MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Mar 15 00:16:20 2010
Length of input sequence	439 amino acids
Number of nanomers from input sequence	431
Number of nanomers with obligatory P1 anchor residue	134
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	43

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	WVSFYAAGL	209	2.8800	48.00
2	LRGAGALTA	11	1.7000	28.33
3	FVPVLRSAI	358	1.0500	17.50
4	WGFVNAWVS	203	0.8700	14.50
5	FTFNGGQYA	138	0.7400	12.33
6	FAMNNGVPW	218	0.4400	7.33
7	FVNAWVSFY	205	0.4000	6.67
8	VPRMNPTHL	228	0.3900	6.50

9	VMQQLATFC	76	0.2900	4.83
10	MQQLATFCA	77	0.2000	3.33
11	LRGSRPATS	415	0.2000	3.33
12	FVKFATGPV	339	0.1800	3.00
13	VKFATGPVG	340	-0.1300	0
14	MNNGVPWSV	220	-0.3800	0
15	VRALLSGPG	67	-0.4000	0
16	LLRGAGALT	10	-0.5000	0
17	WELTYAELA	96	-0.5000	0
18	LRSAINSHG	362	-0.7000	0
19	VLSEGPAYS	383	-0.7000	0
20	FYAAGLFAM	212	-0.7200	0
21	LNTLLARDQ	112	-0.8100	0
22	FFAANPDEL	40	-0.9000	0
23	WRYQTFDRA	288	-1.0000	0
24	FDRADGLDF	293	-1.0000	0
25	WEKIAALMD	400	-1.0000	0
26	LTFFFAANP	37	-1.2200	0
27	LLDLNTLLA	109	-1.3000	0
28	WSFAEFLDA	179	-1.3000	0
29	LIGESRLFV	351	-1.3000	0
30	YQTFDRADG	290	-1.3200	0
31	FFFAANPDE	39	-1.3300	0
32	LFSVGKAGI	274	-1.3500	0
33	VVNEFQRRY	54	-1.4100	0
34	MRVVNEFQR	52	-1.4500	0
35	FLFYNKQLF	155	-1.5000	0
36	VLMAWELTY	92	-1.6000	0
37	FSVGKAGIA	275	-1.6000	0
38	LLSGPGVMQ	70	-1.7000	0
39	FLEAVQFYA	243	-1.7000	0
40	VGNLAVLSE	378	-1.8000	0
41	YPDIKVRAL	62	-1.8100	0
42	LAIAATSRR	324	-1.9000	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	LRGAGALTA	11	2.7000	45.00
2	WVSFYAAGL	209	1.8800	31.33
3	VPRMNPTHL	228	1.3900	23.17
4	VMQQLATFC	76	1.2900	21.50
5	MQQLATFCA	77	1.2000	20.00
6	LRGSRPATS	415	1.2000	20.00
7	FVPVLRSAI	358	1.0500	17.50
8	VKFATGPVG	340	0.8700	14.50
9	FTFNGGQYA	138	0.7400	12.33
10	MNNGVPWSV	220	0.6200	10.33
11	VRALLSGPG	67	0.6000	10.00
12	LLRGAGALT	10	0.5000	8.33
13	FAMNNGVPW	218	0.4400	7.33
14	FVNAWVSFY	205	0.4000	6.67
15	LRSAINSHG	362	0.3000	5.00
16	VLSEGPAYS	383	0.3000	5.00
17	LNTLLARDQ	112	0.1900	3.17
18	FVKFATGPV	339	0.1800	3.00
19	WGFVNAWVS	203	-0.1300	0
20	LTFFFAANP	37	-0.2200	0
21	LLDLNTLLA	109	-0.3000	0
22	LIGESRLFV	351	-0.3000	0
23	LFSVGKAGI	274	-0.3500	0
24	VVNEFQRRY	54	-0.4100	0
25	MRVVNEFQR	52	-0.4500	0
26	VLMAWELTY	92	-0.6000	0
27	LLSGPGVMQ	70	-0.7000	0
28	FYAAGLFAM	212	-0.7200	0
29	VGNLAVLSE	378	-0.8000	0
30	FFAANPDEL	40	-0.9000	0

31	LAIAATSRR	324	-0.9000	0
32	VPVLRSAIN	359	-0.9000	0
33	VLLDLNTLL	108	-0.9100	0
34	VLRGSRPAT	414	-0.9300	0
35	FDRADGLDF	293	-1.0000	0
36	VTGLAIAAT	321	-1.0000	0
37	IGALYETFT	131	-1.1100	0
38	VNAWVSFYA	206	-1.3000	0
39	FFFAANPDE	39	-1.3300	0
40	LARDQAFAA	116	-1.4000	0
41	VGKAGIALA	277	-1.4000	0
42	MDRYFGPVL	407	-1.4300	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	LRGSRPATS	415	4.7000	49.47
2	LKSDSIGAL	126	4.3600	45.89
3	VLLDLNTLL	108	3.5600	37.47
4	LARDQAFAA	116	3.5000	36.84
5	VLRGSRPAT	414	3.4000	35.79
6	FVNAWVSFY	205	3.1700	33.37
7	FVPVLRSAI	358	3.0700	32.32
8	LFSVGKAGI	274	2.9000	30.53
9	LAIAATSRR	324	2.8700	30.21
10	LRGAGALTA	11	2.6000	27.37
11	VRALLSGPG	67	2.6000	27.37
12	LPIGPRGRA	306	2.6000	27.37
13	VLRSAINSH	361	2.5100	26.42
14	MQQLATFCA	77	2.5000	26.32
15	FYADLTNKH	249	2.4100	25.37
16	VGQALIGES	347	2.4000	25.26
17	MRVVNEFQR	52	2.3000	24.21

18	VKFATGPVG	340	2.3000	24.21
19	LRSAINSHG	362	2.2700	23.89
20	LDFDVAPLP	299	2.2000	23.16
21	LRPRMRVVN	48	2.1000	22.11
22	VGNLAVLSE	378	2.1000	22.11
23	MNNGVPWSV	220	2.0000	21.05
24	FLFYNKQLF	155	1.9000	20.00
25	LIGESRLFV	351	1.8000	18.95
26	VLSEGPAYS	383	1.8000	18.95
27	FYAAGLFAM	212	1.7000	17.89
28	VAPLPIGPR	303	1.6000	16.84
29	LTKQGRSGR	191	1.5700	16.53
30	LNFDHDGFL	236	1.5600	16.42
31	VLMAWELTY	92	1.5000	15.79
32	LTYAELADR	98	1.5000	15.79
33	IKVRALLSG	65	1.4000	14.74
34	FGPVLRGSR	411	1.4000	14.74
35	FVKFATGPV	339	1.3000	13.68
36	VGKAGIALA	277	1.2000	12.63
37	LFYNKQLFD	156	1.1000	11.58
38	LLRGAGALT	10	1.0000	10.53
39	LLSGPGVMQ	70	1.0000	10.53
40	LSGPGVMQQ	71	1.0000	10.53
41	VMQQLATFC	76	1.0000	10.53
42	LFDDAGVPP	162	1.0000	10.53
43	LDLNTLLAR	110	0.8000	8.42

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	FYADLTNKH	249	3.9900	43.85
2	LRGSRPATS	415	3.3000	36.26
3	FVPVLRSAI	358	3.1700	34.84

4	FVNAWVSFY	205	2.8700	31.54
5	LARDQAFAA	116	2.5000	27.47
6	LKSDSIGAL	126	2.4000	26.37
7	VLRSAINSH	361	2.0900	22.97
8	FATGPVGQA	342	1.8000	19.78
9	VLRGSRPAT	414	1.7000	18.68
10	LRGAGALTA	11	1.6000	17.58
11	VLLDLNTLL	108	1.6000	17.58
12	LPIGPRGRA	306	1.6000	17.58
13	MQQLATFCA	77	1.5000	16.48
14	WGFVNAWVS	203	1.4000	15.38
15	FVKFATGPV	339	1.3000	14.29
16	FYAAGLFAM	212	1.2000	13.19
17	FAAELKSDS	122	1.0700	11.76
18	FLFYNKQLF	155	1.0000	10.99
19	LFSVGKAGI	274	1.0000	10.99
20	WRYQTFDRA	288	1.0000	10.99
21	VGQALIGES	347	1.0000	10.99
22	FGPVLRGSR	411	0.9000	9.89
23	FSVGKAGIA	275	0.8000	8.79
24	LLSGPGVMQ	70	0.7000	7.69
25	LSGPGVMQQ	71	0.7000	7.69
26	FQRRYPDIK	58	0.5000	5.49
27	VLSEGPAYS	383	0.4000	4.40
28	LAIAATSRR	324	0.3700	4.07
29	LRPRMRVVN	48	0.3000	3.30
30	WVSFYAAGL	209	0.3000	3.30
31	VAPSAAEQQ	259	0.3000	3.30
32	VRALLSGPG	67	0.2000	2.20
33	FTFNGGQYA	138	0.2000	2.20
34	VGKAGIALA	277	0.2000	2.20
35	YQTFDRADG	290	0.2000	2.20
36	LDFDVAPLP	299	0.2000	2.20
37	FCAGGKCPD	83	0.1000	1.10

38	FAMNNGVPW	218	0.1000	1.10

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	LRGSRPATS	415	4.3000	48.86
2	VLRSAINSH	361	3.7800	42.95
3	FYADLTNKH	249	3.6800	41.82
4	LRGAGALTA	11	3.1000	35.23
5	VLLDLNTLL	108	2.6000	29.55
6	LARDQAFAA	116	2.0000	22.73
7	LKSDSIGAL	126	2.0000	22.73
8	LFSVGKAGI	274	2.0000	22.73
9	FVPVLRSAI	358	1.9000	21.59
10	VAPSAAEQQ	259	1.7000	19.32
11	FVNAWVSFY	205	1.6000	18.18
12	LLSGPGVMQ	70	1.5800	17.95
13	LSGPGVMQQ	71	1.4000	15.91
14	VLSEGPAYS	383	1.4000	15.91
15	LIGESRLFV	351	1.3000	14.77
16	VLRGSRPAT	414	1.3000	14.77
17	LLDLNTLLA	109	1.2000	13.64
18	VGKAGIALA	277	1.2000	13.64
19	LPIGPRGRA	306	1.2000	13.64
20	VGNLAVLSE	378	1.2000	13.64
21	LRPRMRVVN	48	1.1800	13.41
22	LAIAATSRR	324	1.1000	12.50
23	VMQQLATFC	76	1.0000	11.36
24	MQQLATFCA	77	1.0000	11.36
25	IGPRGRAAC	308	0.8000	9.09
26	VLMAWELTY	92	0.7000	7.95
27	VGQALIGES	347	0.6000	6.82
28	LRSAINSHG	362	0.6000	6.82

29	IKVRALLSG	65	0.5000	5.68
30	LFYNKQLFD	156	0.5000	5.68
31	LLRGAGALT	10	0.3000	3.41
32	WRYQTFDRA	288	0.3000	3.41
33	LMAWELTYA	93	0.2000	2.27
34	MNNGVPWSV	220	0.2000	2.27
35	IGVTGLAIA	319	0.2000	2.27
36	LNTLLARDQ	112	0.1000	1.14
37	FLFYNKQLF	155	0.1000	1.14
38	LFDDAGVPP	162	-0.1200	0
39	FQRRYPDIK	58	-0.2000	0
40	VRALLSGPG	67	-0.2000	0
41	LDLNTLLAR	110	-0.2000	0

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	LRGSRPATS	415	4.3000	48.86
2	VLRSAINSH	361	3.7800	42.95
3	FYADLTNKH	249	3.6800	41.82
4	LRGAGALTA	11	3.1000	35.23
5	VLLDLNTLL	108	2.6000	29.55
6	LARDQAFAA	116	2.0000	22.73
7	LKSDSIGAL	126	2.0000	22.73
8	LFSVGKAGI	274	2.0000	22.73
9	FVPVLRSAI	358	1.9000	21.59
10	VAPSAAEQQ	259	1.7000	19.32
11	FVNAWVSFY	205	1.6000	18.18
12	LLSGPGVMQ	70	1.5800	17.95
13	LSGPGVMQQ	71	1.4000	15.91
14	VLSEGPAYS	383	1.4000	15.91
15	LIGESRLFV	351	1.3000	14.77
16	VLRGSRPAT	414	1.3000	14.77

17	LLDLNTLLA	109	1.2000	13.64
18	VGKAGIALA	277	1.2000	13.64
19	LPIGPRGRA	306	1.2000	13.64
20	VGNLAVLSE	378	1.2000	13.64
21	LRPRMRVVN	48	1.1800	13.41
22	LAIAATSRR	324	1.1000	12.50
23	VMQQLATFC	76	1.0000	11.36
24	MQQLATFCA	77	1.0000	11.36
25	IGPRGRAAC	308	0.8000	9.09
26	VLMAWELTY	92	0.7000	7.95
27	VGQALIGES	347	0.6000	6.82
28	LRSAINSHG	362	0.6000	6.82
29	IKVRALLSG	65	0.5000	5.68
30	LFYNKQLFD	156	0.5000	5.68
31	LLRGAGALT	10	0.3000	3.41
32	WRYQTFDRA	288	0.3000	3.41
33	LMAWELTYA	93	0.2000	2.27
34	MNNGVPWSV	220	0.2000	2.27
35	IGVTGLAIA	319	0.2000	2.27
36	LNTLLARDQ	112	0.1000	1.14
37	FLFYNKQLF	155	0.1000	1.14
38	LFDDAGVPP	162	-0.1200	0
39	FQRRYPDIK	58	-0.2000	0
40	VRALLSGPG	67	-0.2000	0
41	LDLNTLLAR	110	-0.2000	0

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	LRGSRPATS	415	4.3000	48.86
2	VLRSAINSH	361	3.7800	42.95
3	FYADLTNKH	249	3.6800	41.82
4	LRGAGALTA	11	3.1000	35.23

5	VLLDLNTLL	108	2.6000	29.55
6	LARDQAFAA	116	2.0000	22.73
7	LKSDSIGAL	126	2.0000	22.73
8	LFSVGKAGI	274	2.0000	22.73
9	FVPVLRSAI	358	1.9000	21.59
10	VAPSAAEQQ	259	1.7000	19.32
11	FVNAWVSFY	205	1.6000	18.18
12	LLSGPGVMQ	70	1.5800	17.95
13	LSGPGVMQQ	71	1.4000	15.91
14	VLSEGPAYS	383	1.4000	15.91
15	LIGESRLFV	351	1.3000	14.77
16	VLRGSRPAT	414	1.3000	14.77
17	LLDLNTLLA	109	1.2000	13.64
18	VGKAGIALA	277	1.2000	13.64
19	LPIGPRGRA	306	1.2000	13.64
20	VGNLAVLSE	378	1.2000	13.64
21	LRPRMRVVN	48	1.1800	13.41
22	LAIAATSRR	324	1.1000	12.50
23	VMQQLATFC	76	1.0000	11.36
24	MQQLATFCA	77	1.0000	11.36
25	IGPRGRAAC	308	0.8000	9.09
26	VLMAWELTY	92	0.7000	7.95
27	VGQALIGES	347	0.6000	6.82
28	LRSAINSHG	362	0.6000	6.82
29	IKVRALLSG	65	0.5000	5.68
30	LFYNKQLFD	156	0.5000	5.68
31	LLRGAGALT	10	0.3000	3.41
32	WRYQTFDRA	288	0.3000	3.41
33	LMAWELTYA	93	0.2000	2.27
34	MNNGVPWSV	220	0.2000	2.27
35	IGVTGLAIA	319	0.2000	2.27
36	LNTLLARDQ	112	0.1000	1.14
37	FLFYNKQLF	155	0.1000	1.14
38	LFDDAGVPP	162	-0.1200	0

39	FQRRYPDIK	58	-0.2000	0
40	VRALLSGPG	67	-0.2000	0
41	LDLNTLLAR	110	-0.2000	0

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	FVNAWVSFY	205	4.1700	43.89
2	FVPVLRSAI	358	4.0700	42.84
3	LRGSRPATS	415	3.7000	38.95
4	FYADLTNKH	249	3.4100	35.89
5	LKSDSIGAL	126	3.3600	35.37
6	FLFYNKQLF	155	2.9000	30.53
7	FYAAGLFAM	212	2.7000	28.42
8	VLLDLNTLL	108	2.5600	26.95
9	LARDQAFAA	116	2.5000	26.32
10	FGPVLRGSR	411	2.4000	25.26
11	VLRGSRPAT	414	2.4000	25.26
12	FVKFATGPV	339	2.3000	24.21
13	LFSVGKAGI	274	1.9000	20.00
14	LAIAATSRR	324	1.8700	19.68
15	WGFVNAWVS	203	1.8000	18.95
16	FATGPVGQA	342	1.8000	18.95
17	LRGAGALTA	11	1.6000	16.84
18	VRALLSGPG	67	1.6000	16.84
19	YQTFDRADG	290	1.6000	16.84
20	LPIGPRGRA	306	1.6000	16.84
21	VLRSAINSH	361	1.5100	15.89
22	MQQLATFCA	77	1.5000	15.79
23	FAAELKSDS	122	1.4700	15.47
24	FFFAANPDE	39	1.4000	14.74
25	VGQALIGES	347	1.4000	14.74
26	MRVVNEFQR	52	1.3000	13.68

27	VKFATGPVG	340	1.3000	13.68
28	LRSAINSHG	362	1.2700	13.37
29	WVSFYAAGL	209	1.2600	13.26
30	FCAGGKCPD	83	1.2000	12.63
31	LDFDVAPLP	299	1.2000	12.63
32	LRPRMRVVN	48	1.1000	11.58
33	VGNLAVLSE	378	1.1000	11.58
34	MNNGVPWSV	220	1.0000	10.53
35	WRYQTFDRA	288	1.0000	10.53
36	FANAHRRVG	371	1.0000	10.53
37	FSVGKAGIA	275	0.8000	8.42
38	LIGESRLFV	351	0.8000	8.42
39	VLSEGPAYS	383	0.8000	8.42
40	FFAANPDEL	40	0.6600	6.95
41	FERRSLLRG	5	0.6000	6.32
42	FQRRYPDIK	58	0.6000	6.32
43	VAPLPIGPR	303	0.6000	6.32

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRGSRPATS	415	4.3000	48.86
2	VLRSAINSH	361	3.7800	42.95
3	FYADLTNKH	249	3.6800	41.82
4	LRGAGALTA	11	3.1000	35.23
5	VLLDLNTLL	108	2.6000	29.55
6	LARDQAFAA	116	2.0000	22.73
7	LKSDSIGAL	126	2.0000	22.73
8	LFSVGKAGI	274	2.0000	22.73
9	FVPVLRSAI	358	1.9000	21.59
10	VAPSAAEQQ	259	1.7000	19.32
11	FVNAWVSFY	205	1.6000	18.18
12	LLSGPGVMQ	70	1.5800	17.95

13	LSGPGVMQQ	71	1.4000	15.91
14	VLSEGPAYS	383	1.4000	15.91
15	LIGESRLFV	351	1.3000	14.77
16	VLRGSRPAT	414	1.3000	14.77
17	LLDLNTLLA	109	1.2000	13.64
18	VGKAGIALA	277	1.2000	13.64
19	LPIGPRGRA	306	1.2000	13.64
20	VGNLAVLSE	378	1.2000	13.64
21	LRPRMRVVN	48	1.1800	13.41
22	LAIAATSRR	324	1.1000	12.50
23	VMQQLATFC	76	1.0000	11.36
24	MQQLATFCA	77	1.0000	11.36
25	IGPRGRAAC	308	0.8000	9.09
26	VLMAWELTY	92	0.7000	7.95
27	VGQALIGES	347	0.6000	6.82
28	LRSAINSHG	362	0.6000	6.82
29	IKVRALLSG	65	0.5000	5.68
30	LFYNKQLFD	156	0.5000	5.68
31	LLRGAGALT	10	0.3000	3.41
32	WRYQTFDRA	288	0.3000	3.41
33	LMAWELTYA	93	0.2000	2.27
34	MNNGVPWSV	220	0.2000	2.27
35	IGVTGLAIA	319	0.2000	2.27
36	LNTLLARDQ	112	0.1000	1.14
37	FLFYNKQLF	155	0.1000	1.14
38	LFDDAGVPP	162	-0.1200	0
39	FQRRYPDIK	58	-0.2000	0
40	VRALLSGPG	67	-0.2000	0
41	LDLNTLLAR	110	-0.2000	0

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	FYADLTNKH	249	4.8800	56.74
2	LRGSRPATS	415	2.9000	33.72
3	VLLDLNTLL	108	2.6000	30.23
4	WRYQTFDRA	288	2.4000	27.91
5	VLSEGPAYS	383	2.4000	27.91
6	FVNAWVSFY	205	2.3000	26.74
7	LRGAGALTA	11	2.1000	24.42
8	LLDLNTLLA	109	2.1000	24.42
9	VLRSAINSH	361	2.0800	24.19
10	WELTYAELA	96	2.0000	23.26
11	MQQLATFCA	77	1.9000	22.09
12	LRSAINSHG	362	1.5000	17.44
13	LAIAATSRR	324	1.2000	13.95
14	FVKFATGPV	339	1.1000	12.79
15	VMQQLATFC	76	0.8000	9.30
16	VAPSAAEQQ	259	0.8000	9.30
17	VRALLSGPG	67	0.7000	8.14
18	VGNLAVLSE	378	0.7000	8.14
19	FFFAANPDE	39	0.5000	5.81
20	WVSFYAAGL	209	0.4000	4.65
21	FTFNGGQYA	138	0.2000	2.33
22	YNKQLFDDA	158	0.2000	2.33
23	YADLTNKHK	250	0.2000	2.33
24	LARDQAFAA	116	0.1000	1.16
25	WSFAEFLDA	179	0.1000	1.16
26	LNTLLARDQ	112	-0.1000	0
27	FDHDGFLEA	238	-0.1000	0
28	WEKIAALMD	400	-0.1000	0
29	FAMNNGVPW	218	-0.1200	0
30	WGFVNAWVS	203	-0.3000	0
31	FAAELKSDS	122	-0.4000	0
32	IGVTGLAIA	319	-0.4000	0
33	FFAANPDEL	40	-0.5000	0
34	LSGPGVMQQ	71	-0.5000	0

35	MAWELTYAE	94	-0.5000	0
36	VVNEFQRRY	54	-0.6000	0
37	FQRRYPDIK	58	-0.6000	0
38	LFAMNNGVP	217	-0.6000	0
39	VGKAGIALA	277	-0.6000	0
40	LIGESRLFV	351	-0.6000	0
41	VPVLRSAIN	359	-0.6000	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	VNAWVSFYA	206	3.9000	40.62
2	LRGAGALTA	11	3.4000	35.42
3	MQQLATFCA	77	3.0000	31.25
4	LNTLLARDQ	112	2.4000	25.00
5	LRSAINSHG	362	2.3000	23.96
6	LRGSRPATS	415	2.1000	21.88
7	LLDLNTLLA	109	2.0000	20.83
8	LAIAATSRR	324	2.0000	20.83
9	LMAWELTYA	93	1.7000	17.71
10	WGFVNAWVS	203	1.7000	17.71
11	IKVRALLSG	65	1.5000	15.62
12	MNNGVPWSV	220	1.3000	13.54
13	VLRSAINSH	361	1.2800	13.33
14	FVNAWVSFY	205	1.1000	11.46
15	INSHGFANA	366	1.1000	11.46
16	LSGPGVMQQ	71	0.8000	8.33
17	VMQQLATFC	76	0.8000	8.33
18	LYETFTFNG	134	0.6000	6.25
19	WVSFYAAGL	209	0.6000	6.25
20	LFVPVLRSA	357	0.6000	6.25
21	VGNLAVLSE	378	0.6000	6.25
22	LPVTPAWEK	394	0.6000	6.25

23	LLARDQAFA	115	0.5000	5.21
24	FVKFATGPV	339	0.5000	5.21
25	VGKAGIALA	277	0.4000	4.17
26	FYADLTNKH	249	0.1800	1.88
27	VLLDLNTLL	108	0.1000	1.04
28	VQFYADLTN	247	0.1000	1.04
29	LRPRMRVVN	48	-0.1000	0
30	LADRGVLLD	103	-0.1000	0
31	VPRMNPTHL	228	-0.1000	0
32	LAPWAAGCA	22	-0.2000	0
33	LTFFFAANP	37	-0.2000	0
34	FERRSLLRG	5	-0.3000	0
35	LLSGPGVMQ	70	-0.3000	0
36	VLSEGPAYS	383	-0.4000	0
37	VNKPFERRS	1	-0.5000	0
38	VVNEFQRRY	54	-0.5000	0
39	FQRRYPDIK	58	-0.5000	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	MQQLATFCA	77	4.0500	46.02
2	LRSAINSHG	362	3.2000	36.36
3	LLDLNTLLA	109	2.9000	32.95
4	LAIAATSRR	324	2.9000	32.95
5	LRGAGALTA	11	2.7000	30.68
6	LRGSRPATS	415	2.4000	27.27
7	FVKFATGPV	339	2.1000	23.86
8	VRALLSGPG	67	2.0000	22.73
9	FVNAWVSFY	205	2.0000	22.73
10	VNAWVSFYA	206	1.7000	19.32
11	VLRSAINSH	361	1.6800	19.09
12	VLLDLNTLL	108	1.6000	18.18

13	VMQQLATFC	76	1.5000	17.05
14	VGNLAVLSE	378	1.5000	17.05
15	FYADLTNKH	249	1.4800	16.82
16	LNTLLARDQ	112	1.4000	15.91
17	LFAMNNGVP	217	1.4000	15.91
18	VPRMNPTHL	228	1.4000	15.91
19	WVSFYAAGL	209	1.3000	14.77
20	WGFVNAWVS	203	0.8000	9.09
21	VLSEGPAYS	383	0.8000	9.09
22	LSGPGVMQQ	71	0.7000	7.95
23	VPVLRSAIN	359	0.6000	6.82
24	LTFFFAANP	37	0.5000	5.68
25	VGKAGIALA	277	0.4000	4.55
26	LMAWELTYA	93	0.3500	3.98
27	VTGLAIAAT	321	-0.1000	0
28	VGQALIGES	347	-0.1000	0
29	MRVVNEFQR	52	-0.2500	0
30	WRYQTFDRA	288	-0.3000	0
31	FVPVLRSAI	358	-0.3000	0
32	LYETFTFNG	134	-0.3500	0
33	LARDQAFAA	116	-0.4500	0
34	LATFCAGGK	80	-0.5000	0
35	VQFYADLTN	247	-0.6000	0
36	VAPSAAEQQ	259	-0.6000	0
37	VLMAWELTY	92	-0.7000	0
38	FFFAANPDE	39	-0.8000	0
39	LAPWAAGCA	22	-0.9500	0
40	VAPLPIGPR	303	-1.0000	0
41	IGVTGLAIA	319	-1.0000	0
42	MAWELTYAE	94	-1.1000	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	FVNAWVSFY	205	4.1000	43.62
2	FYADLTNKH	249	3.7000	39.36
3	LRSAINSHG	362	3.5000	37.23
4	VGNLAVLSE	378	3.5000	37.23
5	FVKFATGPV	339	3.4000	36.17
6	WVSFYAAGL	209	3.3000	35.11
7	FFFAANPDE	39	3.2000	34.04
8	MQQLATFCA	77	3.0500	32.45
9	WEKIAALMD	400	2.5000	26.60
10	VRALLSGPG	67	2.3000	24.47
11	LLDLNTLLA	109	1.9000	20.21
12	LAIAATSRR	324	1.9000	20.21
13	VLRSAINSH	361	1.9000	20.21
14	WGFVNAWVS	203	1.8000	19.15
15	WERPWSFAE	175	1.7500	18.62
16	LRGAGALTA	11	1.7000	18.09
17	VLLDLNTLL	108	1.6000	17.02
18	VPVLRSAIN	359	1.6000	17.02
19	VPRMNPTHL	228	1.4000	14.89
20	LRGSRPATS	415	1.4000	14.89
21	LNTLLARDQ	112	1.2000	12.77
22	YETFTFNGG	135	1.0000	10.64
23	MAWELTYAE	94	0.9000	9.57
24	FVPVLRSAI	358	0.9000	9.57
25	LFAMNNGVP	217	0.8000	8.51
26	VNAWVSFYA	206	0.7000	7.45
27	WRYQTFDRA	288	0.7000	7.45
28	WEFVKFATG	337	0.6000	6.38
29	LSGPGVMQQ	71	0.5000	5.32
30	VMQQLATFC	76	0.5000	5.32
31	FYAAGLFAM	212	0.4500	4.79
32	VQFYADLTN	247	0.4000	4.26
33	YQTFDRADG	290	0.1000	1.06

34	LYETFTFNG	134	-0.0500	0
35	LTFFFAANP	37	-0.1000	0
36	MNPTHLNFD	231	-0.2000	0
37	VTGLAIAAT	321	-0.2000	0
38	VLSEGPAYS	383	-0.2000	0
39	FYNKQLFDD	157	-0.2500	0
40	LFYNKQLFD	156	-0.3000	0
41	WSFAEFLDA	179	-0.3000	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	FVKFATGPV	339	3.1000	35.23
2	MQQLATFCA	77	3.0500	34.66
3	FVNAWVSFY	205	3.0000	34.09
4	FYADLTNKH	249	2.4800	28.18
5	WVSFYAAGL	209	2.3000	26.14
6	LRSAINSHG	362	2.2000	25.00
7	LLDLNTLLA	109	1.9000	21.59
8	LAIAATSRR	324	1.9000	21.59
9	WGFVNAWVS	203	1.8000	20.45
10	LRGAGALTA	11	1.7000	19.32
11	LRGSRPATS	415	1.4000	15.91
12	VRALLSGPG	67	1.0000	11.36
13	VNAWVSFYA	206	0.7000	7.95
14	WRYQTFDRA	288	0.7000	7.95
15	FVPVLRSAI	358	0.7000	7.95
16	VLRSAINSH	361	0.6800	7.73
17	VLLDLNTLL	108	0.6000	6.82
18	VMQQLATFC	76	0.5000	5.68
19	VGNLAVLSE	378	0.5000	5.68
20	LNTLLARDQ	112	0.4000	4.55
21	LFAMNNGVP	217	0.4000	4.55

22	VPRMNPTHL	228	0.4000	4.55
23	FFFAANPDE	39	0.2000	2.27
24	VLSEGPAYS	383	-0.2000	0
25	WEKIAALMD	400	-0.2000	0
26	LSGPGVMQQ	71	-0.3000	0
27	YETFTFNGG	135	-0.3000	0
28	WSFAEFLDA	179	-0.3000	0
29	VPVLRSAIN	359	-0.4000	0
30	LTFFFAANP	37	-0.5000	0
31	WELTYAELA	96	-0.5000	0
32	YADLTNKHK	250	-0.6000	0
33	VGKAGIALA	277	-0.6000	0
34	LMAWELTYA	93	-0.6500	0
35	FYAAGLFAM	212	-0.6500	0
36	WEFVKFATG	337	-0.7000	0
37	FAEFLDAAQ	181	-0.8000	0
38	VTGLAIAAT	321	-1.1000	0
39	VGQALIGES	347	-1.1000	0
40	YQTFDRADG	290	-1.2000	0
41	MRVVNEFQR	52	-1.2500	0
42	WERPWSFAE	175	-1.2500	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	LRSAINSHG	362	4.5000	47.87
2	VGNLAVLSE	378	4.5000	47.87
3	MQQLATFCA	77	4.0500	43.09
4	VRALLSGPG	67	3.3000	35.11
5	FVNAWVSFY	205	3.1000	32.98
6	LLDLNTLLA	109	2.9000	30.85
7	LAIAATSRR	324	2.9000	30.85
8	VLRSAINSH	361	2.9000	30.85

9	LRGAGALTA	11	2.7000	28.72
10	FYADLTNKH	249	2.7000	28.72
11	VLLDLNTLL	108	2.6000	27.66
12	VPVLRSAIN	359	2.6000	27.66
13	VPRMNPTHL	228	2.4000	25.53
14	FVKFATGPV	339	2.4000	25.53
15	LRGSRPATS	415	2.4000	25.53
16	WVSFYAAGL	209	2.3000	24.47
17	FFFAANPDE	39	2.2000	23.40
18	LNTLLARDQ	112	2.2000	23.40
19	MAWELTYAE	94	1.9000	20.21
20	LFAMNNGVP	217	1.8000	19.15
21	VNAWVSFYA	206	1.7000	18.09
22	LSGPGVMQQ	71	1.5000	15.96
23	VMQQLATFC	76	1.5000	15.96
24	WEKIAALMD	400	1.5000	15.96
25	VQFYADLTN	247	1.4000	14.89
26	LYETFTFNG	134	0.9500	10.11
27	LTFFFAANP	37	0.9000	9.57
28	WGFVNAWVS	203	0.8000	8.51
29	MNPTHLNFD	231	0.8000	8.51
30	VTGLAIAAT	321	0.8000	8.51
31	VLSEGPAYS	383	0.8000	8.51
32	WERPWSFAE	175	0.7500	7.98
33	LFYNKQLFD	156	0.7000	7.45
34	LTGLSQAVD	424	0.7000	7.45
35	VLMAWELTY	92	0.4000	4.26
36	VGKAGIALA	277	0.4000	4.26
37	LMAWELTYA	93	0.3500	3.72
38	LEAVQFYAD	244	0.3000	3.19
39	VAPSAAEQQ	259	0.2000	2.13
40	VGQALIGES	347	-0.1000	0
41	FVPVLRSAI	358	-0.1000	0

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	FYADLTNKH	249	4.3000	47.78
2	FVNAWVSFY	205	3.6000	40.00
3	VLLDLNTLL	108	3.5600	39.56
4	LRGSRPATS	415	3.3000	36.67
5	LRSAINSHG	362	2.9000	32.22
6	VLSEGPAYS	383	2.8000	31.11
7	LAIAATSRR	324	2.7000	30.00
8	WRYQTFDRA	288	2.4000	26.67
9	LRGAGALTA	11	2.1000	23.33
10	VRALLSGPG	67	2.1000	23.33
11	LLDLNTLLA	109	2.1000	23.33
12	FVKFATGPV	339	2.1000	23.33
13	VGNLAVLSE	378	2.1000	23.33
14	WELTYAELA	96	2.0000	22.22
15	FFFAANPDE	39	1.9000	21.11
16	MQQLATFCA	77	1.9000	21.11
17	VLRSAINSH	361	1.5000	16.67
18	WVSFYAAGL	209	1.3600	15.11
19	WEKIAALMD	400	1.0000	11.11
20	MAWELTYAE	94	0.9000	10.00
21	VMQQLATFC	76	0.8000	8.89
22	VVNEFQRRY	54	0.7000	7.78
23	LYETFTFNG	134	0.7000	7.78
24	FAANPDELR	41	0.5000	5.56
25	FFAANPDEL	40	0.4600	5.11
26	LFAMNNGVP	217	0.4000	4.44
27	LIGESRLFV	351	0.4000	4.44
28	YADLTNKHK	250	0.3000	3.33
29	LKSDSIGAL	126	0.2600	2.89
30	FTFNGGQYA	138	0.2000	2.22

31	YNKQLFDDA	158	0.2000	2.22
32	VPVLRSAIN	359	0.2000	2.22
33	LARDQAFAA	116	0.1000	1.11
34	LFYNKQLFD	156	0.1000	1.11
35	WSFAEFLDA	179	0.1000	1.11
36	WGFVNAWVS	203	0.1000	1.11
37	VAPSAAEQQ	259	0.1000	1.11
38	VPRMNPTHL	228	-0.0400	0
39	FYAAGLFAM	212	-0.1000	0

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	MQQLATFCA	77	4.0500	46.02
2	LRSAINSHG	362	3.2000	36.36
3	LLDLNTLLA	109	2.9000	32.95
4	LAIAATSRR	324	2.9000	32.95
5	LRGAGALTA	11	2.7000	30.68
6	LRGSRPATS	415	2.4000	27.27
7	FVKFATGPV	339	2.1000	23.86
8	VRALLSGPG	67	2.0000	22.73
9	FVNAWVSFY	205	2.0000	22.73
10	VNAWVSFYA	206	1.7000	19.32
11	VLRSAINSH	361	1.6800	19.09
12	VLLDLNTLL	108	1.6000	18.18
13	VMQQLATFC	76	1.5000	17.05
14	VGNLAVLSE	378	1.5000	17.05
15	FYADLTNKH	249	1.4800	16.82
16	LNTLLARDQ	112	1.4000	15.91
17	LFAMNNGVP	217	1.4000	15.91
18	VPRMNPTHL	228	1.4000	15.91
19	WVSFYAAGL	209	1.3000	14.77
20	WGFVNAWVS	203	0.8000	9.09

21	VLSEGPAYS	383	0.8000	9.09
22	LSGPGVMQQ	71	0.7000	7.95
23	VPVLRSAIN	359	0.6000	6.82
24	LTFFFAANP	37	0.5000	5.68
25	VGKAGIALA	277	0.4000	4.55
26	LMAWELTYA	93	0.3500	3.98
27	VTGLAIAAT	321	-0.1000	0
28	VGQALIGES	347	-0.1000	0
29	MRVVNEFQR	52	-0.2500	0
30	WRYQTFDRA	288	-0.3000	0
31	FVPVLRSAI	358	-0.3000	0
32	LYETFTFNG	134	-0.3500	0
33	LARDQAFAA	116	-0.4500	0
34	LATFCAGGK	80	-0.5000	0
35	VQFYADLTN	247	-0.6000	0
36	VAPSAAEQQ	259	-0.6000	0
37	VLMAWELTY	92	-0.7000	0
38	FFFAANPDE	39	-0.8000	0
39	LAPWAAGCA	22	-0.9500	0
40	VAPLPIGPR	303	-1.0000	0
41	IGVTGLAIA	319	-1.0000	0
42	MAWELTYAE	94	-1.1000	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	FYADLTNKH	249	4.8800	56.74
2	LRGSRPATS	415	2.9000	33.72
3	VLLDLNTLL	108	2.6000	30.23
4	WRYQTFDRA	288	2.4000	27.91
5	VLSEGPAYS	383	2.4000	27.91
6	FVNAWVSFY	205	2.3000	26.74
7	LRGAGALTA	11	2.1000	24.42

8	LLDLNTLLA	109	2.1000	24.42
9	VLRSAINSH	361	2.0800	24.19
10	WELTYAELA	96	2.0000	23.26
11	MQQLATFCA	77	1.9000	22.09
12	LRSAINSHG	362	1.5000	17.44
13	LAIAATSRR	324	1.2000	13.95
14	FVKFATGPV	339	1.1000	12.79
15	VMQQLATFC	76	0.8000	9.30
16	VAPSAAEQQ	259	0.8000	9.30
17	VRALLSGPG	67	0.7000	8.14
18	VGNLAVLSE	378	0.7000	8.14
19	FFFAANPDE	39	0.5000	5.81
20	WVSFYAAGL	209	0.4000	4.65
21	FTFNGGQYA	138	0.2000	2.33
22	YNKQLFDDA	158	0.2000	2.33
23	YADLTNKHK	250	0.2000	2.33
24	LARDQAFAA	116	0.1000	1.16
25	WSFAEFLDA	179	0.1000	1.16
26	LNTLLARDQ	112	-0.1000	0
27	FDHDGFLEA	238	-0.1000	0
28	WEKIAALMD	400	-0.1000	0
29	FAMNNGVPW	218	-0.1200	0
30	WGFVNAWVS	203	-0.3000	0
31	FAAELKSDS	122	-0.4000	0
32	IGVTGLAIA	319	-0.4000	0
33	FFAANPDEL	40	-0.5000	0
34	LSGPGVMQQ	71	-0.5000	0
35	MAWELTYAE	94	-0.5000	0
36	VVNEFQRRY	54	-0.6000	0
37	FQRRYPDIK	58	-0.6000	0
38	LFAMNNGVP	217	-0.6000	0
39	VGKAGIALA	277	-0.6000	0
40	LIGESRLFV	351	-0.6000	0
41	VPVLRSAIN	359	-0.6000	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	FVPVLRSAI	358	6.0000	51.72
2	WVSFYAAGL	209	5.9000	50.86
3	FVKFATGPV	339	4.2200	36.38
4	FVNAWVSFY	205	4.2000	36.21
5	FYAAGLFAM	212	4.1000	35.34
6	LRGAGALTA	11	3.6000	31.03
7	YPDIKVRAL	62	3.5000	30.17
8	WELTYAELA	96	3.4000	29.31
9	WGFVNAWVS	203	3.3000	28.45
10	LFSVGKAGI	274	3.2000	27.59
11	VLLDLNTLL	108	3.1000	26.72
12	FDRADGLDF	293	3.1000	26.72
13	FLFYNKQLF	155	3.0000	25.86
14	VLRSAINSH	361	2.9000	25.00
15	VPRMNPTHL	228	2.6000	22.41
16	FFAANPDEL	40	2.4000	20.69
17	VLMAWELTY	92	2.2000	18.97
18	WEKIAALMD	400	2.2000	18.97
19	FAMNNGVPW	218	2.1000	18.10
20	MNNGVPWSV	220	2.1000	18.10
21	LRGSRPATS	415	2.1000	18.10
22	WERPWSFAE	175	2.0000	17.24
23	LIGESRLFV	351	2.0000	17.24
24	WSFAEFLDA	179	1.9000	16.38
25	MSTADLFSV	269	1.9000	16.38
26	IALAGHWRY	282	1.7000	14.66
27	LKSDSIGAL	126	1.6000	13.79
28	LYETFTFNG	134	1.5200	13.10
29	MQQLATFCA	77	1.4200	12.24
30	MRVVNEFQR	52	1.4000	12.07

31	VNAWVSFYA	206	1.4000	12.07
32	VGNLAVLSE	378	1.2000	10.34
33	VVNEFQRRY	54	0.9000	7.76
34	MNPTHLNFD	231	0.8000	6.90
35	FLEAVQFYA	243	0.8000	6.90
36	VAPSAAEQQ	259	0.8000	6.90
37	VSFYAAGLF	210	0.7000	6.03
38	LPVTPAWEK	394	0.7000	6.03
39	LRSAINSHG	362	0.6000	5.17
40	FFFAANPDE	39	0.5000	4.31
41	IGVTGLAIA	319	0.5000	4.31
42	LSQAVDEVL	427	0.5000	4.31
43	FYADLTNKH	249	0.4200	3.62

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	FVPVLRSAI	358	6.0000	51.72
2	WVSFYAAGL	209	5.9000	50.86
3	FVKFATGPV	339	4.2200	36.38
4	FVNAWVSFY	205	4.2000	36.21
5	FYAAGLFAM	212	4.1000	35.34
6	LRGAGALTA	11	3.6000	31.03
7	YPDIKVRAL	62	3.5000	30.17
8	WELTYAELA	96	3.4000	29.31
9	WGFVNAWVS	203	3.3000	28.45
10	LFSVGKAGI	274	3.2000	27.59
11	VLLDLNTLL	108	3.1000	26.72
12	FDRADGLDF	293	3.1000	26.72
13	FLFYNKQLF	155	3.0000	25.86
14	VLRSAINSH	361	2.9000	25.00
15	VPRMNPTHL	228	2.6000	22.41
16	FFAANPDEL	40	2.4000	20.69

17	VLMAWELTY	92	2.2000	18.97
18	WEKIAALMD	400	2.2000	18.97
19	FAMNNGVPW	218	2.1000	18.10
20	MNNGVPWSV	220	2.1000	18.10
21	LRGSRPATS	415	2.1000	18.10
22	WERPWSFAE	175	2.0000	17.24
23	LIGESRLFV	351	2.0000	17.24
24	WSFAEFLDA	179	1.9000	16.38
25	MSTADLFSV	269	1.9000	16.38
26	IALAGHWRY	282	1.7000	14.66
27	LKSDSIGAL	126	1.6000	13.79
28	LYETFTFNG	134	1.5200	13.10
29	MQQLATFCA	77	1.4200	12.24
30	MRVVNEFQR	52	1.4000	12.07
31	VNAWVSFYA	206	1.4000	12.07
32	VGNLAVLSE	378	1.2000	10.34
33	VVNEFQRRY	54	0.9000	7.76
34	MNPTHLNFD	231	0.8000	6.90
35	FLEAVQFYA	243	0.8000	6.90
36	VAPSAAEQQ	259	0.8000	6.90
37	VSFYAAGLF	210	0.7000	6.03
38	LPVTPAWEK	394	0.7000	6.03
39	LRSAINSHG	362	0.6000	5.17
40	FFFAANPDE	39	0.5000	4.31
41	IGVTGLAIA	319	0.5000	4.31
42	LSQAVDEVL	427	0.5000	4.31
43	FYADLTNKH	249	0.4200	3.62

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	LRPRMRVVN	48	4.3000	50.00
2	FLFYNKQLF	155	4.0000	46.51

3	FYNKQLFDD	157	4.0000	46.51
4	FERRSLLRG	5	3.3000	38.37
5	IKVRALLSG	65	3.1000	36.05
6	IGPRGRAAC	308	3.1000	36.05
7	YQTFDRADG	290	3.0000	34.88
8	VGNLAVLSE	378	2.9000	33.72
9	WVSFYAAGL	209	2.8000	32.56
10	FVNAWVSFY	205	2.6000	30.23
11	FVKFATGPV	339	2.5000	29.07
12	FVPVLRSAI	358	2.3000	26.74
13	LLARDQAFA	115	2.0000	23.26
14	LADRGVLLD	103	1.9000	22.09
15	VRALLSGPG	67	1.6000	18.60
16	LRGSRPATS	415	1.6000	18.60
17	LFSVGKAGI	274	1.5000	17.44
18	FQRRYPDIK	58	1.3000	15.12
19	FCAGGKCPD	83	1.3000	15.12
20	LNTLLARDQ	112	1.2000	13.95
21	FANAHRRVG	371	1.2000	13.95
22	LRGAGALTA	11	1.1000	12.79
23	FFFAANPDE	39	1.1000	12.79
24	WGFVNAWVS	203	1.1000	12.79
25	VSFYAAGLF	210	1.1000	12.79
26	VQFYADLTN	247	1.1000	12.79
27	LTNKHKVAP	253	1.1000	12.79
28	WEKIAALMD	400	1.1000	12.79
29	LFYNKQLFD	156	1.0000	11.63
30	FYAAGLFAM	212	0.9000	10.47
31	MQQLATFCA	77	0.8000	9.30
32	FYADLTNKH	249	0.7000	8.14
33	FGPVLRGSR	411	0.6000	6.98
34	LTGLSQAVD	424	0.6000	6.98
35	VGQALIGES	347	0.4000	4.65
36	VLRSAINSH	361	0.4000	4.65

37	VLSEGPAYS	383	0.4000	4.65
38	VTGLAIAAT	321	0.3000	3.49
39	YFGPVLRGS	410	0.3000	3.49
40	VGKAGIALA	277	0.2000	2.33
41	VPVLRSAIN	359	0.2000	2.33
42	LSGPGVMQQ	71	0.1000	1.16
43	WERPWSFAE	175	0.1000	1.16

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	FLFYNKQLF	155	3.1000	38.75
2	IGPRGRAAC	308	3.1000	38.75
3	LRPRMRVVN	48	2.3000	28.75
4	FVKFATGPV	339	2.2000	27.50
5	FVPVLRSAI	358	2.1000	26.25
6	FERRSLLRG	5	2.0000	25.00
7	FQRRYPDIK	58	2.0000	25.00
8	LLARDQAFA	115	2.0000	25.00
9	IKVRALLSG	65	1.8000	22.50
10	WVSFYAAGL	209	1.8000	22.50
11	YQTFDRADG	290	1.7000	21.25
12	LRGSRPATS	415	1.6000	20.00
13	FVNAWVSFY	205	1.5000	18.75
14	FYNKQLFDD	157	1.3000	16.25
15	LFSVGKAGI	274	1.3000	16.25
16	LRGAGALTA	11	1.1000	13.75
17	WGFVNAWVS	203	1.1000	13.75
18	MQQLATFCA	77	0.8000	10.00
19	LTNKHKVAP	253	0.7000	8.75
20	FGPVLRGSR	411	0.6000	7.50
21	LNTLLARDQ	112	0.4000	5.00
22	VGQALIGES	347	0.4000	5.00

23	VLSEGPAYS	383	0.4000	5.00
24	VRALLSGPG	67	0.3000	3.75
25	YFGPVLRGS	410	0.3000	3.75
26	VSFYAAGLF	210	0.2000	2.50
27	VGKAGIALA	277	0.2000	2.50
28	LLDLNTLLA	109	-0.1000	0
29	FANAHRRVG	371	-0.1000	0
30	VGNLAVLSE	378	-0.1000	0
31	FYAAGLFAM	212	-0.2000	0
32	FAAELKSDS	122	-0.3000	0
33	FATGPVGQA	342	-0.3000	0
34	LPIGPRGRA	306	-0.5000	0
35	FYADLTNKH	249	-0.5200	0
36	VTGLAIAAT	321	-0.6000	0
37	LSGPGVMQQ	71	-0.7000	0
38	LIGESRLFV	351	-0.7000	0
39	LADRGVLLD	103	-0.8000	0
40	VAPLPIGPR	303	-0.8000	0
41	IGVTGLAIA	319	-0.8000	0
42	VLRSAINSH	361	-0.8200	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	IGPRGRAAC	308	4.1000	51.25
2	LRPRMRVVN	48	3.3000	41.25
3	LLARDQAFA	115	3.0000	37.50
4	IKVRALLSG	65	2.8000	35.00
5	LRGSRPATS	415	2.6000	32.50
6	LFSVGKAGI	274	2.3000	28.75
7	LRGAGALTA	11	2.1000	26.25
8	FLFYNKQLF	155	2.1000	26.25
9	MQQLATFCA	77	1.8000	22.50

10	LTNKHKVAP	253	1.7000	21.25
11	LNTLLARDQ	112	1.4000	17.50
12	VGQALIGES	347	1.4000	17.50
13	VLSEGPAYS	383	1.4000	17.50
14	VRALLSGPG	67	1.3000	16.25
15	VSFYAAGLF	210	1.2000	15.00
16	VGKAGIALA	277	1.2000	15.00
17	FVKFATGPV	339	1.2000	15.00
18	FVPVLRSAI	358	1.1000	13.75
19	FERRSLLRG	5	1.0000	12.50
20	FQRRYPDIK	58	1.0000	12.50
21	LLDLNTLLA	109	0.9000	11.25
22	VGNLAVLSE	378	0.9000	11.25
23	WVSFYAAGL	209	0.8000	10.00
24	YQTFDRADG	290	0.7000	8.75
25	FVNAWVSFY	205	0.5000	6.25
26	LPIGPRGRA	306	0.5000	6.25
27	VTGLAIAAT	321	0.4000	5.00
28	LSGPGVMQQ	71	0.3000	3.75
29	FYNKQLFDD	157	0.3000	3.75
30	LIGESRLFV	351	0.3000	3.75
31	LADRGVLLD	103	0.2000	2.50
32	VAPLPIGPR	303	0.2000	2.50
33	IGVTGLAIA	319	0.2000	2.50
34	VLRSAINSH	361	0.1800	2.25
35	MVNKPFERR	0	0.1000	1.25
36	WGFVNAWVS	203	0.1000	1.25
37	VQFYADLTN	247	0.1000	1.25
38	LFVPVLRSA	357	-0.1000	0
39	LAPWAAGCA	22	-0.2000	0

ALLELE: DRB1_0806	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LRPRMRVVN	48	5.3000	61.63
2	IKVRALLSG	65	4.1000	47.67
3	IGPRGRAAC	308	4.1000	47.67
4	VGNLAVLSE	378	3.9000	45.35
5	LLARDQAFA	115	3.0000	34.88
6	FLFYNKQLF	155	3.0000	34.88
7	FYNKQLFDD	157	3.0000	34.88
8	LADRGVLLD	103	2.9000	33.72
9	VRALLSGPG	67	2.6000	30.23
10	LRGSRPATS	415	2.6000	30.23
11	LFSVGKAGI	274	2.5000	29.07
12	FERRSLLRG	5	2.3000	26.74
13	LNTLLARDQ	112	2.2000	25.58
14	LRGAGALTA	11	2.1000	24.42
15	VSFYAAGLF	210	2.1000	24.42
16	VQFYADLTN	247	2.1000	24.42
17	LTNKHKVAP	253	2.1000	24.42
18	LFYNKQLFD	156	2.0000	23.26
19	YQTFDRADG	290	2.0000	23.26
20	MQQLATFCA	77	1.8000	20.93
21	WVSFYAAGL	209	1.8000	20.93
22	FVNAWVSFY	205	1.6000	18.60
23	LTGLSQAVD	424	1.6000	18.60
24	FVKFATGPV	339	1.5000	17.44
25	VGQALIGES	347	1.4000	16.28
26	VLRSAINSH	361	1.4000	16.28
27	VLSEGPAYS	383	1.4000	16.28
28	VTGLAIAAT	321	1.3000	15.12
29	FVPVLRSAI	358	1.3000	15.12
30	VGKAGIALA	277	1.2000	13.95
31	VPVLRSAIN	359	1.2000	13.95
32	LSGPGVMQQ	71	1.1000	12.79
33	LLDLNTLLA	109	0.9000	10.47

34	VVNEFQRRY	54	0.8000	9.30
35	VLMAWELTY	92	0.8000	9.30
36	LRSAINSHG	362	0.8000	9.30
37	LIGESRLFV	351	0.6000	6.98
38	LKSDSIGAL	126	0.5000	5.81
39	LPIGPRGRA	306	0.5000	5.81
40	LTFFFAANP	37	0.4000	4.65
41	IAATSRRKD	326	0.4000	4.65
42	FQRRYPDIK	58	0.3000	3.49
43	FCAGGKCPD	83	0.3000	3.49

ALLELE: DRB1_0813	Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	FLFYNKQLF	155	4.1000	47.13
2	FVPVLRSAI	358	3.9000	44.83
3	LRPRMRVVN	48	3.3000	37.93
4	FVNAWVSFY	205	3.3000	37.93
5	FQRRYPDIK	58	3.2000	36.78
6	IGPRGRAAC	308	3.1000	35.63
7	FERRSLLRG	5	2.6000	29.89
8	IKVRALLSG	65	2.4000	27.59
9	FYNKQLFDD	157	2.1500	24.71
10	LLARDQAFA	115	2.0000	22.99
11	WVSFYAAGL	209	1.8000	20.69
12	LRGAGALTA	11	1.7000	19.54
13	LTNKHKVAP	253	1.7000	19.54
14	YQTFDRADG	290	1.7000	19.54
15	MQQLATFCA	77	1.6500	18.97
16	WGFVNAWVS	203	1.6000	18.39
17	LRGSRPATS	415	1.6000	18.39
18	FAAELKSDS	122	1.5000	17.24
19	FVKFATGPV	339	1.5000	17.24

20	FYADLTNKH	249	1.4800	17.01
21	LFSVGKAGI	274	1.3000	14.94
22	VLRSAINSH	361	1.1800	13.56
23	MVNKPFERR	0	0.8000	9.20
24	LAIAATSRR	324	0.8000	9.20
25	LMAWELTYA	93	0.7000	8.05
26	FYAAGLFAM	212	0.6500	7.47
27	LLDLNTLLA	109	0.5000	5.75
28	VPRMNPTHL	228	0.5000	5.75
29	VGNLAVLSE	378	0.5000	5.75
30	VLSEGPAYS	383	0.4000	4.60
31	LSGPGVMQQ	71	0.3000	3.45
32	LRSAINSHG	362	0.3000	3.45
33	VGKAGIALA	277	0.2000	2.30
34	LNTLLARDQ	112	0.1000	1.15
35	FTFNGGQYA	138	-0.1000	0
36	LIGESRLFV	351	-0.1000	0
37	FGPVLRGSR	411	-0.1000	0
38	LADRGVLLD	103	-0.2000	0
39	VQFYADLTN	247	-0.3000	0
40	VGQALIGES	347	-0.3000	0
41	VNAWVSFYA	206	-0.3500	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	FERRSLLRG	5	5.1000	50.50
2	IKVRALLSG	65	4.9000	48.51
3	LRPRMRVVN	48	4.8000	47.52
4	VGNLAVLSE	378	4.7000	46.53
5	FYNKQLFDD	157	4.5000	44.55
6	FLFYNKQLF	155	4.1000	40.59
7	LADRGVLLD	103	3.7000	36.63

8	IGPRGRAAC	308	3.1000	30.69
9	YQTFDRADG	290	3.0000	29.70
10	LRGAGALTA	11	2.9000	28.71
11	VQFYADLTN	247	2.9000	28.71
12	WEKIAALMD	400	2.9000	28.71
13	LFYNKQLFD	156	2.8000	27.72
14	WVSFYAAGL	209	2.8000	27.72
15	FVNAWVSFY	205	2.6000	25.74
16	FVKFATGPV	339	2.6000	25.74
17	FVPVLRSAI	358	2.3000	22.77
18	FFFAANPDE	39	2.2500	22.28
19	LLARDQAFA	115	2.0000	19.80
20	WGFVNAWVS	203	1.9000	18.81
21	VRALLSGPG	67	1.7000	16.83
22	LSGPGVMQQ	71	1.7000	16.83
23	LLDLNTLLA	109	1.7000	16.83
24	VLMAWELTY	92	1.6000	15.84
25	LTNKHKVAP	253	1.6000	15.84
26	LRGSRPATS	415	1.6000	15.84
27	LFSVGKAGI	274	1.5000	14.85
28	LNTLLARDQ	112	1.4000	13.86
29	FYAAGLFAM	212	1.4000	13.86
30	LIGESRLFV	351	1.4000	13.86
31	FANAHRRVG	371	1.4000	13.86
32	MQQLATFCA	77	1.3000	12.87
33	FCAGGKCPD	83	1.3000	12.87
34	VSFYAAGLF	210	1.2000	11.88
35	FQRRYPDIK	58	1.0000	9.90
36	FYADLTNKH	249	1.0000	9.90
37	VLRSAINSH	361	0.7000	6.93
38	FGPVLRGSR	411	0.7000	6.93
39	WERPWSFAE	175	0.6000	5.94
40	WSFAEFLDA	179	0.6000	5.94
41	LTGLSQAVD	424	0.6000	5.94

42	VGQALIGES	347	0.5000	4.95
43	YFGPVLRGS	410	0.5000	4.95

ALLELE: DRB1_1101	Threshold for 3 % with score: 1.1	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LRGAGALTA	11	2.9000	34.94
2	FVKFATGPV	339	2.2000	26.51
3	FVPVLRSAI	358	2.2000	26.51
4	LLDLNTLLA	109	2.1000	25.30
5	VGNLAVLSE	378	2.1000	25.30
6	WGFVNAWVS	203	2.0000	24.10
7	LRGSRPATS	415	1.9000	22.89
8	MQQLATFCA	77	1.7000	20.48
9	WVSFYAAGL	209	1.7000	20.48
10	YQTFDRADG	290	1.6000	19.28
11	FVNAWVSFY	205	1.5000	18.07
12	LFSVGKAGI	274	1.4000	16.87
13	LNTLLARDQ	112	1.0000	12.05
14	FERRSLLRG	5	0.8000	9.64
15	VRALLSGPG	67	0.8000	9.64
16	WEKIAALMD	400	0.8000	9.64
17	FGPVLRGSR	411	0.8000	9.64
18	IKVRALLSG	65	0.6000	7.23
19	WSFAEFLDA	179	0.6000	7.23
20	VLMAWELTY	92	0.5000	6.02
21	VGQALIGES	347	0.5000	6.02
22	LIGESRLFV	351	0.4000	4.82
23	FLFYNKQLF	155	0.3000	3.61
24	FYAAGLFAM	212	0.3000	3.61
25	LSGPGVMQQ	71	0.2000	2.41
26	VGKAGIALA	277	0.2000	2.41
27	LFYNKQLFD	156	0.1000	1.20

28	IGPRGRAAC	308	0.1000	1.20
29	FANAHRRVG	371	0.1000	1.20
30	LRPRMRVVN	48	-0.2000	0
31	VTGLAIAAT	321	-0.2000	0
32	YFGPVLRGS	410	-0.2000	0
33	VLRSAINSH	361	-0.2200	0
34	VAPLPIGPR	303	-0.3000	0
35	VLSEGPAYS	383	-0.3000	0
36	IGVTGLAIA	319	-0.4000	0
37	LDLNTLLAR	110	-0.6000	0
38	MRVVNEFQR	52	-0.7000	0
39	FFFAANPDE	39	-0.7500	0
40	WELTYAELA	96	-0.8000	0
41	VNAWVSFYA	206	-0.8000	0
42	FDRADGLDF	293	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MQQLATFCA	77	3.0000	35.71
2	LRGSRPATS	415	3.0000	35.71
3	LNTLLARDQ	112	2.9000	34.52
4	LRGAGALTA	11	2.8000	33.33
5	LRPRMRVVN	48	2.2000	26.19
6	VNAWVSFYA	206	2.0000	23.81
7	IGPRGRAAC	308	2.0000	23.81
8	VLRSAINSH	361	1.9800	23.57
9	VVNEFQRRY	54	1.4000	16.67
10	IKVRALLSG	65	1.4000	16.67
11	VNEFQRRYP	55	1.3000	15.48
12	LLDLNTLLA	109	1.3000	15.48
13	LAGHWRYQT	284	1.3000	15.48
14	VGNLAVLSE	378	1.3000	15.48

15	VLSEGPAYS	383	1.3000	15.48
16	LTNKHKVAP	253	1.2000	14.29
17	VGKAGIALA	277	1.2000	14.29
18	LFVPVLRSA	357	1.2000	14.29
19	LMAWELTYA	93	1.1000	13.10
20	FLFYNKQLF	155	1.1000	13.10
21	WVSFYAAGL	209	1.1000	13.10
22	LFSVGKAGI	274	1.1000	13.10
23	INSHGFANA	366	1.1000	13.10
24	YQTFDRADG	290	1.0000	11.90
25	LLARDQAFA	115	0.9000	10.71
26	FVNAWVSFY	205	0.9000	10.71
27	LIGESRLFV	351	0.9000	10.71
28	VMQQLATFC	76	0.8000	9.52
29	FANAHRRVG	371	0.7000	8.33
30	YFGPVLRGS	410	0.6000	7.14
31	WGFVNAWVS	203	0.5000	5.95
32	FVKFATGPV	339	0.5000	5.95
33	VLMAWELTY	92	0.4000	4.76
34	LAIAATSRR	324	0.4000	4.76
35	VGQALIGES	347	0.4000	4.76
36	LTFFFAANP	37	0.3000	3.57
37	FYNKQLFDD	157	0.3000	3.57
38	FYAAGLFAM	212	0.3000	3.57
39	IALAGHWRY	282	0.3000	3.57
40	FVPVLRSAI	358	0.3000	3.57
41	LSGPGVMQQ	71	0.1000	1.19
42	LFYNKQLFD	156	0.1000	1.19
43	IGVTGLAIA	319	0.1000	1.19

ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score

1	LRGAGALTA	11	3.9000	46.99
2	LLDLNTLLA	109	3.1000	37.35
3	VGNLAVLSE	378	3.1000	37.35
4	LRGSRPATS	415	2.9000	34.94
5	MQQLATFCA	77	2.7000	32.53
6	LFSVGKAGI	274	2.4000	28.92
7	LNTLLARDQ	112	2.0000	24.10
8	VRALLSGPG	67	1.8000	21.69
9	IKVRALLSG	65	1.6000	19.28
10	VLMAWELTY	92	1.5000	18.07
11	VGQALIGES	347	1.5000	18.07
12	LIGESRLFV	351	1.4000	16.87
13	LSGPGVMQQ	71	1.2000	14.46
14	VGKAGIALA	277	1.2000	14.46
15	FVKFATGPV	339	1.2000	14.46
16	FVPVLRSAI	358	1.2000	14.46
17	LFYNKQLFD	156	1.1000	13.25
18	IGPRGRAAC	308	1.1000	13.25
19	WGFVNAWVS	203	1.0000	12.05
20	LRPRMRVVN	48	0.8000	9.64
21	VTGLAIAAT	321	0.8000	9.64
22	VLRSAINSH	361	0.7800	9.40
23	WVSFYAAGL	209	0.7000	8.43
24	VAPLPIGPR	303	0.7000	8.43
25	VLSEGPAYS	383	0.7000	8.43
26	YQTFDRADG	290	0.6000	7.23
27	IGVTGLAIA	319	0.6000	7.23
28	FVNAWVSFY	205	0.5000	6.02
29	LDLNTLLAR	110	0.4000	4.82
30	MRVVNEFQR	52	0.3000	3.61
31	VNAWVSFYA	206	0.2000	2.41
32	VKFATGPVG	340	0.1500	1.81
33	LTFFFAANP	37	-0.1000	0
34	LMAWELTYA	93	-0.1000	0

35	LDAAQALTK	185	-0.1000	0
36	LPIGPRGRA	306	-0.1000	0
37	FERRSLLRG	5	-0.2000	0
38	LAPWAAGCA	22	-0.2000	0
39	LAVLSEGPA	381	-0.2000	0

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	LRGAGALTA	11	3.9000	46.99
2	LLDLNTLLA	109	3.1000	37.35
3	VGNLAVLSE	378	3.1000	37.35
4	LRGSRPATS	415	2.9000	34.94
5	MQQLATFCA	77	2.7000	32.53
6	LFSVGKAGI	274	2.4000	28.92
7	LNTLLARDQ	112	2.0000	24.10
8	VRALLSGPG	67	1.8000	21.69
9	IKVRALLSG	65	1.6000	19.28
10	VLMAWELTY	92	1.5000	18.07
11	VGQALIGES	347	1.5000	18.07
12	LIGESRLFV	351	1.4000	16.87
13	LSGPGVMQQ	71	1.2000	14.46
14	VGKAGIALA	277	1.2000	14.46
15	FVKFATGPV	339	1.2000	14.46
16	FVPVLRSAI	358	1.2000	14.46
17	LFYNKQLFD	156	1.1000	13.25
18	IGPRGRAAC	308	1.1000	13.25
19	WGFVNAWVS	203	1.0000	12.05
20	LRPRMRVVN	48	0.8000	9.64
21	VTGLAIAAT	321	0.8000	9.64
22	VLRSAINSH	361	0.7800	9.40
23	WVSFYAAGL	209	0.7000	8.43
24	VAPLPIGPR	303	0.7000	8.43

25	VLSEGPAYS	383	0.7000	8.43
26	YQTFDRADG	290	0.6000	7.23
27	IGVTGLAIA	319	0.6000	7.23
28	FVNAWVSFY	205	0.5000	6.02
29	LDLNTLLAR	110	0.4000	4.82
30	MRVVNEFQR	52	0.3000	3.61
31	VNAWVSFYA	206	0.2000	2.41
32	VKFATGPVG	340	0.1500	1.81
33	LTFFFAANP	37	-0.1000	0
34	LMAWELTYA	93	-0.1000	0
35	LDAAQALTK	185	-0.1000	0
36	LPIGPRGRA	306	-0.1000	0
37	FERRSLLRG	5	-0.2000	0
38	LAPWAAGCA	22	-0.2000	0
39	LAVLSEGPA	381	-0.2000	0

ALLELE: DRB1_1107	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	LRGSRPATS	415	4.3000	47.25
2	LARDQAFAA	116	3.5000	38.46
3	LKSDSIGAL	126	3.4000	37.36
4	VLRSAINSH	361	3.0900	33.96
5	FYADLTNKH	249	2.9900	32.86
6	VLRGSRPAT	414	2.7000	29.67
7	LRGAGALTA	11	2.6000	28.57
8	VLLDLNTLL	108	2.6000	28.57
9	LPIGPRGRA	306	2.6000	28.57
10	MQQLATFCA	77	2.5000	27.47
11	FVPVLRSAI	358	2.1700	23.85
12	LFSVGKAGI	274	2.0000	21.98
13	VGQALIGES	347	2.0000	21.98
14	FVNAWVSFY	205	1.8700	20.55

15	LLSGPGVMQ	70	1.7000	18.68
16	LSGPGVMQQ	71	1.7000	18.68
17	VLSEGPAYS	383	1.4000	15.38
18	LAIAATSRR	324	1.3700	15.05
19	LRPRMRVVN	48	1.3000	14.29
20	VAPSAAEQQ	259	1.3000	14.29
21	VRALLSGPG	67	1.2000	13.19
22	VGKAGIALA	277	1.2000	13.19
23	LDFDVAPLP	299	1.2000	13.19
24	VMQQLATFC	76	1.0000	10.99
25	MNNGVPWSV	220	1.0000	10.99
26	VKFATGPVG	340	0.9000	9.89
27	LRSAINSHG	362	0.8700	9.56
28	MRVVNEFQR	52	0.8000	8.79
29	IGPRGRAAC	308	0.8000	8.79
30	FATGPVGQA	342	0.8000	8.79
31	LIGESRLFV	351	0.8000	8.79
32	LLDLNTLLA	109	0.7000	7.69
33	VGNLAVLSE	378	0.7000	7.69
34	LNFDHDGFL	236	0.6000	6.59
35	LNTLLARDQ	112	0.4000	4.40
36	WGFVNAWVS	203	0.4000	4.40
37	LLRGAGALT	10	0.3000	3.30
38	FVKFATGPV	339	0.3000	3.30
39	VLMAWELTY	92	0.2000	2.20
40	LMAWELTYA	93	0.2000	2.20
41	VNAWVSFYA	206	0.2000	2.20
42	FYAAGLFAM	212	0.2000	2.20
43	IGVTGLAIA	319	0.2000	2.20

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

Rank	Sequence	At Position	Score	% of Highest Score

1	FLFYNKQLF	155	2.1000	25.00
2	WVSFYAAGL	209	2.1000	25.00
3	MQQLATFCA	77	2.0000	23.81
4	YQTFDRADG	290	2.0000	23.81
5	LRGSRPATS	415	2.0000	23.81
6	LNTLLARDQ	112	1.9000	22.62
7	FVNAWVSFY	205	1.9000	22.62
8	LRGAGALTA	11	1.8000	21.43
9	FANAHRRVG	371	1.7000	20.24
10	YFGPVLRGS	410	1.6000	19.05
11	WGFVNAWVS	203	1.5000	17.86
12	FVKFATGPV	339	1.5000	17.86
13	FYNKQLFDD	157	1.3000	15.48
14	FYAAGLFAM	212	1.3000	15.48
15	FVPVLRSAI	358	1.3000	15.48
16	LRPRMRVVN	48	1.2000	14.29
17	VNAWVSFYA	206	1.0000	11.90
18	IGPRGRAAC	308	1.0000	11.90
19	VLRSAINSH	361	0.9800	11.67
20	FQRRYPDIK	58	0.8000	9.52
21	WRYQTFDRA	288	0.7000	8.33
22	FERRSLLRG	5	0.6000	7.14
23	FYADLTNKH	249	0.4800	5.71
24	VVNEFQRRY	54	0.4000	4.76
25	IKVRALLSG	65	0.4000	4.76
26	VNEFQRRYP	55	0.3000	3.57
27	LLDLNTLLA	109	0.3000	3.57
28	LAGHWRYQT	284	0.3000	3.57
29	VGNLAVLSE	378	0.3000	3.57
30	VLSEGPAYS	383	0.3000	3.57
31	LTNKHKVAP	253	0.2000	2.38
32	VGKAGIALA	277	0.2000	2.38
33	LFVPVLRSA	357	0.2000	2.38
34	LMAWELTYA	93	0.1000	1.19

35	FLEAVQFYA	243	0.1000	1.19
36	LFSVGKAGI	274	0.1000	1.19
37	INSHGFANA	366	0.1000	1.19
38	LLARDQAFA	115	-0.1000	0
39	LIGESRLFV	351	-0.1000	0
40	VMQQLATFC	76	-0.2000	0
41	FTFNGGQYA	138	-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	FLFYNKQLF	155	4.0000	45.45
2	YQTFDRADG	290	3.4000	38.64
3	FVNAWVSFY	205	3.2000	36.36
4	FANAHRRVG	371	3.1000	35.23
5	WVSFYAAGL	209	3.0600	34.77
6	FYAAGLFAM	212	2.8000	31.82
7	FVKFATGPV	339	2.5000	28.41
8	FYNKQLFDD	157	2.4000	27.27
9	LRGSRPATS	415	2.4000	27.27
10	FVPVLRSAI	358	2.2000	25.00
11	FERRSLLRG	5	2.0000	22.73
12	LRPRMRVVN	48	2.0000	22.73
13	MQQLATFCA	77	2.0000	22.73
14	YFGPVLRGS	410	2.0000	22.73
15	WGFVNAWVS	203	1.9000	21.59
16	LRGAGALTA	11	1.8000	20.45
17	IKVRALLSG	65	1.8000	20.45
18	VVNEFQRRY	54	1.7000	19.32
19	VGNLAVLSE	378	1.7000	19.32
20	VNEFQRRYP	55	1.3000	14.77
21	LNTLLARDQ	112	1.2000	13.64
22	LTNKHKVAP	253	1.2000	13.64

23	VNAWVSFYA	206	1.0000	11.36
24	LFSVGKAGI	274	1.0000	11.36
25	LAGHWRYQT	284	1.0000	11.36
26	IGPRGRAAC	308	1.0000	11.36
27	FQRRYPDIK	58	0.9000	10.23
28	LAIAATSRR	324	0.9000	10.23
29	LIGESRLFV	351	0.9000	10.23
30	VLMAWELTY	92	0.7000	7.95
31	WRYQTFDRA	288	0.7000	7.95
32	VLSEGPAYS	383	0.7000	7.95
33	IALAGHWRY	282	0.6000	6.82
34	MVNKPFERR	0	0.5000	5.68
35	MRVVNEFQR	52	0.5000	5.68
36	LTYAELADR	98	0.5000	5.68
37	VRALLSGPG	67	0.4000	4.55
38	FAAELKSDS	122	0.4000	4.55
39	VLRSAINSH	361	0.4000	4.55
40	LTFFFAANP	37	0.3000	3.41
41	LLDLNTLLA	109	0.3000	3.41
42	LRSAINSHG	362	0.3000	3.41
43	FFFAANPDE	39	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MQQLATFCA	77	3.0000	35.71
2	LRGSRPATS	415	3.0000	35.71
3	LNTLLARDQ	112	2.9000	34.52
4	LRGAGALTA	11	2.8000	33.33
5	LRPRMRVVN	48	2.2000	26.19
6	VNAWVSFYA	206	2.0000	23.81
7	IGPRGRAAC	308	2.0000	23.81
8	VLRSAINSH	361	1.9800	23.57

9	VVNEFQRRY	54	1.4000	16.67
10	IKVRALLSG	65	1.4000	16.67
11	VNEFQRRYP	55	1.3000	15.48
12	LLDLNTLLA	109	1.3000	15.48
13	LAGHWRYQT	284	1.3000	15.48
14	VGNLAVLSE	378	1.3000	15.48
15	VLSEGPAYS	383	1.3000	15.48
16	LTNKHKVAP	253	1.2000	14.29
17	VGKAGIALA	277	1.2000	14.29
18	LFVPVLRSA	357	1.2000	14.29
19	LMAWELTYA	93	1.1000	13.10
20	FLFYNKQLF	155	1.1000	13.10
21	WVSFYAAGL	209	1.1000	13.10
22	LFSVGKAGI	274	1.1000	13.10
23	INSHGFANA	366	1.1000	13.10
24	YQTFDRADG	290	1.0000	11.90
25	LLARDQAFA	115	0.9000	10.71
26	FVNAWVSFY	205	0.9000	10.71
27	LIGESRLFV	351	0.9000	10.71
28	VMQQLATFC	76	0.8000	9.52
29	FANAHRRVG	371	0.7000	8.33
30	YFGPVLRGS	410	0.6000	7.14
31	WGFVNAWVS	203	0.5000	5.95
32	FVKFATGPV	339	0.5000	5.95
33	VLMAWELTY	92	0.4000	4.76
34	LAIAATSRR	324	0.4000	4.76
35	VGQALIGES	347	0.4000	4.76
36	LTFFFAANP	37	0.3000	3.57
37	FYNKQLFDD	157	0.3000	3.57
38	FYAAGLFAM	212	0.3000	3.57
39	IALAGHWRY	282	0.3000	3.57
40	FVPVLRSAI	358	0.3000	3.57
41	LSGPGVMQQ	71	0.1000	1.19
42	LFYNKQLFD	156	0.1000	1.19

43	IGVTGLAIA	319	0.1000	1.19

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	VGNLAVLSE	378	3.5000	40.23
2	FVKFATGPV	339	3.2000	36.78
3	FVPVLRSAI	358	3.1000	35.63
4	YQTFDRADG	290	3.0000	34.48
5	LRGAGALTA	11	2.9000	33.33
6	FVNAWVSFY	205	2.8000	32.18
7	WVSFYAAGL	209	2.6600	30.57
8	WGFVNAWVS	203	2.4000	27.59
9	LFSVGKAGI	274	2.3000	26.44
10	FGPVLRGSR	411	2.3000	26.44
11	LRGSRPATS	415	2.3000	26.44
12	FERRSLLRG	5	2.2000	25.29
13	VRALLSGPG	67	2.2000	25.29
14	FLFYNKQLF	155	2.2000	25.29
15	LLDLNTLLA	109	2.1000	24.14
16	IKVRALLSG	65	2.0000	22.99
17	WEKIAALMD	400	1.9000	21.84
18	VLMAWELTY	92	1.8000	20.69
19	FYAAGLFAM	212	1.8000	20.69
20	MQQLATFCA	77	1.7000	19.54
21	FANAHRRVG	371	1.5000	17.24
22	LIGESRLFV	351	1.4000	16.09
23	LFYNKQLFD	156	1.2000	13.79
24	VAPLPIGPR	303	1.2000	13.79
25	FDRADGLDF	293	1.1000	12.64
26	LDLNTLLAR	110	0.9000	10.34
27	VGQALIGES	347	0.9000	10.34
28	MRVVNEFQR	52	0.8000	9.20

29	FFFAANPDE	39	0.6500	7.47
30	LRPRMRVVN	48	0.6000	6.90
31	WSFAEFLDA	179	0.6000	6.90
32	VKFATGPVG	340	0.5500	6.32
33	LTYAELADR	98	0.5000	5.75
34	VTGLAIAAT	321	0.5000	5.75
35	LAIAATSRR	324	0.5000	5.75
36	LNTLLARDQ	112	0.3000	3.45
37	WEFVKFATG	337	0.3000	3.45
38	VGKAGIALA	277	0.2000	2.30
39	YFGPVLRGS	410	0.2000	2.30
40	FYNKQLFDD	157	0.1000	1.15
41	IGPRGRAAC	308	0.1000	1.15
42	VLSEGPAYS	383	0.1000	1.15

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	LRGSRPATS	415	3.4000	38.64
2	LRPRMRVVN	48	3.0000	34.09
3	MQQLATFCA	77	3.0000	34.09
4	FLFYNKQLF	155	3.0000	34.09
5	LRGAGALTA	11	2.8000	31.82
6	IKVRALLSG	65	2.8000	31.82
7	VVNEFQRRY	54	2.7000	30.68
8	VGNLAVLSE	378	2.7000	30.68
9	YQTFDRADG	290	2.4000	27.27
10	VNEFQRRYP	55	2.3000	26.14
11	LNTLLARDQ	112	2.2000	25.00
12	FVNAWVSFY	205	2.2000	25.00
13	LTNKHKVAP	253	2.2000	25.00
14	FANAHRRVG	371	2.1000	23.86
15	WVSFYAAGL	209	2.0600	23.41

16	VNAWVSFYA	206	2.0000	22.73
17	LFSVGKAGI	274	2.0000	22.73
18	LAGHWRYQT	284	2.0000	22.73
19	IGPRGRAAC	308	2.0000	22.73
20	LAIAATSRR	324	1.9000	21.59
21	LIGESRLFV	351	1.9000	21.59
22	FYAAGLFAM	212	1.8000	20.45
23	VLMAWELTY	92	1.7000	19.32
24	VLSEGPAYS	383	1.7000	19.32
25	IALAGHWRY	282	1.6000	18.18
26	MVNKPFERR	0	1.5000	17.05
27	MRVVNEFQR	52	1.5000	17.05
28	LTYAELADR	98	1.5000	17.05
29	FVKFATGPV	339	1.5000	17.05
30	VRALLSGPG	67	1.4000	15.91
31	FYNKQLFDD	157	1.4000	15.91
32	VLRSAINSH	361	1.4000	15.91
33	LTFFFAANP	37	1.3000	14.77
34	LLDLNTLLA	109	1.3000	14.77
35	LRSAINSHG	362	1.3000	14.77
36	LFYNKQLFD	156	1.2000	13.64
37	LTKQGRSGR	191	1.2000	13.64
38	VGKAGIALA	277	1.2000	13.64
39	LFVPVLRSA	357	1.2000	13.64
40	FVPVLRSAI	358	1.2000	13.64
41	LMAWELTYA	93	1.1000	12.50
42	VKFATGPVG	340	1.1000	12.50
43	INSHGFANA	366	1.1000	12.50

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	FLFYNKQLF	155	4.0000	45.45

2	YQTFDRADG	290	3.4000	38.64
3	FVNAWVSFY	205	3.2000	36.36
4	FANAHRRVG	371	3.1000	35.23
5	WVSFYAAGL	209	3.0600	34.77
6	FYAAGLFAM	212	2.8000	31.82
7	FVKFATGPV	339	2.5000	28.41
8	FYNKQLFDD	157	2.4000	27.27
9	LRGSRPATS	415	2.4000	27.27
10	FVPVLRSAI	358	2.2000	25.00
11	FERRSLLRG	5	2.0000	22.73
12	LRPRMRVVN	48	2.0000	22.73
13	MQQLATFCA	77	2.0000	22.73
14	YFGPVLRGS	410	2.0000	22.73
15	WGFVNAWVS	203	1.9000	21.59
16	LRGAGALTA	11	1.8000	20.45
17	IKVRALLSG	65	1.8000	20.45
18	VVNEFQRRY	54	1.7000	19.32
19	VGNLAVLSE	378	1.7000	19.32
20	VNEFQRRYP	55	1.3000	14.77
21	LNTLLARDQ	112	1.2000	13.64
22	LTNKHKVAP	253	1.2000	13.64
23	VNAWVSFYA	206	1.0000	11.36
24	LFSVGKAGI	274	1.0000	11.36
25	LAGHWRYQT	284	1.0000	11.36
26	IGPRGRAAC	308	1.0000	11.36
27	FQRRYPDIK	58	0.9000	10.23
28	LAIAATSRR	324	0.9000	10.23
29	LIGESRLFV	351	0.9000	10.23
30	VLMAWELTY	92	0.7000	7.95
31	WRYQTFDRA	288	0.7000	7.95
32	VLSEGPAYS	383	0.7000	7.95
33	IALAGHWRY	282	0.6000	6.82
34	MVNKPFERR	0	0.5000	5.68
35	MRVVNEFQR	52	0.5000	5.68

36	LTYAELADR	98	0.5000	5.68
37	VRALLSGPG	67	0.4000	4.55
38	FAAELKSDS	122	0.4000	4.55
39	VLRSAINSH	361	0.4000	4.55
40	LTFFFAANP	37	0.3000	3.41
41	LLDLNTLLA	109	0.3000	3.41
42	LRSAINSHG	362	0.3000	3.41
43	FFFAANPDE	39	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VGNLAVLSE	378	4.3000	47.78
2	LRPRMRVVN	48	4.2000	46.67
3	LNTLLARDQ	112	3.7000	41.11
4	VLRSAINSH	361	3.2000	35.56
5	MQQLATFCA	77	3.0000	33.33
6	FYNKQLFDD	157	3.0000	33.33
7	LRGSRPATS	415	3.0000	33.33
8	LRGAGALTA	11	2.8000	31.11
9	LFYNKQLFD	156	2.8000	31.11
10	IKVRALLSG	65	2.7000	30.00
11	VVNEFQRRY	54	2.5000	27.78
12	YQTFDRADG	290	2.3000	25.56
13	LAGHWRYQT	284	2.2000	24.44
14	WVSFYAAGL	209	2.1000	23.33
15	IAATSRRKD	326	2.1000	23.33
16	FLFYNKQLF	155	2.0000	22.22
17	FVNAWVSFY	205	2.0000	22.22
18	VNAWVSFYA	206	2.0000	22.22
19	IGPRGRAAC	308	2.0000	22.22
20	FANAHRRVG	371	2.0000	22.22
21	VNEFQRRYP	55	1.7000	18.89

22	LTNKHKVAP	253	1.6000	17.78
23	VLMAWELTY	92	1.5000	16.67
24	LADRGVLLD	103	1.5000	16.67
25	FYAAGLFAM	212	1.4000	15.56
26	IALAGHWRY	282	1.4000	15.56
27	VRALLSGPG	67	1.3000	14.44
28	LLDLNTLLA	109	1.3000	14.44
29	MNPTHLNFD	231	1.3000	14.44
30	LFSVGKAGI	274	1.3000	14.44
31	VLSEGPAYS	383	1.3000	14.44
32	LTGLSQAVD	424	1.3000	14.44
33	VPWSVPRMN	224	1.2000	13.33
34	VGKAGIALA	277	1.2000	13.33
35	LIGESRLFV	351	1.2000	13.33
36	LFVPVLRSA	357	1.2000	13.33
37	LRSAINSHG	362	1.2000	13.33
38	LMAWELTYA	93	1.1000	12.22
39	INSHGFANA	366	1.1000	12.22
40	VQFYADLTN	247	1.0000	11.11
41	VTGLAIAAT	321	1.0000	11.11
42	VKFATGPVG	340	1.0000	11.11
43	FERRSLLRG	5	0.9000	10.00

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	VGNLAVLSE	378	3.5000	40.23
2	FVKFATGPV	339	3.2000	36.78
3	FVPVLRSAI	358	3.1000	35.63
4	YQTFDRADG	290	3.0000	34.48
5	LRGAGALTA	11	2.9000	33.33
6	FVNAWVSFY	205	2.8000	32.18
7	WVSFYAAGL	209	2.6600	30.57

8	WGFVNAWVS	203	2.4000	27.59
9	LFSVGKAGI	274	2.3000	26.44
10	FGPVLRGSR	411	2.3000	26.44
11	LRGSRPATS	415	2.3000	26.44
12	FERRSLLRG	5	2.2000	25.29
13	VRALLSGPG	67	2.2000	25.29
14	FLFYNKQLF	155	2.2000	25.29
15	LLDLNTLLA	109	2.1000	24.14
16	IKVRALLSG	65	2.0000	22.99
17	WEKIAALMD	400	1.9000	21.84
18	VLMAWELTY	92	1.8000	20.69
19	FYAAGLFAM	212	1.8000	20.69
20	MQQLATFCA	77	1.7000	19.54
21	FANAHRRVG	371	1.5000	17.24
22	LIGESRLFV	351	1.4000	16.09
23	LFYNKQLFD	156	1.2000	13.79
24	VAPLPIGPR	303	1.2000	13.79
25	FDRADGLDF	293	1.1000	12.64
26	LDLNTLLAR	110	0.9000	10.34
27	VGQALIGES	347	0.9000	10.34
28	MRVVNEFQR	52	0.8000	9.20
29	FFFAANPDE	39	0.6500	7.47
30	LRPRMRVVN	48	0.6000	6.90
31	WSFAEFLDA	179	0.6000	6.90
32	VKFATGPVG	340	0.5500	6.32
33	LTYAELADR	98	0.5000	5.75
34	VTGLAIAAT	321	0.5000	5.75
35	LAIAATSRR	324	0.5000	5.75
36	LNTLLARDQ	112	0.3000	3.45
37	WEFVKFATG	337	0.3000	3.45
38	VGKAGIALA	277	0.2000	2.30
39	YFGPVLRGS	410	0.2000	2.30
40	FYNKQLFDD	157	0.1000	1.15
41	IGPRGRAAC	308	0.1000	1.15

42	VLSEGPAYS	383	0.1000	1.15

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	FVPVLRSAI	358	2.2000	32.35
2	FVKFATGPV	339	2.1000	30.88
3	LRGSRPATS	415	1.9000	27.94
4	WVSFYAAGL	209	1.7000	25.00
5	YQTFDRADG	290	1.6000	23.53
6	FVNAWVSFY	205	1.5000	22.06
7	LFSVGKAGI	274	1.4000	20.59
8	MQQLATFCA	77	1.2000	17.65
9	WGFVNAWVS	203	1.2000	17.65
10	LRGAGALTA	11	1.1000	16.18
11	LNTLLARDQ	112	0.8000	11.76
12	VRALLSGPG	67	0.7000	10.29
13	FGPVLRGSR	411	0.7000	10.29
14	VGQALIGES	347	0.4000	5.88
15	LLDLNTLLA	109	0.3000	4.41
16	VGNLAVLSE	378	0.3000	4.41
17	FLFYNKQLF	155	0.2000	2.94
18	VGKAGIALA	277	0.2000	2.94
19	IGPRGRAAC	308	0.1000	1.47
20	FANAHRRVG	371	-0.1000	0
21	FYAAGLFAM	212	-0.2000	0
22	VTGLAIAAT	321	-0.2000	0
23	VLSEGPAYS	383	-0.3000	0
24	VAPLPIGPR	303	-0.4000	0
25	IGVTGLAIA	319	-0.4000	0
26	YFGPVLRGS	410	-0.4000	0
27	VLRSAINSH	361	-0.5200	0
28	LRPRMRVVN	48	-0.7000	0

29	FERRSLLRG	5	-1.0000	0
30	FQRRYPDIK	58	-1.0000	0
31	LTYAELADR	98	-1.0000	0
32	LLARDQAFA	115	-1.0000	0
33	FAAELKSDS	122	-1.0000	0
34	LAIAATSRR	324	-1.0000	0
35	FATGPVGQA	342	-1.0000	0
36	WEKIAALMD	400	-1.0000	0
37	LTFFFAANP	37	-1.1000	0
38	FTFNGGQYA	138	-1.1000	0
39	WEFVKFATG	337	-1.1000	0
40	MRVVNEFQR	52	-1.2000	0
41	IKVRALLSG	65	-1.2000	0
42	WSFAEFLDA	179	-1.2000	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	LRGAGALTA	11	3.9000	46.99
2	LLDLNTLLA	109	3.1000	37.35
3	VGNLAVLSE	378	3.1000	37.35
4	LRGSRPATS	415	2.9000	34.94
5	MQQLATFCA	77	2.7000	32.53
6	LFSVGKAGI	274	2.4000	28.92
7	LNTLLARDQ	112	2.0000	24.10
8	VRALLSGPG	67	1.8000	21.69
9	IKVRALLSG	65	1.6000	19.28
10	VLMAWELTY	92	1.5000	18.07
11	VGQALIGES	347	1.5000	18.07
12	LIGESRLFV	351	1.4000	16.87
13	LSGPGVMQQ	71	1.2000	14.46
14	VGKAGIALA	277	1.2000	14.46
15	FVKFATGPV	339	1.2000	14.46

16	FVPVLRSAI	358	1.2000	14.46
17	LFYNKQLFD	156	1.1000	13.25
18	IGPRGRAAC	308	1.1000	13.25
19	WGFVNAWVS	203	1.0000	12.05
20	LRPRMRVVN	48	0.8000	9.64
21	VTGLAIAAT	321	0.8000	9.64
22	VLRSAINSH	361	0.7800	9.40
23	WVSFYAAGL	209	0.7000	8.43
24	VAPLPIGPR	303	0.7000	8.43
25	VLSEGPAYS	383	0.7000	8.43
26	YQTFDRADG	290	0.6000	7.23
27	IGVTGLAIA	319	0.6000	7.23
28	FVNAWVSFY	205	0.5000	6.02
29	LDLNTLLAR	110	0.4000	4.82
30	MRVVNEFQR	52	0.3000	3.61
31	VNAWVSFYA	206	0.2000	2.41
32	VKFATGPVG	340	0.1500	1.81
33	LTFFFAANP	37	-0.1000	0
34	LMAWELTYA	93	-0.1000	0
35	LDAAQALTK	185	-0.1000	0
36	LPIGPRGRA	306	-0.1000	0
37	FERRSLLRG	5	-0.2000	0
38	LAPWAAGCA	22	-0.2000	0
39	LAVLSEGPA	381	-0.2000	0

ALLELE: DRB1_1321	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.9

Rank	Sequence	At Position	Score	% of Highest Score
1	VGNLAVLSE	378	5.1000	57.30
2	WEKIAALMD	400	3.5000	39.33
3	LRGAGALTA	11	2.9000	32.58
4	YQTFDRADG	290	2.9000	32.58
5	LFYNKQLFD	156	2.8000	31.46

6	WVSFYAAGL	209	2.7000	30.34
7	FVNAWVSFY	205	2.6000	29.21
8	FVKFATGPV	339	2.5000	28.09
9	FVPVLRSAI	358	2.4000	26.97
10	FFFAANPDE	39	2.2500	25.28
11	FERRSLLRG	5	2.1000	23.60
12	VRALLSGPG	67	2.1000	23.60
13	LLDLNTLLA	109	2.1000	23.60
14	WGFVNAWVS	203	2.0000	22.47
15	IKVRALLSG	65	1.9000	21.35
16	LRGSRPATS	415	1.9000	21.35
17	LRPRMRVVN	48	1.8000	20.22
18	LNTLLARDQ	112	1.8000	20.22
19	MQQLATFCA	77	1.7000	19.10
20	FYNKQLFDD	157	1.7000	19.10
21	VLMAWELTY	92	1.6000	17.98
22	LFSVGKAGI	274	1.6000	17.98
23	FYAAGLFAM	212	1.4000	15.73
24	FANAHRRVG	371	1.4000	15.73
25	FLFYNKQLF	155	1.2000	13.48
26	LSGPGVMQQ	71	1.0000	11.24
27	VLRSAINSH	361	1.0000	11.24
28	LTGLSQAVD	424	1.0000	11.24
29	FGPVLRGSR	411	0.8000	8.99
30	LADRGVLLD	103	0.7000	7.87
31	VTGLAIAAT	321	0.7000	7.87
32	LIGESRLFV	351	0.7000	7.87
33	FCAGGKCPD	83	0.6000	6.74
34	WSFAEFLDA	179	0.6000	6.74
35	VPVLRSAIN	359	0.6000	6.74
36	VGQALIGES	347	0.5000	5.62
37	VKFATGPVG	340	0.4500	5.06
38	WSGNFLFYN	151	0.3000	3.37
39	FYADLTNKH	249	0.3000	3.37

40	VGKAGIALA	277	0.2000	2.25
41	WEFVKFATG	337	0.2000	2.25
42	FDRADGLDF	293	0.1000	1.12
43	IGPRGRAAC	308	0.1000	1.12

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	MQQLATFCA	77	3.0000	35.71
2	LRGSRPATS	415	3.0000	35.71
3	LNTLLARDQ	112	2.9000	34.52
4	LRGAGALTA	11	2.8000	33.33
5	LRPRMRVVN	48	2.2000	26.19
6	VNAWVSFYA	206	2.0000	23.81
7	IGPRGRAAC	308	2.0000	23.81
8	VLRSAINSH	361	1.9800	23.57
9	VVNEFQRRY	54	1.4000	16.67
10	IKVRALLSG	65	1.4000	16.67
11	VNEFQRRYP	55	1.3000	15.48
12	LLDLNTLLA	109	1.3000	15.48
13	LAGHWRYQT	284	1.3000	15.48
14	VGNLAVLSE	378	1.3000	15.48
15	VLSEGPAYS	383	1.3000	15.48
16	LTNKHKVAP	253	1.2000	14.29
17	VGKAGIALA	277	1.2000	14.29
18	LFVPVLRSA	357	1.2000	14.29
19	LMAWELTYA	93	1.1000	13.10
20	FLFYNKQLF	155	1.1000	13.10
21	WVSFYAAGL	209	1.1000	13.10
22	LFSVGKAGI	274	1.1000	13.10
23	INSHGFANA	366	1.1000	13.10
24	YQTFDRADG	290	1.0000	11.90
25	LLARDQAFA	115	0.9000	10.71

26	FVNAWVSFY	205	0.9000	10.71
27	LIGESRLFV	351	0.9000	10.71
28	VMQQLATFC	76	0.8000	9.52
29	FANAHRRVG	371	0.7000	8.33
30	YFGPVLRGS	410	0.6000	7.14
31	WGFVNAWVS	203	0.5000	5.95
32	FVKFATGPV	339	0.5000	5.95
33	VLMAWELTY	92	0.4000	4.76
34	LAIAATSRR	324	0.4000	4.76
35	VGQALIGES	347	0.4000	4.76
36	LTFFFAANP	37	0.3000	3.57
37	FYNKQLFDD	157	0.3000	3.57
38	FYAAGLFAM	212	0.3000	3.57
39	IALAGHWRY	282	0.3000	3.57
40	FVPVLRSAI	358	0.3000	3.57
41	LSGPGVMQQ	71	0.1000	1.19
42	LFYNKQLFD	156	0.1000	1.19
43	IGVTGLAIA	319	0.1000	1.19

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	FLFYNKQLF	155	2.1000	25.00
2	WVSFYAAGL	209	2.1000	25.00
3	MQQLATFCA	77	2.0000	23.81
4	YQTFDRADG	290	2.0000	23.81
5	LRGSRPATS	415	2.0000	23.81
6	LNTLLARDQ	112	1.9000	22.62
7	FVNAWVSFY	205	1.9000	22.62
8	LRGAGALTA	11	1.8000	21.43
9	FANAHRRVG	371	1.7000	20.24
10	YFGPVLRGS	410	1.6000	19.05
11	WGFVNAWVS	203	1.5000	17.86

12	FVKFATGPV	339	1.5000	17.86
13	FYNKQLFDD	157	1.3000	15.48
14	FYAAGLFAM	212	1.3000	15.48
15	FVPVLRSAI	358	1.3000	15.48
16	LRPRMRVVN	48	1.2000	14.29
17	VNAWVSFYA	206	1.0000	11.90
18	IGPRGRAAC	308	1.0000	11.90
19	VLRSAINSH	361	0.9800	11.67
20	FQRRYPDIK	58	0.8000	9.52
21	WRYQTFDRA	288	0.7000	8.33
22	FERRSLLRG	5	0.6000	7.14
23	FYADLTNKH	249	0.4800	5.71
24	VVNEFQRRY	54	0.4000	4.76
25	IKVRALLSG	65	0.4000	4.76
26	VNEFQRRYP	55	0.3000	3.57
27	LLDLNTLLA	109	0.3000	3.57
28	LAGHWRYQT	284	0.3000	3.57
29	VGNLAVLSE	378	0.3000	3.57
30	VLSEGPAYS	383	0.3000	3.57
31	LTNKHKVAP	253	0.2000	2.38
32	VGKAGIALA	277	0.2000	2.38
33	LFVPVLRSA	357	0.2000	2.38
34	LMAWELTYA	93	0.1000	1.19
35	FLEAVQFYA	243	0.1000	1.19
36	LFSVGKAGI	274	0.1000	1.19
37	INSHGFANA	366	0.1000	1.19
38	LLARDQAFA	115	-0.1000	0
39	LIGESRLFV	351	-0.1000	0
40	VMQQLATFC	76	-0.2000	0
41	FTFNGGQYA	138	-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	LRGSRPATS	415	3.4000	38.64
2	LRPRMRVVN	48	3.0000	34.09
3	MQQLATFCA	77	3.0000	34.09
4	FLFYNKQLF	155	3.0000	34.09
5	LRGAGALTA	11	2.8000	31.82
6	IKVRALLSG	65	2.8000	31.82
7	VVNEFQRRY	54	2.7000	30.68
8	VGNLAVLSE	378	2.7000	30.68
9	YQTFDRADG	290	2.4000	27.27
10	VNEFQRRYP	55	2.3000	26.14
11	LNTLLARDQ	112	2.2000	25.00
12	FVNAWVSFY	205	2.2000	25.00
13	LTNKHKVAP	253	2.2000	25.00
14	FANAHRRVG	371	2.1000	23.86
15	WVSFYAAGL	209	2.0600	23.41
16	VNAWVSFYA	206	2.0000	22.73
17	LFSVGKAGI	274	2.0000	22.73
18	LAGHWRYQT	284	2.0000	22.73
19	IGPRGRAAC	308	2.0000	22.73
20	LAIAATSRR	324	1.9000	21.59
21	LIGESRLFV	351	1.9000	21.59
22	FYAAGLFAM	212	1.8000	20.45
23	VLMAWELTY	92	1.7000	19.32
24	VLSEGPAYS	383	1.7000	19.32
25	IALAGHWRY	282	1.6000	18.18
26	MVNKPFERR	0	1.5000	17.05
27	MRVVNEFQR	52	1.5000	17.05
28	LTYAELADR	98	1.5000	17.05
29	FVKFATGPV	339	1.5000	17.05
30	VRALLSGPG	67	1.4000	15.91
31	FYNKQLFDD	157	1.4000	15.91
32	VLRSAINSH	361	1.4000	15.91
33	LTFFFAANP	37	1.3000	14.77

34	LLDLNTLLA	109	1.3000	14.77
35	LRSAINSHG	362	1.3000	14.77
36	LFYNKQLFD	156	1.2000	13.64
37	LTKQGRSGR	191	1.2000	13.64
38	VGKAGIALA	277	1.2000	13.64
39	LFVPVLRSA	357	1.2000	13.64
40	FVPVLRSAI	358	1.2000	13.64
41	LMAWELTYA	93	1.1000	12.50
42	VKFATGPVG	340	1.1000	12.50
43	INSHGFANA	366	1.1000	12.50

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	LRGSRPATS	415	3.4000	38.64
2	LRPRMRVVN	48	3.0000	34.09
3	MQQLATFCA	77	3.0000	34.09
4	FLFYNKQLF	155	3.0000	34.09
5	LRGAGALTA	11	2.8000	31.82
6	IKVRALLSG	65	2.8000	31.82
7	VVNEFQRRY	54	2.7000	30.68
8	VGNLAVLSE	378	2.7000	30.68
9	YQTFDRADG	290	2.4000	27.27
10	VNEFQRRYP	55	2.3000	26.14
11	LNTLLARDQ	112	2.2000	25.00
12	FVNAWVSFY	205	2.2000	25.00
13	LTNKHKVAP	253	2.2000	25.00
14	FANAHRRVG	371	2.1000	23.86
15	WVSFYAAGL	209	2.0600	23.41
16	VNAWVSFYA	206	2.0000	22.73
17	LFSVGKAGI	274	2.0000	22.73
18	LAGHWRYQT	284	2.0000	22.73
19	IGPRGRAAC	308	2.0000	22.73

20	LAIAATSRR	324	1.9000	21.59
21	LIGESRLFV	351	1.9000	21.59
22	FYAAGLFAM	212	1.8000	20.45
23	VLMAWELTY	92	1.7000	19.32
24	VLSEGPAYS	383	1.7000	19.32
25	IALAGHWRY	282	1.6000	18.18
26	MVNKPFERR	0	1.5000	17.05
27	MRVVNEFQR	52	1.5000	17.05
28	LTYAELADR	98	1.5000	17.05
29	FVKFATGPV	339	1.5000	17.05
30	VRALLSGPG	67	1.4000	15.91
31	FYNKQLFDD	157	1.4000	15.91
32	VLRSAINSH	361	1.4000	15.91
33	LTFFFAANP	37	1.3000	14.77
34	LLDLNTLLA	109	1.3000	14.77
35	LRSAINSHG	362	1.3000	14.77
36	LFYNKQLFD	156	1.2000	13.64
37	LTKQGRSGR	191	1.2000	13.64
38	VGKAGIALA	277	1.2000	13.64
39	LFVPVLRSA	357	1.2000	13.64
40	FVPVLRSAI	358	1.2000	13.64
41	LMAWELTYA	93	1.1000	12.50
42	VKFATGPVG	340	1.1000	12.50
43	INSHGFANA	366	1.1000	12.50

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	VQFYADLTN	247	4.8000	48.98
2	LRGAGALTA	11	4.3000	43.88
3	WVSFYAAGL	209	4.2000	42.86
4	LIGESRLFV	351	3.9000	39.80
5	FVKFATGPV	339	3.7600	38.37

6	FVPVLRSAI	358	3.6000	36.73
7	VNAWVSFYA	206	3.2000	32.65
8	MDRYFGPVL	407	3.2000	32.65
9	IKVRALLSG	65	3.1000	31.63
10	MQQLATFCA	77	3.0600	31.22
11	VLLDLNTLL	108	3.0000	30.61
12	LRPRMRVVN	48	2.8000	28.57
13	LAGHWRYQT	284	2.8000	28.57
14	YQTFDRADG	290	2.8000	28.57
15	VLRGSRPAT	414	2.8000	28.57
16	VSFYAAGLF	210	2.6000	26.53
17	LRSAINSHG	362	2.6000	26.53
18	VRALLSGPG	67	2.5000	25.51
19	VLMAWELTY	92	2.4000	24.49
20	MRVVNEFQR	52	2.3000	23.47
21	FLFYNKQLF	155	2.3000	23.47
22	LTFFFAANP	37	2.1000	21.43
23	LLDLNTLLA	109	2.0600	21.02
24	LLRGAGALT	10	2.0000	20.41
25	MNNGVPWSV	220	2.0000	20.41
26	LPIGPRGRA	306	2.0000	20.41
27	IGPRGRAAC	308	2.0000	20.41
28	LMAWELTYA	93	1.9000	19.39
29	VKFATGPVG	340	1.9000	19.39
30	INSHGFANA	366	1.8000	18.37
31	LARDQAFAA	116	1.7000	17.35
32	VPRMNPTHL	228	1.7000	17.35
33	MSTADLFSV	269	1.6000	16.33
34	LFSVGKAGI	274	1.6000	16.33
35	LRGSRPATS	415	1.6000	16.33
36	FYAAGLFAM	212	1.5800	16.12
37	LKSDSIGAL	126	1.4500	14.80
38	VNEFQRRYP	55	1.4000	14.29
39	LFAMNNGVP	217	1.4000	14.29

40	FERRSLLRG	5	1.3000	13.27
41	LNFDHDGFL	236	1.3000	13.27
42	VGNLAVLSE	378	1.2000	12.24
43	YETFTFNGG	135	1.1000	11.22

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	WVSFYAAGL	209	5.2000	53.06
2	FVKFATGPV	339	4.7600	48.57
3	FVPVLRSAI	358	4.6000	46.94
4	VQFYADLTN	247	3.8000	38.78
5	YQTFDRADG	290	3.8000	38.78
6	LRGAGALTA	11	3.3000	33.67
7	FLFYNKQLF	155	3.3000	33.67
8	LIGESRLFV	351	2.9000	29.59
9	FYAAGLFAM	212	2.5800	26.33
10	FERRSLLRG	5	2.3000	23.47
11	VNAWVSFYA	206	2.2000	22.45
12	MDRYFGPVL	407	2.2000	22.45
13	IKVRALLSG	65	2.1000	21.43
14	YETFTFNGG	135	2.1000	21.43
15	WSFAEFLDA	179	2.1000	21.43
16	MQQLATFCA	77	2.0600	21.02
17	VLLDLNTLL	108	2.0000	20.41
18	LRPRMRVVN	48	1.8000	18.37
19	WGFVNAWVS	203	1.8000	18.37
20	LAGHWRYQT	284	1.8000	18.37
21	VLRGSRPAT	414	1.8000	18.37
22	FVNAWVSFY	205	1.7000	17.35
23	VSFYAAGLF	210	1.6000	16.33
24	LRSAINSHG	362	1.6000	16.33
25	VRALLSGPG	67	1.5000	15.31

26	VLMAWELTY	92	1.4000	14.29
27	FDRADGLDF	293	1.4000	14.29
28	MRVVNEFQR	52	1.3000	13.27
29	WRYQTFDRA	288	1.2000	12.24
30	LTFFFAANP	37	1.1000	11.22
31	LLDLNTLLA	109	1.0600	10.82
32	LLRGAGALT	10	1.0000	10.20
33	MNNGVPWSV	220	1.0000	10.20
34	LPIGPRGRA	306	1.0000	10.20
35	IGPRGRAAC	308	1.0000	10.20
36	FGPVLRGSR	411	1.0000	10.20
37	LMAWELTYA	93	0.9000	9.18
38	VKFATGPVG	340	0.9000	9.18
39	FTFNGGQYA	138	0.8000	8.16
40	INSHGFANA	366	0.8000	8.16
41	FFFAANPDE	39	0.7000	7.14
42	LARDQAFAA	116	0.7000	7.14
43	VPRMNPTHL	228	0.7000	7.14

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	VQFYADLTN	247	4.8000	48.98
2	LRGAGALTA	11	4.3000	43.88
3	WVSFYAAGL	209	4.2000	42.86
4	LIGESRLFV	351	3.9000	39.80
5	FVKFATGPV	339	3.7600	38.37
6	FVPVLRSAI	358	3.6000	36.73
7	VNAWVSFYA	206	3.2000	32.65
8	MDRYFGPVL	407	3.2000	32.65
9	IKVRALLSG	65	3.1000	31.63
10	MQQLATFCA	77	3.0600	31.22
11	VLLDLNTLL	108	3.0000	30.61

12	LRPRMRVVN	48	2.8000	28.57
13	LAGHWRYQT	284	2.8000	28.57
14	YQTFDRADG	290	2.8000	28.57
15	VLRGSRPAT	414	2.8000	28.57
16	VSFYAAGLF	210	2.6000	26.53
17	LRSAINSHG	362	2.6000	26.53
18	VRALLSGPG	67	2.5000	25.51
19	VLMAWELTY	92	2.4000	24.49
20	MRVVNEFQR	52	2.3000	23.47
21	FLFYNKQLF	155	2.3000	23.47
22	LTFFFAANP	37	2.1000	21.43
23	LLDLNTLLA	109	2.0600	21.02
24	LLRGAGALT	10	2.0000	20.41
25	MNNGVPWSV	220	2.0000	20.41
26	LPIGPRGRA	306	2.0000	20.41
27	IGPRGRAAC	308	2.0000	20.41
28	LMAWELTYA	93	1.9000	19.39
29	VKFATGPVG	340	1.9000	19.39
30	INSHGFANA	366	1.8000	18.37
31	LARDQAFAA	116	1.7000	17.35
32	VPRMNPTHL	228	1.7000	17.35
33	MSTADLFSV	269	1.6000	16.33
34	LFSVGKAGI	274	1.6000	16.33
35	LRGSRPATS	415	1.6000	16.33
36	FYAAGLFAM	212	1.5800	16.12
37	LKSDSIGAL	126	1.4500	14.80
38	VNEFQRRYP	55	1.4000	14.29
39	LFAMNNGVP	217	1.4000	14.29
40	FERRSLLRG	5	1.3000	13.27
41	LNFDHDGFL	236	1.3000	13.27
42	VGNLAVLSE	378	1.2000	12.24
43	YETFTFNGG	135	1.1000	11.22

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	MRVVNEFQR	52	4.8000	48.98
2	FGPVLRGSR	411	3.7000	37.76
3	WGFVNAWVS	203	3.5000	35.71
4	FVPVLRSAI	358	3.2000	32.65
5	WVSFYAAGL	209	3.0000	30.61
6	VPRMNPTHL	228	2.7000	27.55
7	LNTLLARDQ	112	2.4000	24.49
8	FVNAWVSFY	205	2.4000	24.49
9	LPVTPAWEK	394	2.4000	24.49
10	VRALLSGPG	67	2.3000	23.47
11	LRGAGALTA	11	2.0000	20.41
12	LAIAATSRR	324	2.0000	20.41
13	FYAAGLFAM	212	1.9000	19.39
14	LRGSRPATS	415	1.8000	18.37
15	LATFCAGGK	80	1.7000	17.35
16	FQRRYPDIK	58	1.6000	16.33
17	FLFYNKQLF	155	1.6000	16.33
18	YADLTNKHK	250	1.6000	16.33
19	VAPLPIGPR	303	1.6000	16.33
20	VVNEFQRRY	54	1.5000	15.31
21	MQQLATFCA	77	1.5000	15.31
22	VLMAWELTY	92	1.3000	13.27
23	LTYAELADR	98	1.3000	13.27
24	FVKFATGPV	339	1.1000	11.22
25	LDAAQALTK	185	1.0000	10.20
26	FDRADGLDF	293	0.9000	9.18
27	FANAHRRVG	371	0.9000	9.18
28	FFAANPDEL	40	0.8000	8.16
29	YPDIKVRAL	62	0.8000	8.16
30	LFSVGKAGI	274	0.8000	8.16
31	VSFYAAGLF	210	0.7000	7.14

32	WEFVKFATG	337	0.7000	7.14
33	WELTYAELA	96	0.5000	5.10
34	IALAGHWRY	282	0.5000	5.10
35	WEKIAALMD	400	0.5000	5.10
36	YFGPVLRGS	410	0.5000	5.10
37	VKFATGPVG	340	0.4000	4.08
38	VLRSAINSH	361	0.3000	3.06
39	LRSAINSHG	362	0.3000	3.06
40	LYETFTFNG	134	0.1000	1.02
41	IAALMDRYF	403	0.1000	1.02

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MRVVNEFQR	52	4.8000	48.98
2	FGPVLRGSR	411	3.7000	37.76
3	WGFVNAWVS	203	3.5000	35.71
4	FVPVLRSAI	358	3.2000	32.65
5	WVSFYAAGL	209	3.0000	30.61
6	VPRMNPTHL	228	2.7000	27.55
7	LNTLLARDQ	112	2.4000	24.49
8	FVNAWVSFY	205	2.4000	24.49
9	LPVTPAWEK	394	2.4000	24.49
10	VRALLSGPG	67	2.3000	23.47
11	LRGAGALTA	11	2.0000	20.41
12	LAIAATSRR	324	2.0000	20.41
13	FYAAGLFAM	212	1.9000	19.39
14	LRGSRPATS	415	1.8000	18.37
15	LATFCAGGK	80	1.7000	17.35
16	FQRRYPDIK	58	1.6000	16.33
17	FLFYNKQLF	155	1.6000	16.33
18	YADLTNKHK	250	1.6000	16.33
19	VAPLPIGPR	303	1.6000	16.33

20	VVNEFQRRY	54	1.5000	15.31
21	MQQLATFCA	77	1.5000	15.31
22	VLMAWELTY	92	1.3000	13.27
23	LTYAELADR	98	1.3000	13.27
24	FVKFATGPV	339	1.1000	11.22
25	LDAAQALTK	185	1.0000	10.20
26	FDRADGLDF	293	0.9000	9.18
27	FANAHRRVG	371	0.9000	9.18
28	FFAANPDEL	40	0.8000	8.16
29	YPDIKVRAL	62	0.8000	8.16
30	LFSVGKAGI	274	0.8000	8.16
31	VSFYAAGLF	210	0.7000	7.14
32	WEFVKFATG	337	0.7000	7.14
33	WELTYAELA	96	0.5000	5.10
34	IALAGHWRY	282	0.5000	5.10
35	WEKIAALMD	400	0.5000	5.10
36	YFGPVLRGS	410	0.5000	5.10
37	VKFATGPVG	340	0.4000	4.08
38	VLRSAINSH	361	0.3000	3.06
39	LRSAINSHG	362	0.3000	3.06
40	LYETFTFNG	134	0.1000	1.02
41	IAALMDRYF	403	0.1000	1.02