22
62	VTVAHQLHL	857	1.1000	11.22
63	YGRGEPADA	72	1.0000	10.20
64	YAGAEGADV	143	1.0000	10.20
65	LGLFTKRSH	588	1.0000	10.20
66	LLRVGIFSW	654	0.9500	9.69
67	WITHAPKLG	662	0.9000	9.18
68	VRNPNLDSA	713	0.9000	9.18
69	VRNRLSAKQ	729	0.9000	9.18
70	IQLHEPTMW	741	0.9000	9.18
71	LRPGDFYRP	51	0.8000	8.16
72	FYRPAHQNV	56	0.8000	8.16
73	LHPGQMVIV	215	0.8000	8.16
74	LDFMRSCSI	236	0.8000	8.16
75	VFPSGRKEV	446	0.8000	8.16
76	FEGWTPLAQ	476	0.8000	8.16
77	VFRAPNDQV	604	0.8000	8.16
78	VANGISLHN	806	0.8000	8.16
79	ILLHRPDAF	824	0.8000	8.16
80	VGVHGAEAV	692	0.7000	7.14
81	VVEITSIGD	783	0.7000	7.14
82	VSGTHNFVA	799	0.7000	7.14
83	VLGGMLLSK	33	0.6000	6.12
84	YGYAGAEGA	141	0.6000	6.12
85	IFSLEMSKS	252	0.6000	6.12
86	VDYLQLMTS	334	0.6000	6.12
87	MKFEGWTPL	474	0.6000	6.12

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRMVARPMI	436	5.8000	59.18
2	VVQYGYAGA	138	5.0000	51.02
3	LRQKANLKL	323	4.6000	46.94
4	LIVVDYLQL	331	4.6000	46.94
5	VGIFSWITH	657	4.4000	44.90
6	VVDYLQLMT	333	4.2000	42.86
7	MVARPMINV	438	4.2000	42.86
8	LSRFANMAR	865	4.2000	42.86
9	LKVGDRIAA	485	4.1000	41.84
10	MRSGERPMV	421	4.0000	40.82
11	LLLRVGIFS	653	3.9000	39.80
12	VILLHRPDA	823	3.9000	39.80
13	LISLARMIG	511	3.7000	37.76
14	IRHRMASVI	244	3.6000	36.73
15	VALFLRHLW	612	3.6000	36.73
16	VRFLRHVGV	686	3.6000	36.73
17	LRLASGREV	457	3.5000	35.71
18	LGGHDSWRL	669	3.5000	35.71
19	LRVGIFSWI	655	3.4000	34.69
20	LFIDDSPNL	303	3.3000	33.67
21	VIVAARPGV	221	3.2000	32.65
22	LRRIGGAPY	93	3.1000	31.63
23	VMRLLSAEA	263	2.9000	29.59
24	LRHVGVHGA	689	2.9000	29.59
25	IGGAPYLHT	96	2.8000	28.57
26	VVAISQLNR	371	2.8000	28.57
27	LFLRHLWSA	614	2.8000	28.57
28	LRHLWSAGG	616	2.7000	27.55
29	ISLHNSLEQ	810	2.7000	27.55
30	LRESGCLTA	394	2.6000	26.53
31	LRADTGAEV	407	2.6000	26.53
32	INVFPSGRK	444	2.6000	26.53
33	MVIVAARPG	220	2.5000	25.51
34	FMKFEGWTP	473	2.5000	25.51
35	LRQLKGPVR	706	2.5000	25.51
36	IVAEKALLR	121	2.4000	24.49
37	VAFGELMRS	415	2.4000	24.49

38	IVMRLLSAE	262	2.3000	23.47
39	WSLDERLRM	430	2.2800	23.27
40	LRRLVEAGT	128	2.2000	22.45
41	LKLIVVDYL	329	2.2000	22.45
42	WLAGLGLFT	584	2.2000	22.45
43	IVVDYLQLM	332	2.1800	22.24
44	LDLYGRGEP	69	2.1000	21.43
45	LQLMTSGKK	337	2.1000	21.43
46	FSRHLKLLA	356	2.1000	21.43
47	VTVAHQLHL	857	2.1000	21.43
48	LGLFTKRSH	588	2.0000	20.41
49	LLRVGIFSW	654	1.9500	19.90
50	VRNPNLDSA	713	1.9000	19.39
51	VRNRLSAKQ	729	1.9000	19.39
52	IQLHEPTMW	741	1.9000	19.39
53	LRPGDFYRP	51	1.8000	18.37
54	LHPGQMVIV	215	1.8000	18.37
55	LDFMRSCSI	236	1.8000	18.37
56	VFPSGRKEV	446	1.8000	18.37
57	VFRAPNDQV	604	1.8000	18.37
58	FLRHVGVHG	688	1.8000	18.37
59	VANGISLHN	806	1.8000	18.37
60	ILLHRPDAF	824	1.8000	18.37
61	FRLRLASGR	455	1.7000	17.35
62	VGVHGAEAV	692	1.7000	17.35
63	VVEITSIGD	783	1.7000	17.35
64	VSGTHNFVA	799	1.7000	17.35
65	VLGGMLLSK	33	1.6000	16.33
66	IFSLEMSKS	252	1.6000	16.33
67	VDYLQLMTS	334	1.6000	16.33
68	MKFEGWTPL	474	1.6000	16.33
69	LHRPDAFDR	826	1.6000	16.33
70	LAKHRNGPT	846	1.6000	16.33
71	FVALEDLLQ	174	1.5000	15.31
72	FMRSCSIRH	238	1.5000	15.31
73	LHIHGAKDQ	677	1.5000	15.31
74	LKGPVRNPN	709	1.5000	15.31
75	LSAKQMMDI	733	1.5000	15.31
76	VALEDLLQP	175	1.4000	14.29
77	LEMSKSEIV	255	1.4000	14.29
78	VFRLRLASG	454	1.4000	14.29

79	IRYEPVDEA	529	1.4000	14.29
80	MLLSKDAIA	37	1.3000	13.27
81	LLRRIGGAP	92	1.3000	13.27
82	IASSGGLAR	191	1.3000	13.27
83	MRLLSAEAK	264	1.3000	13.27
84	VAISQLNRG	372	1.3000	13.27
85	VHGAEAVAA	694	1.3000	13.27
86	VWAQVRNRL	725	1.3000	13.27
87	LHLSRFANM	863	1.2800	13.06

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	LQLMTSGKK	337	5.7000	58.16
2	MVIVAARPG	220	5.4000	55.10
3	LTMMEIRAK	311	4.7000	47.96
4	MRLLSAEAK	264	4.6000	46.94
5	LRRIGGAPY	93	4.2000	42.86
6	MINVFPSGR	443	4.2000	42.86
7	VVAISQLNR	371	4.1000	41.84
8	WKHSPSRSR	749	4.1000	41.84
9	WRLHIHGAK	675	3.9000	39.80
10	MRSCSIRHR	239	3.8000	38.78
11	LLSAEAKIK	266	3.8000	38.78
12	FRLRLASGR	455	3.8000	38.78
13	MMEIRAKAR	313	3.6000	36.73
14	LRQLKGPVR	706	3.4000	34.69
15	YLQLMTSGK	336	3.3000	33.67
16	FMRSCSIRH	238	3.0000	30.61
17	LRMVARPMI	436	3.0000	30.61
18	LRLASGREV	457	3.0000	30.61
19	LAGLGLFTK	585	3.0000	30.61
20	LHRPDAFDR	826	3.0000	30.61
21	YRPAHQNVY	57	2.9000	29.59
22	IVAEKALLR	121	2.9000	29.59
23	YGRQPPQDL	19	2.7000	27.55
24	YYGSTSRRL	638	2.7000	27.55

25	LIVVDYLQL	331	2.6000	26.53
26	FILAKHRNG	844	2.6000	26.53
27	INVFPSGRK	444	2.5000	25.51
28	FSWITHAPK	660	2.5000	25.51
29	LERLRPGDF	48	2.4000	24.49
30	LRHVGVHGA	689	2.4000	24.49
31	IVAARPGVG	222	2.3000	23.47
32	WDPTNGQGR	628	2.2000	22.45
33	YGSTSRRLI	639	2.2000	22.45
34	FVALEDLLQ	174	2.0000	20.41
35	WTRLARRMS	288	2.0000	20.41
36	IRAKARRLR	316	2.0000	20.41
37	LRHLWSAGG	616	1.9000	19.39
38	YYASIVAEK	117	1.8000	18.37
39	WAQVRNRLS	726	1.8000	18.37
40	VVILLHRPD	822	1.8000	18.37
41	IASSGGLAR	191	1.5000	15.31
42	VIFSLEMSK	251	1.5000	15.31
43	VWSLDERLR	429	1.5000	15.31
44	LFTKRSHEK	590	1.5000	15.31
45	LHIHGAKDQ	677	1.5000	15.31
46	LAQLKVGDR	482	1.4000	14.29
47	VEATGSHPF	465	1.3000	13.27
48	LLRVGIFSW	654	1.2000	12.24
49	WITHAPKLG	662	1.2000	12.24
50	IHGAKDQVR	679	1.2000	12.24
51	LISTVPTAA	105	1.1000	11.22
52	LWSAGGSVR	619	1.1000	11.22
53	VLGGMLLSK	33	0.9000	9.18
54	LDFMRSCSI	236	0.9000	9.18
55	VMRLLSAEA	263	0.9000	9.18
56	LKLIVVDYL	329	0.9000	9.18
57	LTASTRILR	400	0.9000	9.18
58	LLLRVGIFS	653	0.9000	9.18
59	VGIFSWITH	657	0.9000	9.18
60	VRFLRHVGV	686	0.9000	9.18
61	IKLSDMRSG	273	0.8000	8.16
62	YEPVDEANL	531	0.8000	8.16
63	VEITSIGDQ	784	0.8000	8.16
64	IRHRMASVI	244	0.7000	7.14
65	LGLFTKRSH	588	0.7000	7.14

66	IADVLERLR	44	0.6000	6.12
67	VTVAAELDR	81	0.6000	6.12
68	YASIVAEKA	118	0.6000	6.12
69	MIGDGSCLK	517	0.6000	6.12
70	LRPARQRLP	566	0.6000	6.12
71	VYYGSTSRR	637	0.6000	6.12
72	VFRLRLASG	454	0.5000	5.10
73	YGYAGAEGA	141	0.4000	4.08
74	FEGWTPLAQ	476	0.4000	4.08
75	LISLARMIG	511	0.4000	4.08
76	YLAARVPSL	558	0.4000	4.08
77	VVEITSIGD	783	0.4000	4.08
78	VAHQLHLSR	859	0.4000	4.08
79	LSRFANMAR	865	0.4000	4.08
80	LRRLVEAGT	128	0.3000	3.06
81	IYDVADRRL	162	0.3000	3.06
82	LARMIGDGS	514	0.3000	3.06
83	VAQLLLRVG	650	0.3000	3.06
84	FDGTVSGTH	795	0.3000	3.06
85	LVEAGTRVV	131	0.2000	2.04
86	VPSLRPARQ	563	0.2000	2.04
87	VRNRLSAKQ	729	0.2000	2.04

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	LQLMTSGKK	337	5.7000	58.16
2	MVIVAARPG	220	5.4000	55.10
3	LTMMEIRAK	311	4.7000	47.96
4	MRLLSAEAK	264	4.6000	46.94
5	LRRIGGAPY	93	4.2000	42.86
6	MINVFPSGR	443	4.2000	42.86
7	VVAISQLNR	371	4.1000	41.84
8	WKHSPSRSR	749	4.1000	41.84
9	WRLHIHGAK	675	3.9000	39.80
10	MRSCSIRHR	239	3.8000	38.78
11	LLSAEAKIK	266	3.8000	38.78

12	FRLRLASGR	455	3.8000	38.78
13	MMEIRAKAR	313	3.6000	36.73
14	LRQLKGPVR	706	3.4000	34.69
15	YLQLMTSGK	336	3.3000	33.67
16	FMRSCSIRH	238	3.0000	30.61
17	LRMVARPMI	436	3.0000	30.61
18	LRLASGREV	457	3.0000	30.61
19	LAGLGLFTK	585	3.0000	30.61
20	LHRPDAFDR	826	3.0000	30.61
21	YRPAHQNVY	57	2.9000	29.59
22	IVAEKALLR	121	2.9000	29.59
23	YGRQPPQDL	19	2.7000	27.55
24	YYGSTSRRL	638	2.7000	27.55
25	LIVVDYLQL	331	2.6000	26.53
26	FILAKHRNG	844	2.6000	26.53
27	INVFPSGRK	444	2.5000	25.51
28	FSWITHAPK	660	2.5000	25.51
29	LERLRPGDF	48	2.4000	24.49
30	LRHVGVHGA	689	2.4000	24.49
31	IVAARPGVG	222	2.3000	23.47
32	WDPTNGQGR	628	2.2000	22.45
33	YGSTSRRLI	639	2.2000	22.45
34	FVALEDLLQ	174	2.0000	20.41
35	WTRLARRMS	288	2.0000	20.41
36	IRAKARRLR	316	2.0000	20.41
37	LRHLWSAGG	616	1.9000	19.39
38	YYASIVAEK	117	1.8000	18.37
39	WAQVRNRLS	726	1.8000	18.37
40	VVILLHRPD	822	1.8000	18.37
41	IASSGGLAR	191	1.5000	15.31
42	VIFSLEMSK	251	1.5000	15.31
43	VWSLDERLR	429	1.5000	15.31
44	LFTKRSHEK	590	1.5000	15.31
45	LHIHGAKDQ	677	1.5000	15.31
46	LAQLKVGDR	482	1.4000	14.29
47	VEATGSHPF	465	1.3000	13.27
48	LLRVGIFSW	654	1.2000	12.24
49	WITHAPKLG	662	1.2000	12.24
50	IHGAKDQVR	679	1.2000	12.24
51	LISTVPTAA	105	1.1000	11.22
52	LWSAGGSVR	619	1.1000	11.22

53	VLGGMLLSK	33	0.9000	9.18
54	LDFMRSCSI	236	0.9000	9.18
55	VMRLLSAEA	263	0.9000	9.18
56	LKLIVVDYL	329	0.9000	9.18
57	LTASTRILR	400	0.9000	9.18
58	LLLRVGIFS	653	0.9000	9.18
59	VGIFSWITH	657	0.9000	9.18
60	VRFLRHVGV	686	0.9000	9.18
61	IKLSDMRSG	273	0.8000	8.16
62	YEPVDEANL	531	0.8000	8.16
63	VEITSIGDQ	784	0.8000	8.16
64	IRHRMASVI	244	0.7000	7.14
65	LGLFTKRSH	588	0.7000	7.14
66	IADVLERLR	44	0.6000	6.12
67	VTVAAELDR	81	0.6000	6.12
68	YASIVAEKA	118	0.6000	6.12
69	MIGDGSCLK	517	0.6000	6.12
70	LRPARQRLP	566	0.6000	6.12
71	VYYGSTSRR	637	0.6000	6.12
72	VFRLRLASG	454	0.5000	5.10
73	YGYAGAEGA	141	0.4000	4.08
74	FEGWTPLAQ	476	0.4000	4.08
75	LISLARMIG	511	0.4000	4.08
76	YLAARVPSL	558	0.4000	4.08
77	VVEITSIGD	783	0.4000	4.08
78	VAHQLHLSR	859	0.4000	4.08
79	LSRFANMAR	865	0.4000	4.08
80	LRRLVEAGT	128	0.3000	3.06
81	IYDVADRRL	162	0.3000	3.06
82	LARMIGDGS	514	0.3000	3.06
83	VAQLLLRVG	650	0.3000	3.06
84	FDGTVSGTH	795	0.3000	3.06
85	LVEAGTRVV	131	0.2000	2.04
86	VPSLRPARQ	563	0.2000	2.04
87	VRNRLSAKQ	729	0.2000	2.04