MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Mar 30 23:40:40 2010
Length of input sequence	414 amino acids
Number of nanomers from input sequence	406
Number of nanomers with obligatory P1 anchor residue	126
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	41

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	WRTATALPA	344	2.5000	41.67
2	LVLVSALRA	298	2.3500	39.17
3	LRVLPPQDY	117	1.7000	28.33
4	WHVECAAIA	228	0.9000	15.00
5	WRDLAQAEV	99	0.3000	5.00
6	MLACGAAYV	142	0.3000	5.00
7	LGLLAGHYR	316	0.2000	3.33
8	FGYESGYDR	171	0.1000	1.67

9	VSALRAQDV	301	0.1000	1.67
10	YFRADATLQ	162	-0.0100	0
11	YVGATEAIA	125	-0.1000	0
12	IEKMLACGA	139	-0.1000	0
13	VLPGRGPQL	10	-0.1300	0
14	WRAARPGEP	207	-0.2000	0
15	YVTFDLIHR	58	-0.2200	0
16	FTAAHAECV	260	-0.3000	0
17	YVHAGMIGW	278	-0.3000	0
18	LRLYDSADR	18	-0.5000	0
19	LACGAAYVI	143	-0.5000	0
20	IDALLGVDL	405	-0.5000	0
21	IAALDGWVT	377	-0.6800	0
22	LRAQDVEPS	304	-0.7000	0
23	VRRYLADDL	363	-0.7000	0
24	FDLIHRLWL	61	-0.8000	0
25	LRLCEERGG	183	-0.9100	0
26	MQSWYCPPV	0	-1.0300	0
27	LGHAATYVT	52	-1.2000	0
28	ITPYDATHL	44	-1.2100	0
29	MVELIEKML	135	-1.3000	0
30	VELIEKMLA	136	-1.3100	0
31	VPVLPGRGP	8	-1.4100	0
32	FRADATLQF	163	-1.5000	0
33	WYCPPVPVL	3	-1.5300	0
34	VRPVAPGSK	28	-1.5500	0
35	VRLGLLAGH	314	-1.6000	0
36	MIGWDGHKM	283	-1.6200	0
37	YVCGITPYD	40	-1.6300	0
38	VARVRRYLA	360	-1.6500	0
39	FARHYVHAG	274	-1.8000	0

ALLELE: DRB1_0102	Threshold for 3 % with score:	Highest Score achievable by any peptide: 6

	0.7	

Rank	Sequence	At Position	Score	% of Highest Score
1	LVLVSALRA	298	3.3500	55.83
2	LRVLPPQDY	117	2.7000	45.00
3	WRTATALPA	344	1.5000	25.00
4	MLACGAAYV	142	1.3000	21.67
5	LGLLAGHYR	316	1.2000	20.00
6	VSALRAQDV	301	1.1000	18.33
7	VCGITPYDA	41	1.0000	16.67
8	IEKMLACGA	139	0.9000	15.00
9	VLPGRGPQL	10	0.8700	14.50
10	LRLYDSADR	18	0.5000	8.33
11	LACGAAYVI	143	0.5000	8.33
12	IDALLGVDL	405	0.5000	8.33
13	IAALDGWVT	377	0.3200	5.33
14	LRAQDVEPS	304	0.3000	5.00
15	VRRYLADDL	363	0.3000	5.00
16	FGYESGYDR	171	0.1000	1.67
17	LRLCEERGG	183	0.0900	1.50
18	MQSWYCPPV	0	-0.0300	0
19	WHVECAAIA	228	-0.1000	0
20	LGHAATYVT	52	-0.2000	0
21	ITPYDATHL	44	-0.2100	0
22	MVELIEKML	135	-0.3000	0
23	FTAAHAECV	260	-0.3000	0
24	VELIEKMLA	136	-0.3100	0
25	VPVLPGRGP	8	-0.4100	0
26	VRPVAPGSK	28	-0.5500	0
27	VRLGLLAGH	314	-0.6000	0
28	MIGWDGHKM	283	-0.6200	0
29	VARVRRYLA	360	-0.6500	0
30	WRDLAQAEV	99	-0.7000	0
31	FDLIHRLWL	61	-0.8000	0
32	LHYVQNITD	75	-0.8500	0

33	LFCEDMAAL	109	-0.9000	0
34	MSKSRGNLV	291	-0.9000	0
35	MAALRVLPP	114	-1.0000	0
36	YFRADATLQ	162	-1.0100	0
37	YVGATEAIA	125	-1.1000	0
38	LWLDLGHEL	67	-1.2000	0
39	MLRLCEERG	182	-1.2000	0
40	WRAARPGEP	207	-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	FRADATLQF	163	5.4000	56.84
2	WVTDAVEYG	383	4.8000	50.53
3	YVIDREMGE	149	4.3000	45.26
4	LRAQDVEPS	304	4.3000	45.26
5	VELIEKMLA	136	4.0000	42.11
6	LRVLPPQDY	117	3.4000	35.79
7	VRLGLLAGH	314	3.4000	35.79
8	LVLVSALRA	298	3.3000	34.74
9	VAPGSKATM	31	3.2000	33.68
10	VTFDLIHRL	59	2.9600	31.16
11	VRPVAPGSK	28	2.9000	30.53
12	IALSRIGSG	235	2.9000	30.53
13	IGWDGHKMS	284	2.9000	30.53
14	LVSALRAQD	300	2.7000	28.42
15	LRLYDSADR	18	2.6000	27.37
16	YVCGITPYD	40	2.5000	26.32
17	MYVCGITPY	39	2.3000	24.21
18	LAQAEVALF	102	2.1000	22.11
19	LWRAARPGE	206	2.0000	21.05
20	VECAAIALS	230	1.9000	20.00
21	IQGGGSDLI	246	1.8000	18.95

22	VEPSAVRLG	309	1.8000	18.95
23	VLPGRGPQL	10	1.7600	18.53
24	LAGHYRADR	319	1.7000	17.89
25	LWLDLGHEL	67	1.6600	17.47
26	VARVRRYLA	360	1.6500	17.37
27	YLADDLDTP	366	1.6000	16.84
28	IHRLWLDLG	64	1.5000	15.79
29	WRAARPGEP	207	1.5000	15.79
30	VHAGMIGWD	279	1.5000	15.79
31	LQFGYESGY	169	1.4700	15.47
32	MQSWYCPPV	0	1.4000	14.74
33	WRTATALPA	344	1.4000	14.74
34	MLACGAAYV	142	1.3000	13.68
35	LRLCEERGG	183	1.3000	13.68
36	VLVSALRAQ	299	1.3000	13.68
37	YRADRFWSQ	323	1.3000	13.68
38	LHRWRTATA	341	1.3000	13.68
39	VRRYLADDL	363	1.2600	13.26
40	YVTFDLIHR	58	1.2000	12.63
41	VVARVRRYL	359	1.1600	12.21

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	FRADATLQF	163	4.5000	49.45
2	WVTDAVEYG	383	4.4000	48.35
3	YVIDREMGE	149	3.9000	42.86
4	VELIEKMLA	136	3.0000	32.97
5	YRADRFWSQ	323	3.0000	32.97
6	VRLGLLAGH	314	2.9800	32.75
7	LRAQDVEPS	304	2.9000	31.87
8	YVCGITPYD	40	2.4000	26.37
9	WRTATALPA	344	2.4000	26.37

10	LVLVSALRA	298	2.3000	25.27
11	FGPGRPGWH	221	1.9800	21.76
12	YFRADATLQ	162	1.9000	20.88
13	VRPVAPGSK	28	1.8000	19.78
14	YLADDLDTP	366	1.6000	17.58
15	WRAARPGEP	207	1.5000	16.48
16	IGWDGHKMS	284	1.5000	16.48
17	LRVLPPQDY	117	1.1000	12.09
18	VTFDLIHRL	59	1.0000	10.99
19	VLVSALRAQ	299	1.0000	10.99
20	YVGATEAIA	125	0.9000	9.89
21	WYCPPVPVL	3	0.8000	8.79
22	YVQNITDID	77	0.8000	8.79
23	YVHAGMIGW	278	0.8000	8.79
24	VAPGSKATM	31	0.7000	7.69
25	YVTFDLIHR	58	0.7000	7.69
26	VARVRRYLA	360	0.6500	7.14
27	LVSALRAQD	300	0.6000	6.59
28	FERADRDGV	89	0.5000	5.49
29	VECAAIALS	230	0.5000	5.49
30	IALSRIGSG	235	0.5000	5.49
31	FDLIHRLWL	61	0.4000	4.40
32	WHVECAAIA	228	0.3000	3.30
33	LHRWRTATA	341	0.3000	3.30
34	VCGITPYDA	41	0.1500	1.65
35	LRLYDSADR	18	0.1000	1.10
36	FCEDMAALR	110	0.1000	1.10
37	FARHYVHAG	274	0.1000	1.10
38	WRDLAQAEV	99	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score

1	LRAQDVEPS	304	4.3000	48.86
2	FRADATLQF	163	4.0000	45.45
3	VRLGLLAGH	314	3.9800	45.23
4	LVLVSALRA	298	3.8000	43.18
5	WVTDAVEYG	383	3.8000	43.18
6	VELIEKMLA	136	3.7000	42.05
7	IGWDGHKMS	284	3.1000	35.23
8	VTFDLIHRL	59	2.8000	31.82
9	YVIDREMGE	149	2.6000	29.55
10	LRVLPPQDY	117	2.2000	25.00
11	WRTATALPA	344	1.9000	21.59
12	VAPGSKATM	31	1.7000	19.32
13	VLVSALRAQ	299	1.7000	19.32
14	LVSALRAQD	300	1.6000	18.18
15	LWLDLGHEL	67	1.5000	17.05
16	VECAAIALS	230	1.5000	17.05
17	VRPVAPGSK	28	1.4000	15.91
18	LHRWRTATA	341	1.3000	14.77
19	IQGGGSDLI	246	1.2000	13.64
20	YRADRFWSQ	323	1.2000	13.64
21	LRLYDSADR	18	1.1000	12.50
22	MYVCGITPY	39	1.0000	11.36
23	YFRADATLQ	162	0.9000	10.23
24	YLADDLDTP	366	0.9000	10.23
25	MAALRVLPP	114	0.6000	6.82
26	VRRYLADDL	363	0.6000	6.82
27	VARVRRYLA	360	0.5000	5.68
28	LVATAIDAL	400	0.5000	5.68
29	IHRLWLDLG	64	0.4000	4.55
30	MLACGAAYV	142	0.3000	3.41
31	LAQAEVALF	102	0.2000	2.27
32	LAGHYRADR	319	0.2000	2.27
33	YVQNITDID	77	0.1000	1.14
34	IEKMLACGA	139	0.1000	1.14

35	IALSRIGSG	235	0.1000	1.14
36	VEPSAVRLG	309	0.1000	1.14
37	FDLIHRLWL	61	-0.1000	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	LRAQDVEPS	304	4.3000	48.86
2	FRADATLQF	163	4.0000	45.45
3	VRLGLLAGH	314	3.9800	45.23
4	LVLVSALRA	298	3.8000	43.18
5	WVTDAVEYG	383	3.8000	43.18
6	VELIEKMLA	136	3.7000	42.05
7	IGWDGHKMS	284	3.1000	35.23
8	VTFDLIHRL	59	2.8000	31.82
9	YVIDREMGE	149	2.6000	29.55
10	LRVLPPQDY	117	2.2000	25.00
11	WRTATALPA	344	1.9000	21.59
12	VAPGSKATM	31	1.7000	19.32
13	VLVSALRAQ	299	1.7000	19.32
14	LVSALRAQD	300	1.6000	18.18
15	LWLDLGHEL	67	1.5000	17.05
16	VECAAIALS	230	1.5000	17.05
17	VRPVAPGSK	28	1.4000	15.91
18	LHRWRTATA	341	1.3000	14.77
19	IQGGGSDLI	246	1.2000	13.64
20	YRADRFWSQ	323	1.2000	13.64
21	LRLYDSADR	18	1.1000	12.50
22	MYVCGITPY	39	1.0000	11.36
23	YFRADATLQ	162	0.9000	10.23
24	YLADDLDTP	366	0.9000	10.23
25	MAALRVLPP	114	0.6000	6.82
26	VRRYLADDL	363	0.6000	6.82

27	VARVRRYLA	360	0.5000	5.68
28	LVATAIDAL	400	0.5000	5.68
29	IHRLWLDLG	64	0.4000	4.55
30	MLACGAAYV	142	0.3000	3.41
31	LAQAEVALF	102	0.2000	2.27
32	LAGHYRADR	319	0.2000	2.27
33	YVQNITDID	77	0.1000	1.14
34	IEKMLACGA	139	0.1000	1.14
35	IALSRIGSG	235	0.1000	1.14
36	VEPSAVRLG	309	0.1000	1.14
37	FDLIHRLWL	61	-0.1000	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	LRAQDVEPS	304	4.3000	48.86
2	FRADATLQF	163	4.0000	45.45
3	VRLGLLAGH	314	3.9800	45.23
4	LVLVSALRA	298	3.8000	43.18
5	WVTDAVEYG	383	3.8000	43.18
6	VELIEKMLA	136	3.7000	42.05
7	IGWDGHKMS	284	3.1000	35.23
8	VTFDLIHRL	59	2.8000	31.82
9	YVIDREMGE	149	2.6000	29.55
10	LRVLPPQDY	117	2.2000	25.00
11	WRTATALPA	344	1.9000	21.59
12	VAPGSKATM	31	1.7000	19.32
13	VLVSALRAQ	299	1.7000	19.32
14	LVSALRAQD	300	1.6000	18.18
15	LWLDLGHEL	67	1.5000	17.05
16	VECAAIALS	230	1.5000	17.05
17	VRPVAPGSK	28	1.4000	15.91
18	LHRWRTATA	341	1.3000	14.77

19	IQGGGSDLI	246	1.2000	13.64
20	YRADRFWSQ	323	1.2000	13.64
21	LRLYDSADR	18	1.1000	12.50
22	MYVCGITPY	39	1.0000	11.36
23	YFRADATLQ	162	0.9000	10.23
24	YLADDLDTP	366	0.9000	10.23
25	MAALRVLPP	114	0.6000	6.82
26	VRRYLADDL	363	0.6000	6.82
27	VARVRRYLA	360	0.5000	5.68
28	LVATAIDAL	400	0.5000	5.68
29	IHRLWLDLG	64	0.4000	4.55
30	MLACGAAYV	142	0.3000	3.41
31	LAQAEVALF	102	0.2000	2.27
32	LAGHYRADR	319	0.2000	2.27
33	YVQNITDID	77	0.1000	1.14
34	IEKMLACGA	139	0.1000	1.14
35	IALSRIGSG	235	0.1000	1.14
36	VEPSAVRLG	309	0.1000	1.14
37	FDLIHRLWL	61	-0.1000	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	FRADATLQF	163	6.4000	67.37
2	WVTDAVEYG	383	5.8000	61.05
3	YVIDREMGE	149	5.3000	55.79
4	YVCGITPYD	40	3.5000	36.84
5	LRAQDVEPS	304	3.3000	34.74
6	VELIEKMLA	136	3.0000	31.58
7	YLADDLDTP	366	2.6000	27.37
8	WRAARPGEP	207	2.5000	26.32
9	LRVLPPQDY	117	2.4000	25.26
10	VRLGLLAGH	314	2.4000	25.26

11	WRTATALPA	344	2.4000	25.26
12	LVLVSALRA	298	2.3000	24.21
13	YRADRFWSQ	323	2.3000	24.21
14	VAPGSKATM	31	2.2000	23.16
15	YVTFDLIHR	58	2.2000	23.16
16	VTFDLIHRL	59	1.9600	20.63
17	VRPVAPGSK	28	1.9000	20.00
18	YVQNITDID	77	1.9000	20.00
19	IALSRIGSG	235	1.9000	20.00
20	IGWDGHKMS	284	1.9000	20.00
21	WYCPPVPVL	3	1.7600	18.53
22	LVSALRAQD	300	1.7000	17.89
23	LRLYDSADR	18	1.6000	16.84
24	FCEDMAALR	110	1.6000	16.84
25	FERADRDGV	89	1.5000	15.79
26	FARHYVHAG	274	1.5000	15.79
27	FGPGRPGWH	221	1.4000	14.74
28	FDLIHRLWL	61	1.3600	14.32
29	MYVCGITPY	39	1.3000	13.68
30	YFRADATLQ	162	1.2000	12.63
31	FWSQQVLDE	328	1.2000	12.63
32	LAQAEVALF	102	1.1000	11.58
33	LWRAARPGE	206	1.0000	10.53
34	YDRDTMLRL	177	0.9600	10.11
35	WRDLAQAEV	99	0.9000	9.47
36	YVGATEAIA	125	0.9000	9.47
37	VECAAIALS	230	0.9000	9.47
38	IQGGGSDLI	246	0.8000	8.42
39	YVHAGMIGW	278	0.8000	8.42
40	VEPSAVRLG	309	0.8000	8.42
41	VLPGRGPQL	10	0.7600	8.00

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

	2.08	8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LRAQDVEPS	304	4.3000	48.86
2	FRADATLQF	163	4.0000	45.45
3	VRLGLLAGH	314	3.9800	45.23
4	LVLVSALRA	298	3.8000	43.18
5	WVTDAVEYG	383	3.8000	43.18
6	VELIEKMLA	136	3.7000	42.05
7	IGWDGHKMS	284	3.1000	35.23
8	VTFDLIHRL	59	2.8000	31.82
9	YVIDREMGE	149	2.6000	29.55
10	LRVLPPQDY	117	2.2000	25.00
11	WRTATALPA	344	1.9000	21.59
12	VAPGSKATM	31	1.7000	19.32
13	VLVSALRAQ	299	1.7000	19.32
14	LVSALRAQD	300	1.6000	18.18
15	LWLDLGHEL	67	1.5000	17.05
16	VECAAIALS	230	1.5000	17.05
17	VRPVAPGSK	28	1.4000	15.91
18	LHRWRTATA	341	1.3000	14.77
19	IQGGGSDLI	246	1.2000	13.64
20	YRADRFWSQ	323	1.2000	13.64
21	LRLYDSADR	18	1.1000	12.50
22	MYVCGITPY	39	1.0000	11.36
23	YFRADATLQ	162	0.9000	10.23
24	YLADDLDTP	366	0.9000	10.23
25	MAALRVLPP	114	0.6000	6.82
26	VRRYLADDL	363	0.6000	6.82
27	VARVRRYLA	360	0.5000	5.68
28	LVATAIDAL	400	0.5000	5.68
29	IHRLWLDLG	64	0.4000	4.55
30	MLACGAAYV	142	0.3000	3.41
31	LAQAEVALF	102	0.2000	2.27
32	LAGHYRADR	319	0.2000	2.27

33	YVQNITDID	77	0.1000	1.14
34	IEKMLACGA	139	0.1000	1.14
35	IALSRIGSG	235	0.1000	1.14
36	VEPSAVRLG	309	0.1000	1.14
37	FDLIHRLWL	61	-0.1000	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	FRADATLQF	163	5.2000	60.47
2	LRAQDVEPS	304	3.8000	44.19
3	WVTDAVEYG	383	3.6000	41.86
4	YVQNITDID	77	2.9000	33.72
5	WRTATALPA	344	2.9000	33.72
6	WHVECAAIA	228	2.8000	32.56
7	YFRADATLQ	162	1.9000	22.09
8	LVLVSALRA	298	1.9000	22.09
9	YVIDREMGE	149	1.7000	19.77
10	FARHYVHAG	274	1.7000	19.77
11	YRADRFWSQ	323	1.6000	18.60
12	LRVLPPQDY	117	1.5000	17.44
13	LHRWRTATA	341	1.2000	13.95
14	VLDEATARL	333	1.1000	12.79
15	FWSQQVLDE	328	0.8000	9.30
16	LRLYDSADR	18	0.6000	6.98
17	LVATAIDAL	400	0.4000	4.65
18	YVHAGMIGW	278	0.2800	3.26
19	VTFDLIHRL	59	0.1000	1.16
20	MAALRVLPP	114	0.1000	1.16
21	YVGATEAIA	125	-0.1000	0
22	IGWDGHKMS	284	-0.1000	0
23	VECAAIALS	230	-0.3000	0
24	YLADDLDTP	366	-0.3000	0

25	WRAARPGEP	207	-0.4000	0
26	FPHHEFTAA	255	-0.4000	0
27	VRLGLLAGH	314	-0.4200	0
28	WRDLAQAEV	99	-0.5000	0
29	FTAAHAECV	260	-0.5000	0
30	VLVSALRAQ	299	-0.5000	0
31	YDRDTMLRL	177	-0.6000	0
32	WDGHKMSKS	286	-0.6000	0
33	WLDLGHELH	68	-0.6200	0
34	LHYVQNITD	75	-0.6200	0
35	VELIEKMLA	136	-0.7000	0
36	MLACGAAYV	142	-0.7000	0
37	MYVCGITPY	39	-0.8000	0
38	LGHAATYVT	52	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LHRWRTATA	341	5.0000	52.08
2	LVLVSALRA	298	3.4000	35.42
3	LRLYDSADR	18	2.8000	29.17
4	LLWRAARPG	205	2.7000	28.13
5	LGHAATYVT	52	2.3000	23.96
6	LRVLPPQDY	117	2.2000	22.92
7	LRAQDVEPS	304	2.2000	22.92
8	WRTATALPA	344	2.2000	22.92
9	VLVSALRAQ	299	1.6000	16.67
10	LRLCEERGG	183	1.5000	15.62
11	MIGWDGHKM	283	1.5000	15.62
12	VRLGLLAGH	314	1.4800	15.42
13	VVARVRRYL	359	1.4000	14.58
14	MQSWYCPPV	0	1.3000	13.54
15	LIHRLWLDL	63	1.3000	13.54

16	FARHYVHAG	274	1.3000	13.54
17	VCGITPYDA	41	1.1800	12.29
18	YFRADATLQ	162	1.1000	11.46
19	LHYVQNITD	75	1.0000	10.42
20	VEPSAVRLG	309	1.0000	10.42
21	LPGRGPQLR	11	0.8000	8.33
22	FRADATLQF	163	0.8000	8.33
23	IEKMLACGA	139	0.7000	7.29
24	VECAAIALS	230	0.7000	7.29
25	IYFRADATL	161	0.6000	6.25
26	MYVCGITPY	39	0.4000	4.17
27	IFPHHEFTA	254	0.4000	4.17
28	MLACGAAYV	142	0.3000	3.12
29	LFERADRDG	88	0.2000	2.08
30	LAQAEVALF	102	-0.1000	0
31	LACGAAYVI	143	-0.1000	0
32	YVTFDLIHR	58	-0.2000	0
33	YVHAGMIGW	278	-0.3000	0
34	YRADRFWSQ	323	-0.3000	0
35	YVCGITPYD	40	-0.4000	0
36	LDGWVTDAV	380	-0.4000	0
37	VELIEKMLA	136	-0.4200	0
38	VSALRAQDV	301	-0.5000	0
39	VQNITDIDD	78	-0.5200	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	LVLVSALRA	298	3.9000	44.32
2	LHRWRTATA	341	3.3500	38.07
3	LRAQDVEPS	304	3.1000	35.23
4	LRLYDSADR	18	2.8000	31.82
5	LRVLPPQDY	117	2.5000	28.41

6	IEKMLACGA	139	1.9000	21.59
7	LHYVQNITD	75	1.7800	20.23
8	VRPVAPGSK	28	1.5000	17.05
9	WRTATALPA	344	1.5000	17.05
10	YFRADATLQ	162	1.4000	15.91
11	FRADATLQF	163	1.3000	14.77
12	LGHAATYVT	52	1.2000	13.64
13	VCGITPYDA	41	1.1000	12.50
14	MAALRVLPP	114	0.9000	10.23
15	MYVCGITPY	39	0.7000	7.95
16	VECAAIALS	230	0.7000	7.95
17	VELIEKMLA	136	0.5000	5.68
18	MLACGAAYV	142	0.3000	3.41
19	VRRYLADDL	363	0.3000	3.41
20	YVTFDLIHR	58	0.0800	0.91
21	VQNITDIDD	78	0.0800	0.91
22	LAQAEVALF	102	-0.1000	0
23	VSALRAQDV	301	-0.2000	0
24	VRLGLLAGH	314	-0.2200	0
25	MQSWYCPPV	0	-0.3500	0
26	LSRIGSGLD	237	-0.4000	0
27	LGLLAGHYR	316	-0.4000	0
28	VLDEATARL	333	-0.5000	0
29	YVQNITDID	77	-0.6000	0
30	ITPYDATHL	44	-0.7000	0
31	VLVSALRAQ	299	-0.7000	0
32	YVHAGMIGW	278	-0.7200	0
33	IHRLWLDLG	64	-0.8000	0
34	WHVECAAIA	228	-0.8000	0
35	WVTDAVEYG	383	-0.8000	0
36	MIGWDGHKM	283	-1.0500	0
37	YVGATEAIA	125	-1.1000	0
38	LRLCEERGG	183	-1.1000	0
39	LVATAIDAL	400	-1.1000	0

40	LDGWVTDAV	380	-1.1500	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	LHYVQNITD	75	3.4800	37.02
2	YFRADATLQ	162	3.2000	34.04
3	FRADATLQF	163	3.2000	34.04
4	YVQNITDID	77	3.1000	32.98
5	LVLVSALRA	298	2.9000	30.85
6	LRVLPPQDY	117	2.6000	27.66
7	FWSQQVLDE	328	2.6000	27.66
8	WRTATALPA	344	2.5000	26.60
9	LHRWRTATA	341	2.3500	25.00
10	YVIDREMGE	149	2.1000	22.34
11	LRAQDVEPS	304	2.1000	22.34
12	LRLYDSADR	18	1.8000	19.15
13	VQNITDIDD	78	1.7800	18.94
14	YVCGITPYD	40	1.6000	17.02
15	WVTDAVEYG	383	1.5000	15.96
16	LSRIGSGLD	237	1.3000	13.83
17	YVHAGMIGW	278	1.1800	12.55
18	LGHAATYVT	52	1.1000	11.70
19	YVTFDLIHR	58	1.0800	11.49
20	IEKMLACGA	139	0.9000	9.57
21	MYVCGITPY	39	0.8000	8.51
22	YRADRFWSQ	323	0.6000	6.38
23	FARHYVHAG	274	0.5000	5.32
24	MAALRVLPP	114	0.3000	3.19
25	VRRYLADDL	363	0.3000	3.19
26	WHVECAAIA	228	0.2000	2.13
27	VCGITPYDA	41	0.1000	1.06
28	WRAARPGEP	207	0.1000	1.06

29	VGATEAIAE	126	-0.0200	0
30	WLDLGHELH	68	-0.1000	0
31	YVGATEAIA	125	-0.1000	0
32	LVSALRAQD	300	-0.1000	0
33	VRPVAPGSK	28	-0.2000	0
34	LAQAEVALF	102	-0.2000	0
35	VECAAIALS	230	-0.3000	0
36	MLACGAAYV	142	-0.4000	0
37	WYCPPVPVL	3	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVLVSALRA	298	2.9000	32.95
2	WRTATALPA	344	2.5000	28.41
3	YFRADATLQ	162	2.4000	27.27
4	LHRWRTATA	341	2.3500	26.70
5	FRADATLQF	163	2.3000	26.14
6	LRAQDVEPS	304	2.1000	23.86
7	LRLYDSADR	18	1.8000	20.45
8	LRVLPPQDY	117	1.5000	17.05
9	YVTFDLIHR	58	1.0800	12.27
10	IEKMLACGA	139	0.9000	10.23
11	LHYVQNITD	75	0.7800	8.86
12	VRPVAPGSK	28	0.5000	5.68
13	YVQNITDID	77	0.4000	4.55
14	YVHAGMIGW	278	0.2800	3.18
15	LGHAATYVT	52	0.2000	2.27
16	WHVECAAIA	228	0.2000	2.27
17	WVTDAVEYG	383	0.2000	2.27
18	VCGITPYDA	41	0.1000	1.14
19	MAALRVLPP	114	-0.1000	0
20	YVGATEAIA	125	-0.1000	0

21	YRADRFWSQ	323	-0.2000	0
22	MYVCGITPY	39	-0.3000	0
23	WRDLAQAEV	99	-0.3000	0
24	WRAARPGEP	207	-0.3000	0
25	VECAAIALS	230	-0.3000	0
26	FWSQQVLDE	328	-0.4000	0
27	VELIEKMLA	136	-0.5000	0
28	MLACGAAYV	142	-0.7000	0
29	VRRYLADDL	363	-0.7000	0
30	FARHYVHAG	274	-0.8000	0
31	YVIDREMGE	149	-0.9000	0
32	VQNITDIDD	78	-0.9200	0
33	YVCGITPYD	40	-1.1000	0
34	LAQAEVALF	102	-1.1000	0
35	VSALRAQDV	301	-1.2000	0
36	VRLGLLAGH	314	-1.2200	0
37	WLDLGHELH	68	-1.3200	0
38	MQSWYCPPV	0	-1.3500	0
39	LSRIGSGLD	237	-1.4000	0
40	FTAAHAECV	260	-1.4000	0

ALLELE: DRB1_0410	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	LHYVQNITD	75	4.4800	47.66
2	LVLVSALRA	298	3.9000	41.49
3	LRVLPPQDY	117	3.6000	38.30
4	LHRWRTATA	341	3.3500	35.64
5	LRAQDVEPS	304	3.1000	32.98
6	LRLYDSADR	18	2.8000	29.79
7	VQNITDIDD	78	2.7800	29.57
8	LSRIGSGLD	237	2.3000	24.47
9	YFRADATLQ	162	2.2000	23.40

10	FRADATLQF	163	2.2000	23.40
11	LGHAATYVT	52	2.1000	22.34
12	YVQNITDID	77	2.1000	22.34
13	IEKMLACGA	139	1.9000	20.21
14	MYVCGITPY	39	1.8000	19.15
15	FWSQQVLDE	328	1.6000	17.02
16	WRTATALPA	344	1.5000	15.96
17	MAALRVLPP	114	1.3000	13.83
18	VRRYLADDL	363	1.3000	13.83
19	VCGITPYDA	41	1.1000	11.70
20	YVIDREMGE	149	1.1000	11.70
21	VRLGLLAGH	314	1.0000	10.64
22	VGATEAIAE	126	0.9800	10.43
23	LVSALRAQD	300	0.9000	9.57
24	VRPVAPGSK	28	0.8000	8.51
25	LAQAEVALF	102	0.8000	8.51
26	VECAAIALS	230	0.7000	7.45
27	YVCGITPYD	40	0.6000	6.38
28	MLACGAAYV	142	0.6000	6.38
29	IHRLWLDLG	64	0.5000	5.32
30	VELIEKMLA	136	0.5000	5.32
31	VLDEATARL	333	0.5000	5.32
32	WVTDAVEYG	383	0.5000	5.32
33	ITPYDATHL	44	0.3000	3.19
34	LRLCEERGG	183	0.2000	2.13
35	YVHAGMIGW	278	0.1800	1.91
36	VLVSALRAQ	299	0.1000	1.06
37	VSALRAQDV	301	0.1000	1.06
38	YVTFDLIHR	58	0.0800	0.85
39	MIGWDGHKM	283	0.0500	0.53

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	FRADATLQF	163	7.1000	78.89
2	WVTDAVEYG	383	5.0000	55.56
3	LRAQDVEPS	304	4.2000	46.67
4	YVQNITDID	77	4.0000	44.44
5	YVIDREMGE	149	3.1000	34.44
6	FARHYVHAG	274	3.1000	34.44
7	WRTATALPA	344	2.9000	32.22
8	LRVLPPQDY	117	2.8000	31.11
9	WHVECAAIA	228	2.8000	31.11
10	FWSQQVLDE	328	2.2000	24.44
11	LRLYDSADR	18	2.1000	23.33
12	VLDEATARL	333	2.0600	22.89
13	LVLVSALRA	298	1.9000	21.11
14	LVATAIDAL	400	1.3600	15.11
15	YFRADATLQ	162	1.2000	13.33
16	LHRWRTATA	341	1.2000	13.33
17	YVCGITPYD	40	1.1000	12.22
18	MAALRVLPP	114	1.1000	12.22
19	VTFDLIHRL	59	1.0600	11.78
20	YRADRFWSQ	323	0.9000	10.00
21	LAQAEVALF	102	0.8000	8.89
22	FCEDMAALR	110	0.7000	7.78
23	YLADDLDTP	366	0.7000	7.78
24	YVTFDLIHR	58	0.6800	7.56
25	FGYESGYDR	171	0.6000	6.67
26	WRAARPGEP	207	0.6000	6.67
27	MYVCGITPY	39	0.5000	5.56
28	WRDLAQAEV	99	0.5000	5.56
29	FTAAHAECV	260	0.5000	5.56
30	LHYVQNITD	75	0.4800	5.33
31	YDRDTMLRL	177	0.3600	4.00
32	IHRLWLDLG	64	0.3000	3.33
33	MLACGAAYV	142	0.3000	3.33

34	IGWDGHKMS	284	0.3000	3.33
35	VEPSAVRLG	309	0.3000	3.33
36	LGLLAGHYR	316	0.3000	3.33
37	YVHAGMIGW	278	0.2800	3.11
38	YGGHDAGAP	390	0.2000	2.22
39	LFCEDMAAL	109	0.1600	1.78
40	VECAAIALS	230	0.1000	1.11
41	IQGGGSDLI	246	0.1000	1.11

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	LVLVSALRA	298	3.9000	44.32
2	LHRWRTATA	341	3.3500	38.07
3	LRAQDVEPS	304	3.1000	35.23
4	LRLYDSADR	18	2.8000	31.82
5	LRVLPPQDY	117	2.5000	28.41
6	IEKMLACGA	139	1.9000	21.59
7	LHYVQNITD	75	1.7800	20.23
8	VRPVAPGSK	28	1.5000	17.05
9	WRTATALPA	344	1.5000	17.05
10	YFRADATLQ	162	1.4000	15.91
11	FRADATLQF	163	1.3000	14.77
12	LGHAATYVT	52	1.2000	13.64
13	VCGITPYDA	41	1.1000	12.50
14	MAALRVLPP	114	0.9000	10.23
15	MYVCGITPY	39	0.7000	7.95
16	VECAAIALS	230	0.7000	7.95
17	VELIEKMLA	136	0.5000	5.68
18	MLACGAAYV	142	0.3000	3.41
19	VRRYLADDL	363	0.3000	3.41
20	YVTFDLIHR	58	0.0800	0.91
21	VQNITDIDD	78	0.0800	0.91

22	LAQAEVALF	102	-0.1000	0
23	VSALRAQDV	301	-0.2000	0
24	VRLGLLAGH	314	-0.2200	0
25	MQSWYCPPV	0	-0.3500	0
26	LSRIGSGLD	237	-0.4000	0
27	LGLLAGHYR	316	-0.4000	0
28	VLDEATARL	333	-0.5000	0
29	YVQNITDID	77	-0.6000	0
30	ITPYDATHL	44	-0.7000	0
31	VLVSALRAQ	299	-0.7000	0
32	YVHAGMIGW	278	-0.7200	0
33	IHRLWLDLG	64	-0.8000	0
34	WHVECAAIA	228	-0.8000	0
35	WVTDAVEYG	383	-0.8000	0
36	MIGWDGHKM	283	-1.0500	0
37	YVGATEAIA	125	-1.1000	0
38	LRLCEERGG	183	-1.1000	0
39	LVATAIDAL	400	-1.1000	0
40	LDGWVTDAV	380	-1.1500	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	FRADATLQF	163	5.2000	60.47
2	LRAQDVEPS	304	3.8000	44.19
3	WVTDAVEYG	383	3.6000	41.86
4	YVQNITDID	77	2.9000	33.72
5	WRTATALPA	344	2.9000	33.72
6	WHVECAAIA	228	2.8000	32.56
7	YFRADATLQ	162	1.9000	22.09
8	LVLVSALRA	298	1.9000	22.09
9	YVIDREMGE	149	1.7000	19.77
10	FARHYVHAG	274	1.7000	19.77

11	YRADRFWSQ	323	1.6000	18.60
12	LRVLPPQDY	117	1.5000	17.44
13	LHRWRTATA	341	1.2000	13.95
14	VLDEATARL	333	1.1000	12.79
15	FWSQQVLDE	328	0.8000	9.30
16	LRLYDSADR	18	0.6000	6.98
17	LVATAIDAL	400	0.4000	4.65
18	YVHAGMIGW	278	0.2800	3.26
19	VTFDLIHRL	59	0.1000	1.16
20	MAALRVLPP	114	0.1000	1.16
21	YVGATEAIA	125	-0.1000	0
22	IGWDGHKMS	284	-0.1000	0
23	VECAAIALS	230	-0.3000	0
24	YLADDLDTP	366	-0.3000	0
25	WRAARPGEP	207	-0.4000	0
26	FPHHEFTAA	255	-0.4000	0
27	VRLGLLAGH	314	-0.4200	0
28	WRDLAQAEV	99	-0.5000	0
29	FTAAHAECV	260	-0.5000	0
30	VLVSALRAQ	299	-0.5000	0
31	YDRDTMLRL	177	-0.6000	0
32	WDGHKMSKS	286	-0.6000	0
33	WLDLGHELH	68	-0.6200	0
34	LHYVQNITD	75	-0.6200	0
35	VELIEKMLA	136	-0.7000	0
36	MLACGAAYV	142	-0.7000	0
37	MYVCGITPY	39	-0.8000	0
38	LGHAATYVT	52	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FDLIHRLWL	61	5.3000	45.69

2	LVLVSALRA	298	5.2000	44.83
3	FRADATLQF	163	4.8200	41.55
4	YVHAGMIGW	278	4.7000	40.52
5	WRTATALPA	344	4.4000	37.93
6	LVATAIDAL	400	4.1000	35.34
7	LIHRLWLDL	63	3.9000	33.62
8	VRRYLADDL	363	3.1000	26.72
9	WYCPPVPVL	3	3.0000	25.86
10	YVTFDLIHR	58	3.0000	25.86
11	VGATEAIAE	126	3.0000	25.86
12	LACGAAYVI	143	3.0000	25.86
13	MSKSRGNLV	291	3.0000	25.86
14	VVARVRRYL	359	3.0000	25.86
15	FTAAHAECV	260	2.9000	25.00
16	ITPYDATHL	44	2.7000	23.28
17	LRVLPPQDY	117	2.6000	22.41
18	YDRDTMLRL	177	2.6000	22.41
19	LHYVQNITD	75	2.1000	18.10
20	VTFDLIHRL	59	2.0000	17.24
21	LWLDLGHEL	67	2.0000	17.24
22	MLACGAAYV	142	2.0000	17.24
23	IQGGGSDLI	246	2.0000	17.24
24	MYVCGITPY	39	1.9000	16.38
25	VELIEKMLA	136	1.9000	16.38
26	VLPGRGPQL	10	1.8000	15.52
27	LGHAATYVT	52	1.7200	14.83
28	VCGITPYDA	41	1.5000	12.93
29	YFRADATLQ	162	1.5000	12.93
30	MIGWDGHKM	283	1.5000	12.93
31	IDALLGVDL	405	1.3000	11.21
32	LAQAEVALF	102	1.2000	10.34
33	FARHYVHAG	274	1.2000	10.34
34	VARVRRYLA	360	1.2000	10.34
35	MQSWYCPPV	0	1.1000	9.48

36	LRLYDSADR	18	1.1000	9.48
37	WRAARPGEP	207	1.1000	9.48
38	VEPSAVRLG	309	1.1000	9.48
39	WRDLAQAEV	99	1.0000	8.62
40	LFCEDMAAL	109	1.0000	8.62
41	YVIDREMGE	149	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	FDLIHRLWL	61	5.3000	45.69
2	LVLVSALRA	298	5.2000	44.83
3	FRADATLQF	163	4.8200	41.55
4	YVHAGMIGW	278	4.7000	40.52
5	WRTATALPA	344	4.4000	37.93
6	LVATAIDAL	400	4.1000	35.34
7	LIHRLWLDL	63	3.9000	33.62
8	VRRYLADDL	363	3.1000	26.72
9	WYCPPVPVL	3	3.0000	25.86
10	YVTFDLIHR	58	3.0000	25.86
11	VGATEAIAE	126	3.0000	25.86
12	LACGAAYVI	143	3.0000	25.86
13	MSKSRGNLV	291	3.0000	25.86
14	VVARVRRYL	359	3.0000	25.86
15	FTAAHAECV	260	2.9000	25.00
16	ITPYDATHL	44	2.7000	23.28
17	LRVLPPQDY	117	2.6000	22.41
18	YDRDTMLRL	177	2.6000	22.41
19	LHYVQNITD	75	2.1000	18.10
20	VTFDLIHRL	59	2.0000	17.24
21	LWLDLGHEL	67	2.0000	17.24
22	MLACGAAYV	142	2.0000	17.24
23	IQGGGSDLI	246	2.0000	17.24

24	MYVCGITPY	39	1.9000	16.38
25	VELIEKMLA	136	1.9000	16.38
26	VLPGRGPQL	10	1.8000	15.52
27	LGHAATYVT	52	1.7200	14.83
28	VCGITPYDA	41	1.5000	12.93
29	YFRADATLQ	162	1.5000	12.93
30	MIGWDGHKM	283	1.5000	12.93
31	IDALLGVDL	405	1.3000	11.21
32	LAQAEVALF	102	1.2000	10.34
33	FARHYVHAG	274	1.2000	10.34
34	VARVRRYLA	360	1.2000	10.34
35	MQSWYCPPV	0	1.1000	9.48
36	LRLYDSADR	18	1.1000	9.48
37	WRAARPGEP	207	1.1000	9.48
38	VEPSAVRLG	309	1.1000	9.48
39	WRDLAQAEV	99	1.0000	8.62
40	LFCEDMAAL	109	1.0000	8.62
41	YVIDREMGE	149	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	VVARVRRYL	359	3.8000	44.19
2	LRLYDSADR	18	3.3000	38.37
3	LVSALRAQD	300	3.3000	38.37
4	VRLGLLAGH	314	2.7000	31.40
5	YVIDREMGE	149	2.2000	25.58
6	LVLVSALRA	298	2.1000	24.42
7	LLWRAARPG	205	2.0000	23.26
8	WRTATALPA	344	1.9000	22.09
9	LRVLPPQDY	117	1.8000	20.93
10	YVCGITPYD	40	1.7000	19.77
11	LIEKMLACG	138	1.7000	19.77

12	VRRYLADDL	363	1.7000	19.77
13	FRADATLQF	163	1.6000	18.60
14	YVQNITDID	77	1.5000	17.44
15	VELIEKMLA	136	1.4000	16.28
16	WRAARPGEP	207	1.3000	15.12
17	FWSQQVLDE	328	1.3000	15.12
18	LHRWRTATA	341	1.3000	15.12
19	FGPGRPGWH	221	1.1000	12.79
20	YVTFDLIHR	58	1.0000	11.63
21	LIHRLWLDL	63	0.9000	10.47
22	WRDLAQAEV	99	0.9000	10.47
23	YVGATEAIA	125	0.9000	10.47
24	VRPVAPGSK	28	0.8000	9.30
25	FDLIHRLWL	61	0.7000	8.14
26	LWRAARPGE	206	0.7000	8.14
27	IYFRADATL	161	0.6000	6.98
28	LHYVQNITD	75	0.5000	5.81
29	IEKMLACGA	139	0.5000	5.81
30	LRLCEERGG	183	0.5000	5.81
31	VECAAIALS	230	0.5000	5.81
32	YVHAGMIGW	278	0.5000	5.81
33	YFRADATLQ	162	0.4000	4.65
34	VLVSALRAQ	299	0.4000	4.65
35	VAPGSKATM	31	0.3000	3.49
36	WHVECAAIA	228	0.3000	3.49
37	FARHYVHAG	274	0.3000	3.49
38	VDWRDLAQA	97	0.2000	2.33
39	WVTDAVEYG	383	0.2000	2.33
40	LAQAEVALF	102	0.1000	1.16
41	LSRIGSGLD	237	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	LRLYDSADR	18	3.3000	41.25
2	VVARVRRYL	359	2.8000	35.00
3	LVLVSALRA	298	2.1000	26.25
4	WRTATALPA	344	1.9000	23.75
5	VRPVAPGSK	28	1.5000	18.75
6	VRLGLLAGH	314	1.4800	18.50
7	VELIEKMLA	136	1.4000	17.50
8	LHRWRTATA	341	1.3000	16.25
9	YVTFDLIHR	58	1.0000	12.50
10	YVGATEAIA	125	0.9000	11.25
11	WRAARPGEP	207	0.9000	11.25
12	LRVLPPQDY	117	0.7000	8.75
13	FRADATLQF	163	0.7000	8.75
14	LLWRAARPG	205	0.7000	8.75
15	VRRYLADDL	363	0.7000	8.75
16	WRDLAQAEV	99	0.6000	7.50
17	LVSALRAQD	300	0.6000	7.50
18	IEKMLACGA	139	0.5000	6.25
19	VECAAIALS	230	0.5000	6.25
20	LIEKMLACG	138	0.4000	5.00
21	WHVECAAIA	228	0.3000	3.75
22	VDWRDLAQA	97	0.2000	2.50
23	LIHRLWLDL	63	-0.1000	0
24	VARVRRYLA	360	-0.1000	0
25	FGPGRPGWH	221	-0.1200	0
26	FDLIHRLWL	61	-0.3000	0
27	LRAQDVEPS	304	-0.3000	0
28	IYFRADATL	161	-0.4000	0
29	YFRADATLQ	162	-0.4000	0
30	YVHAGMIGW	278	-0.4000	0
31	VLVSALRAQ	299	-0.4000	0
32	LPGRGPQLR	11	-0.7000	0
33	MAALRVLPP	114	-0.7000	0

34	MLACGAAYV	142	-0.7000	0
35	VAPGSKATM	31	-0.8000	0
36	LAQAEVALF	102	-0.8000	0
37	YVIDREMGE	149	-0.8000	0
38	LRLCEERGG	183	-0.8000	0
39	YRADRFWSQ	323	-0.9000	0
40	YVCGITPYD	40	-1.0000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRLYDSADR	18	4.3000	53.75
2	VVARVRRYL	359	3.8000	47.50
3	LVLVSALRA	298	3.1000	38.75
4	VRPVAPGSK	28	2.5000	31.25
5	VRLGLLAGH	314	2.4800	31.00
6	VELIEKMLA	136	2.4000	30.00
7	LHRWRTATA	341	2.3000	28.75
8	LRVLPPQDY	117	1.7000	21.25
9	LLWRAARPG	205	1.7000	21.25
10	VRRYLADDL	363	1.7000	21.25
11	LVSALRAQD	300	1.6000	20.00
12	IEKMLACGA	139	1.5000	18.75
13	VECAAIALS	230	1.5000	18.75
14	LIEKMLACG	138	1.4000	17.50
15	VDWRDLAQA	97	1.2000	15.00
16	LIHRLWLDL	63	0.9000	11.25
17	WRTATALPA	344	0.9000	11.25
18	VARVRRYLA	360	0.9000	11.25
19	LRAQDVEPS	304	0.7000	8.75
20	IYFRADATL	161	0.6000	7.50
21	VLVSALRAQ	299	0.6000	7.50
22	LPGRGPQLR	11	0.3000	3.75

23	MAALRVLPP	114	0.3000	3.75
24	MLACGAAYV	142	0.3000	3.75
25	VAPGSKATM	31	0.2000	2.50
26	LAQAEVALF	102	0.2000	2.50
27	LRLCEERGG	183	0.2000	2.50
28	VCGITPYDA	41	-0.1000	0
29	YVGATEAIA	125	-0.1000	0
30	WRAARPGEP	207	-0.1000	0
31	VIDREMGEY	150	-0.3000	0
32	FRADATLQF	163	-0.3000	0
33	WRDLAQAEV	99	-0.4000	0
34	LGLLAGHYR	316	-0.4000	0
35	MQSWYCPPV	0	-0.5000	0
36	WHVECAAIA	228	-0.7000	0
37	MIGWDGHKM	283	-0.7000	0
38	IGWDGHKMS	284	-0.7000	0
39	LGHAATYVT	52	-0.8000	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	VVARVRRYL	359	4.8000	55.81
2	LRLYDSADR	18	4.3000	50.00
3	LVSALRAQD	300	4.3000	50.00
4	VRLGLLAGH	314	3.7000	43.02
5	LVLVSALRA	298	3.1000	36.05
6	LLWRAARPG	205	3.0000	34.88
7	LRVLPPQDY	117	2.8000	32.56
8	LIEKMLACG	138	2.7000	31.40
9	VRRYLADDL	363	2.7000	31.40
10	VELIEKMLA	136	2.4000	27.91
11	LHRWRTATA	341	2.3000	26.74
12	LIHRLWLDL	63	1.9000	22.09

13	VRPVAPGSK	28	1.8000	20.93
14	LWRAARPGE	206	1.7000	19.77
15	IYFRADATL	161	1.6000	18.60
16	LHYVQNITD	75	1.5000	17.44
17	IEKMLACGA	139	1.5000	17.44
18	LRLCEERGG	183	1.5000	17.44
19	VECAAIALS	230	1.5000	17.44
20	VLVSALRAQ	299	1.4000	16.28
21	VAPGSKATM	31	1.3000	15.12
22	VDWRDLAQA	97	1.2000	13.95
23	YVIDREMGE	149	1.2000	13.95
24	LAQAEVALF	102	1.1000	12.79
25	LSRIGSGLD	237	1.1000	12.79
26	VHAGMIGWD	279	1.0000	11.63
27	WRTATALPA	344	0.9000	10.47
28	VARVRRYLA	360	0.9000	10.47
29	VIDREMGEY	150	0.8000	9.30
30	YVCGITPYD	40	0.7000	8.14
31	MAALRVLPP	114	0.7000	8.14
32	LRAQDVEPS	304	0.7000	8.14
33	MLACGAAYV	142	0.6000	6.98
34	FRADATLQF	163	0.6000	6.98
35	YVQNITDID	77	0.5000	5.81
36	IALSRIGSG	235	0.5000	5.81
37	MIGWDGHKM	283	0.4000	4.65
38	LPGRGPQLR	11	0.3000	3.49
39	IHRLWLDLG	64	0.3000	3.49
40	WRAARPGEP	207	0.3000	3.49
41	VEPSAVRLG	309	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	LRLYDSADR	18	3.3000	37.93
2	LVLVSALRA	298	2.7000	31.03
3	WRTATALPA	344	2.5000	28.74
4	VVARVRRYL	359	2.5000	28.74
5	VELIEKMLA	136	2.4000	27.59
6	YFRADATLQ	162	2.4000	27.59
7	VRRYLADDL	363	1.9000	21.84
8	YVTFDLIHR	58	1.8800	21.61
9	LRVLPPQDY	117	1.7000	19.54
10	VRLGLLAGH	314	1.4800	17.01
11	LRAQDVEPS	304	1.4000	16.09
12	FRADATLQF	163	1.3000	14.94
13	LHRWRTATA	341	1.3000	14.94
14	ITPYDATHL	44	0.9000	10.34
15	YVGATEAIA	125	0.9000	10.34
16	VRPVAPGSK	28	0.8000	9.20
17	VARVRRYLA	360	0.8000	9.20
18	WRDLAQAEV	99	0.6000	6.90
19	LVSALRAQD	300	0.6000	6.90
20	WVTDAVEYG	383	0.6000	6.90
21	MYVCGITPY	39	0.5000	5.75
22	LIHRLWLDL	63	0.5000	5.75
23	IEKMLACGA	139	0.5000	5.75
24	VECAAIALS	230	0.5000	5.75
25	YVHAGMIGW	278	0.4800	5.52
26	LIEKMLACG	138	0.4000	4.60
27	LLWRAARPG	205	0.4000	4.60
28	LPGRGPQLR	11	0.3000	3.45
29	FDLIHRLWL	61	0.3000	3.45
30	WHVECAAIA	228	0.3000	3.45
31	VDWRDLAQA	97	0.2000	2.30
32	YVIDREMGE	149	0.2000	2.30
33	WRAARPGEP	207	0.2000	2.30
34	FERADRDGV	89	-0.1000	0

35	MAALRVLPP	114	-0.1000	0
36	VCGITPYDA	41	-0.2000	0
37	WLDLGHELH	68	-0.3200	0
38	IYFRADATL	161	-0.4000	0
39	YRADRFWSQ	323	-0.4000	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	VVARVRRYL	359	4.0000	39.60
2	LVLVSALRA	298	3.9000	38.61
3	YVIDREMGE	149	3.8000	37.62
4	WRTATALPA	344	3.7000	36.63
5	FRADATLQF	163	3.4000	33.66
6	LRLYDSADR	18	3.3000	32.67
7	LVSALRAQD	300	3.3000	32.67
8	FWSQQVLDE	328	3.1000	30.69
9	VELIEKMLA	136	3.0000	29.70
10	YVCGITPYD	40	2.8500	28.22
11	LIHRLWLDL	63	2.7000	26.73
12	VRLGLLAGH	314	2.7000	26.73
13	YVTFDLIHR	58	2.6000	25.74
14	FDLIHRLWL	61	2.5000	24.75
15	LLWRAARPG	205	2.2000	21.78
16	LHYVQNITD	75	2.1000	20.79
17	YVHAGMIGW	278	2.1000	20.79
18	LRVLPPQDY	117	1.9000	18.81
19	LWRAARPGE	206	1.8500	18.32
20	LIEKMLACG	138	1.7000	16.83
21	MAALRVLPP	114	1.5000	14.85
22	YFRADATLQ	162	1.5000	14.85
23	WRAARPGEP	207	1.4000	13.86
24	VRRYLADDL	363	1.4000	13.86

25	LHRWRTATA	341	1.3000	12.87
26	WVTDAVEYG	383	1.3000	12.87
27	YVQNITDID	77	1.2000	11.88
28	FGPGRPGWH	221	1.2000	11.88
29	WYCPPVPVL	3	1.0500	10.40
30	FARHYVHAG	274	1.0000	9.90
31	VRPVAPGSK	28	0.9000	8.91
32	WRDLAQAEV	99	0.9000	8.91
33	YVGATEAIA	125	0.9000	8.91
34	LRAQDVEPS	304	0.8000	7.92
35	LRLCEERGG	183	0.7000	6.93
36	YRADRFWSQ	323	0.7000	6.93
37	VGATEAIAE	126	0.6000	5.94
38	IAEMVELIE	132	0.6000	5.94
39	IYFRADATL	161	0.6000	5.94
40	VLVSALRAQ	299	0.6000	5.94
41	VARVRRYLA	360	0.6000	5.94

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	LVLVSALRA	298	4.0000	48.19
2	WRTATALPA	344	3.7000	44.58
3	VELIEKMLA	136	3.6000	43.37
4	YVTFDLIHR	58	2.5000	30.12
5	FDLIHRLWL	61	2.1000	25.30
6	FRADATLQF	163	1.8000	21.69
7	VRPVAPGSK	28	1.7000	20.48
8	MAALRVLPP	114	1.5000	18.07
9	LRAQDVEPS	304	1.4000	16.87
10	LRVLPPQDY	117	1.2000	14.46
11	YVHAGMIGW	278	1.2000	14.46
12	LHRWRTATA	341	1.2000	14.46

13	WRDLAQAEV	99	1.0000	12.05
14	WRAARPGEP	207	1.0000	12.05
15	YVGATEAIA	125	0.9000	10.84
16	VRLGLLAGH	314	0.7800	9.40
17	YFRADATLQ	162	0.7000	8.43
18	FWSQQVLDE	328	0.7000	8.43
19	VARVRRYLA	360	0.7000	8.43
20	LVSALRAQD	300	0.6000	7.23
21	VECAAIALS	230	0.5000	6.02
22	LRLYDSADR	18	0.4000	4.82
23	VCGITPYDA	41	0.2000	2.41
24	IEKMLACGA	139	0.1000	1.20
25	YVIDREMGE	149	0.1000	1.20
26	FARHYVHAG	274	0.1000	1.20
27	VLVSALRAQ	299	0.1000	1.20
28	LGLLAGHYR	316	-0.3000	0
29	WHVECAAIA	228	-0.4000	0
30	MQSWYCPPV	0	-0.4500	0
31	LHYVQNITD	75	-0.5000	0
32	WLDLGHELH	68	-0.5200	0
33	YVCGITPYD	40	-0.5500	0
34	LRLCEERGG	183	-0.6000	0
35	WYCPPVPVL	3	-0.6500	0
36	MLACGAAYV	142	-0.7000	0
37	WVTDAVEYG	383	-0.7000	0
38	FGPGRPGWH	221	-0.7200	0
39	LAQAEVALF	102	-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	LRAQDVEPS	304	3.7000	44.05
2	VVARVRRYL	359	3.5000	41.67

3	LHRWRTATA	341	3.0000	35.71
4	VLVSALRAQ	299	2.8000	33.33
5	LVLVSALRA	298	2.6000	30.95
6	LRLYDSADR	18	2.5000	29.76
7	LRVLPPQDY	117	2.2000	26.19
8	LRLCEERGG	183	2.0000	23.81
9	VRLGLLAGH	314	1.9800	23.57
10	VELIEKMLA	136	1.8000	21.43
11	IFPHHEFTA	254	1.8000	21.43
12	FARHYVHAG	274	1.7000	20.24
13	LAGHYRADR	319	1.7000	20.24
14	LVSALRAQD	300	1.6000	19.05
15	WRTATALPA	344	1.6000	19.05
16	VECAAIALS	230	1.5000	17.86
17	LLWRAARPG	205	1.4000	16.67
18	MIGWDGHKM	283	1.2000	14.29
19	VEPSAVRLG	309	1.2000	14.29
20	MQSWYCPPV	0	0.9000	10.71
21	IEKMLACGA	139	0.9000	10.71
22	VRRYLADDL	363	0.8000	9.52
23	MAALRVLPP	114	0.7000	8.33
24	YVTFDLIHR	58	0.6000	7.14
25	VARVRRYLA	360	0.6000	7.14
26	LGLLAGHYR	316	0.5000	5.95
27	VRPVAPGSK	28	0.3000	3.57
28	MLACGAAYV	142	0.3000	3.57
29	MYVCGITPY	39	0.2000	2.38
30	LAQAEVALF	102	0.2000	2.38
31	LGHAATYVT	52	0.1000	1.19
32	YFRADATLQ	162	0.1000	1.19
33	VCGITPYDA	41	-0.1000	0
34	YVGATEAIA	125	-0.1000	0
35	LIEKMLACG	138	-0.1000	0
36	LGHELHYVQ	71	-0.2000	0

37	VAPGSKATM	31	-0.3000	0
38	IGWDGHKMS	284	-0.3000	0
39	VPVLPGRGP	8	-0.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVLVSALRA	298	5.0000	60.24
2	VELIEKMLA	136	4.6000	55.42
3	VRPVAPGSK	28	2.7000	32.53
4	WRTATALPA	344	2.7000	32.53
5	MAALRVLPP	114	2.5000	30.12
6	LRAQDVEPS	304	2.4000	28.92
7	LRVLPPQDY	117	2.2000	26.51
8	LHRWRTATA	341	2.2000	26.51
9	VRLGLLAGH	314	1.7800	21.45
10	VARVRRYLA	360	1.7000	20.48
11	LVSALRAQD	300	1.6000	19.28
12	YVTFDLIHR	58	1.5000	18.07
13	VECAAIALS	230	1.5000	18.07
14	LRLYDSADR	18	1.4000	16.87
15	VCGITPYDA	41	1.2000	14.46
16	FDLIHRLWL	61	1.1000	13.25
17	IEKMLACGA	139	1.1000	13.25
18	VLVSALRAQ	299	1.1000	13.25
19	VVARVRRYL	359	1.0000	12.05
20	FRADATLQF	163	0.8000	9.64
21	LGLLAGHYR	316	0.7000	8.43
22	MQSWYCPPV	0	0.5500	6.63
23	LHYVQNITD	75	0.5000	6.02
24	LRLCEERGG	183	0.4000	4.82
25	MLACGAAYV	142	0.3000	3.61
26	LAQAEVALF	102	0.2000	2.41

27	YVHAGMIGW	278	0.2000	2.41
28	LGHAATYVT	52	-0.1000	0
29	YVGATEAIA	125	-0.1000	0
30	MIGWDGHKM	283	-0.1000	0
31	LWRAARPGE	206	-0.1500	0
32	MYVCGITPY	39	-0.2000	0
33	LIHRLWLDL	63	-0.3000	0
34	YFRADATLQ	162	-0.3000	0
35	FWSQQVLDE	328	-0.3000	0
36	IALSRIGSG	235	-0.4000	0
37	LAGHYRADR	319	-0.4000	0
38	VAPGSKATM	31	-0.5000	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	LVLVSALRA	298	5.0000	60.24
2	VELIEKMLA	136	4.6000	55.42
3	VRPVAPGSK	28	2.7000	32.53
4	WRTATALPA	344	2.7000	32.53
5	MAALRVLPP	114	2.5000	30.12
6	LRAQDVEPS	304	2.4000	28.92
7	LRVLPPQDY	117	2.2000	26.51
8	LHRWRTATA	341	2.2000	26.51
9	VRLGLLAGH	314	1.7800	21.45
10	VARVRRYLA	360	1.7000	20.48
11	LVSALRAQD	300	1.6000	19.28
12	YVTFDLIHR	58	1.5000	18.07
13	VECAAIALS	230	1.5000	18.07
14	LRLYDSADR	18	1.4000	16.87
15	VCGITPYDA	41	1.2000	14.46
16	FDLIHRLWL	61	1.1000	13.25
17	IEKMLACGA	139	1.1000	13.25

18	VLVSALRAQ	299	1.1000	13.25
19	VVARVRRYL	359	1.0000	12.05
20	FRADATLQF	163	0.8000	9.64
21	LGLLAGHYR	316	0.7000	8.43
22	MQSWYCPPV	0	0.5500	6.63
23	LHYVQNITD	75	0.5000	6.02
24	LRLCEERGG	183	0.4000	4.82
25	MLACGAAYV	142	0.3000	3.61
26	LAQAEVALF	102	0.2000	2.41
27	YVHAGMIGW	278	0.2000	2.41
28	LGHAATYVT	52	-0.1000	0
29	YVGATEAIA	125	-0.1000	0
30	MIGWDGHKM	283	-0.1000	0
31	LWRAARPGE	206	-0.1500	0
32	MYVCGITPY	39	-0.2000	0
33	LIHRLWLDL	63	-0.3000	0
34	YFRADATLQ	162	-0.3000	0
35	FWSQQVLDE	328	-0.3000	0
36	IALSRIGSG	235	-0.4000	0
37	LAGHYRADR	319	-0.4000	0
38	VAPGSKATM	31	-0.5000	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	VELIEKMLA	136	4.0000	43.96
2	VRLGLLAGH	314	3.9800	43.74
3	LRAQDVEPS	304	3.9000	42.86
4	FRADATLQF	163	3.5000	38.46
5	WVTDAVEYG	383	3.4000	37.36
6	LVLVSALRA	298	3.3000	36.26
7	YVIDREMGE	149	2.9000	31.87
8	VRPVAPGSK	28	2.8000	30.77

9	IGWDGHKMS	284	2.5000	27.47
10	LRVLPPQDY	117	2.1000	23.08
11	VTFDLIHRL	59	2.0000	21.98
12	VLVSALRAQ	299	2.0000	21.98
13	YRADRFWSQ	323	2.0000	21.98
14	VAPGSKATM	31	1.7000	18.68
15	VARVRRYLA	360	1.6500	18.13
16	LVSALRAQD	300	1.6000	17.58
17	VECAAIALS	230	1.5000	16.48
18	IALSRIGSG	235	1.5000	16.48
19	YVCGITPYD	40	1.4000	15.38
20	WRTATALPA	344	1.4000	15.38
21	LHRWRTATA	341	1.3000	14.29
22	VCGITPYDA	41	1.1500	12.64
23	LRLYDSADR	18	1.1000	12.09
24	MYVCGITPY	39	1.0000	10.99
25	FGPGRPGWH	221	0.9800	10.77
26	YFRADATLQ	162	0.9000	9.89
27	IQGGGSDLI	246	0.9000	9.89
28	VLPGRGPQL	10	0.8000	8.79
29	LWLDLGHEL	67	0.7000	7.69
30	LWRAARPGE	206	0.6000	6.59
31	YLADDLDTP	366	0.6000	6.59
32	WRAARPGEP	207	0.5000	5.49
33	MQSWYCPPV	0	0.4000	4.40
34	VHAGMIGWD	279	0.4000	4.40
35	VEPSAVRLG	309	0.4000	4.40
36	MLACGAAYV	142	0.3000	3.30
37	VRRYLADDL	363	0.3000	3.30
38	LGHAATYVT	52	0.2500	2.75
39	LAQAEVALF	102	0.2000	2.20
40	IFPHHEFTA	254	0.2000	2.20
41	LAGHYRADR	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	FARHYVHAG	274	2.7000	32.14
2	LRAQDVEPS	304	2.7000	32.14
3	WRTATALPA	344	2.6000	30.95
4	VVARVRRYL	359	2.5000	29.76
5	LHRWRTATA	341	2.0000	23.81
6	VLVSALRAQ	299	1.8000	21.43
7	YVTFDLIHR	58	1.6000	19.05
8	LVLVSALRA	298	1.6000	19.05
9	LRLYDSADR	18	1.5000	17.86
10	LRVLPPQDY	117	1.2000	14.29
11	YFRADATLQ	162	1.1000	13.10
12	FRADATLQF	163	1.0000	11.90
13	LRLCEERGG	183	1.0000	11.90
14	VRLGLLAGH	314	0.9800	11.67
15	YVGATEAIA	125	0.9000	10.71
16	VELIEKMLA	136	0.8000	9.52
17	IFPHHEFTA	254	0.8000	9.52
18	LAGHYRADR	319	0.7000	8.33
19	LVSALRAQD	300	0.6000	7.14
20	FWSQQVLDE	328	0.6000	7.14
21	VECAAIALS	230	0.5000	5.95
22	LLWRAARPG	205	0.4000	4.76
23	WRDLAQAEV	99	0.3000	3.57
24	YRADRFWSQ	323	0.3000	3.57
25	WHVECAAIA	228	0.2000	2.38
26	MIGWDGHKM	283	0.2000	2.38
27	VEPSAVRLG	309	0.2000	2.38
28	MQSWYCPPV	0	-0.1000	0
29	IEKMLACGA	139	-0.1000	0
30	WRAARPGEP	207	-0.1000	0

31	YVHAGMIGW	278	-0.1000	0
32	WVTDAVEYG	383	-0.1000	0
33	YVQNITDID	77	-0.2000	0
34	VRRYLADDL	363	-0.2000	0
35	MAALRVLPP	114	-0.3000	0
36	FERADRDGV	89	-0.4000	0
37	VARVRRYLA	360	-0.4000	0
38	FDLIHRLWL	61	-0.5000	0
39	LGLLAGHYR	316	-0.5000	0
40	YGGHDAGAP	390	-0.6000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FARHYVHAG	274	4.1000	46.59
2	VVARVRRYL	359	3.4600	39.32
3	YVTFDLIHR	58	3.1000	35.23
4	LRAQDVEPS	304	3.1000	35.23
5	LRLYDSADR	18	3.0000	34.09
6	FRADATLQF	163	2.9000	32.95
7	WRTATALPA	344	2.6000	29.55
8	LRVLPPQDY	117	2.5000	28.41
9	LRLCEERGG	183	2.4000	27.27
10	LAGHYRADR	319	2.2000	25.00
11	FWSQQVLDE	328	2.0000	22.73
12	LHRWRTATA	341	2.0000	22.73
13	LLWRAARPG	205	1.8000	20.45
14	MIGWDGHKM	283	1.7000	19.32
15	LVSALRAQD	300	1.7000	19.32
16	LVLVSALRA	298	1.6000	18.18
17	VEPSAVRLG	309	1.6000	18.18
18	WRDLAQAEV	99	1.3000	14.77
19	WVTDAVEYG	383	1.3000	14.77

20	LAQAEVALF	102	1.1000	12.50
21	VLVSALRAQ	299	1.1000	12.50
22	LGLLAGHYR	316	1.0000	11.36
23	MQSWYCPPV	0	0.9000	10.23
24	YVQNITDID	77	0.9000	10.23
25	YVGATEAIA	125	0.9000	10.23
26	WRAARPGEP	207	0.9000	10.23
27	VECAAIALS	230	0.9000	10.23
28	VELIEKMLA	136	0.8000	9.09
29	IFPHHEFTA	254	0.8000	9.09
30	VRRYLADDL	363	0.7600	8.64
31	MAALRVLPP	114	0.7000	7.95
32	FERADRDGV	89	0.6000	6.82
33	MYVCGITPY	39	0.5000	5.68
34	YVIDREMGE	149	0.5000	5.68
35	FDLIHRLWL	61	0.4600	5.23
36	YFRADATLQ	162	0.4000	4.55
37	VRLGLLAGH	314	0.4000	4.55
38	YGGHDAGAP	390	0.4000	4.55
39	YVCGITPYD	40	0.3000	3.41
40	LIEKMLACG	138	0.3000	3.41
41	MLACGAAYV	142	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	LRAQDVEPS	304	3.7000	44.05
2	VVARVRRYL	359	3.5000	41.67
3	LHRWRTATA	341	3.0000	35.71
4	VLVSALRAQ	299	2.8000	33.33
5	LVLVSALRA	298	2.6000	30.95
6	LRLYDSADR	18	2.5000	29.76
7	LRVLPPQDY	117	2.2000	26.19

8	LRLCEERGG	183	2.0000	23.81
9	VRLGLLAGH	314	1.9800	23.57
10	VELIEKMLA	136	1.8000	21.43
11	IFPHHEFTA	254	1.8000	21.43
12	FARHYVHAG	274	1.7000	20.24
13	LAGHYRADR	319	1.7000	20.24
14	LVSALRAQD	300	1.6000	19.05
15	WRTATALPA	344	1.6000	19.05
16	VECAAIALS	230	1.5000	17.86
17	LLWRAARPG	205	1.4000	16.67
18	MIGWDGHKM	283	1.2000	14.29
19	VEPSAVRLG	309	1.2000	14.29
20	MQSWYCPPV	0	0.9000	10.71
21	IEKMLACGA	139	0.9000	10.71
22	VRRYLADDL	363	0.8000	9.52
23	MAALRVLPP	114	0.7000	8.33
24	YVTFDLIHR	58	0.6000	7.14
25	VARVRRYLA	360	0.6000	7.14
26	LGLLAGHYR	316	0.5000	5.95
27	VRPVAPGSK	28	0.3000	3.57
28	MLACGAAYV	142	0.3000	3.57
29	MYVCGITPY	39	0.2000	2.38
30	LAQAEVALF	102	0.2000	2.38
31	LGHAATYVT	52	0.1000	1.19
32	YFRADATLQ	162	0.1000	1.19
33	VCGITPYDA	41	-0.1000	0
34	YVGATEAIA	125	-0.1000	0
35	LIEKMLACG	138	-0.1000	0
36	LGHELHYVQ	71	-0.2000	0
37	VAPGSKATM	31	-0.3000	0
38	IGWDGHKMS	284	-0.3000	0
39	VPVLPGRGP	8	-0.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YVTFDLIHR	58	4.0000	45.98
2	LVLVSALRA	298	4.0000	45.98
3	FRADATLQF	163	3.7000	42.53
4	WRTATALPA	344	3.7000	42.53
5	VELIEKMLA	136	3.6000	41.38
6	FDLIHRLWL	61	3.0600	35.17
7	MAALRVLPP	114	2.5000	28.74
8	LRVLPPQDY	117	2.5000	28.74
9	FWSQQVLDE	328	2.1000	24.14
10	WRDLAQAEV	99	2.0000	22.99
11	WRAARPGEP	207	2.0000	22.99
12	LRLYDSADR	18	1.9000	21.84
13	VRPVAPGSK	28	1.8000	20.69
14	LRAQDVEPS	304	1.8000	20.69
15	LVSALRAQD	300	1.7000	19.54
16	YVIDREMGE	149	1.5000	17.24
17	FARHYVHAG	274	1.5000	17.24
18	YVHAGMIGW	278	1.2000	13.79
19	LGLLAGHYR	316	1.2000	13.79
20	LHRWRTATA	341	1.2000	13.79
21	LAQAEVALF	102	1.1000	12.64
22	VVARVRRYL	359	0.9600	11.03
23	YVGATEAIA	125	0.9000	10.34
24	VECAAIALS	230	0.9000	10.34
25	LRLCEERGG	183	0.8000	9.20
26	VARVRRYLA	360	0.7000	8.05
27	WVTDAVEYG	383	0.7000	8.05
28	LHYVQNITD	75	0.6000	6.90
29	MQSWYCPPV	0	0.5500	6.32
30	YVCGITPYD	40	0.5500	6.32
31	MIGWDGHKM	283	0.4000	4.60

32	WYCPPVPVL	3	0.3100	3.56
33	MLACGAAYV	142	0.3000	3.45
34	LWRAARPGE	206	0.2500	2.87
35	VCGITPYDA	41	0.2000	2.30
36	VRLGLLAGH	314	0.2000	2.30
37	MYVCGITPY	39	0.1000	1.15
38	IEKMLACGA	139	0.1000	1.15
39	LAGHYRADR	319	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	VVARVRRYL	359	4.4600	50.68
2	LRAQDVEPS	304	4.1000	46.59
3	LRLYDSADR	18	4.0000	45.45
4	LRVLPPQDY	117	3.5000	39.77
5	LRLCEERGG	183	3.4000	38.64
6	LAGHYRADR	319	3.2000	36.36
7	FARHYVHAG	274	3.1000	35.23
8	LHRWRTATA	341	3.0000	34.09
9	LLWRAARPG	205	2.8000	31.82
10	MIGWDGHKM	283	2.7000	30.68
11	LVSALRAQD	300	2.7000	30.68
12	LVLVSALRA	298	2.6000	29.55
13	VEPSAVRLG	309	2.6000	29.55
14	YVTFDLIHR	58	2.1000	23.86
15	LAQAEVALF	102	2.1000	23.86
16	VLVSALRAQ	299	2.1000	23.86
17	LGLLAGHYR	316	2.0000	22.73
18	MQSWYCPPV	0	1.9000	21.59
19	FRADATLQF	163	1.9000	21.59
20	VECAAIALS	230	1.9000	21.59
21	VELIEKMLA	136	1.8000	20.45

22	IFPHHEFTA	254	1.8000	20.45
23	VRRYLADDL	363	1.7600	20.00
24	MAALRVLPP	114	1.7000	19.32
25	WRTATALPA	344	1.6000	18.18
26	MYVCGITPY	39	1.5000	17.05
27	VRLGLLAGH	314	1.4000	15.91
28	LIEKMLACG	138	1.3000	14.77
29	MLACGAAYV	142	1.3000	14.77
30	VAPGSKATM	31	1.2000	13.64
31	IHRLWLDLG	64	1.0000	11.36
32	FWSQQVLDE	328	1.0000	11.36
33	IEKMLACGA	139	0.9000	10.23
34	VSGERRFAR	268	0.9000	10.23
35	LGHAATYVT	52	0.8000	9.09
36	LWRAARPGE	206	0.8000	9.09
37	VPVLPGRGP	8	0.6000	6.82
38	VARVRRYLA	360	0.6000	6.82
39	LPGRGPQLR	11	0.5000	5.68
40	LIHRLWLDL	63	0.4600	5.23
41	VRPVAPGSK	28	0.4000	4.55

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	FARHYVHAG	274	4.1000	46.59
2	VVARVRRYL	359	3.4600	39.32
3	YVTFDLIHR	58	3.1000	35.23
4	LRAQDVEPS	304	3.1000	35.23
5	LRLYDSADR	18	3.0000	34.09
6	FRADATLQF	163	2.9000	32.95
7	WRTATALPA	344	2.6000	29.55
8	LRVLPPQDY	117	2.5000	28.41
9	LRLCEERGG	183	2.4000	27.27

10	LAGHYRADR	319	2.2000	25.00
11	FWSQQVLDE	328	2.0000	22.73
12	LHRWRTATA	341	2.0000	22.73
13	LLWRAARPG	205	1.8000	20.45
14	MIGWDGHKM	283	1.7000	19.32
15	LVSALRAQD	300	1.7000	19.32
16	LVLVSALRA	298	1.6000	18.18
17	VEPSAVRLG	309	1.6000	18.18
18	WRDLAQAEV	99	1.3000	14.77
19	WVTDAVEYG	383	1.3000	14.77
20	LAQAEVALF	102	1.1000	12.50
21	VLVSALRAQ	299	1.1000	12.50
22	LGLLAGHYR	316	1.0000	11.36
23	MQSWYCPPV	0	0.9000	10.23
24	YVQNITDID	77	0.9000	10.23
25	YVGATEAIA	125	0.9000	10.23
26	WRAARPGEP	207	0.9000	10.23
27	VECAAIALS	230	0.9000	10.23
28	VELIEKMLA	136	0.8000	9.09
29	IFPHHEFTA	254	0.8000	9.09
30	VRRYLADDL	363	0.7600	8.64
31	MAALRVLPP	114	0.7000	7.95
32	FERADRDGV	89	0.6000	6.82
33	MYVCGITPY	39	0.5000	5.68
34	YVIDREMGE	149	0.5000	5.68
35	FDLIHRLWL	61	0.4600	5.23
36	YFRADATLQ	162	0.4000	4.55
37	VRLGLLAGH	314	0.4000	4.55
38	YGGHDAGAP	390	0.4000	4.55
39	YVCGITPYD	40	0.3000	3.41
40	LIEKMLACG	138	0.3000	3.41
41	MLACGAAYV	142	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	VVARVRRYL	359	4.5000	50.00
2	LVSALRAQD	300	4.3000	47.78
3	LRAQDVEPS	304	3.7000	41.11
4	VLVSALRAQ	299	3.6000	40.00
5	LRVLPPQDY	117	3.3000	36.67
6	LRLCEERGG	183	3.3000	36.67
7	VRLGLLAGH	314	3.2000	35.56
8	FARHYVHAG	274	3.0000	33.33
9	LHRWRTATA	341	3.0000	33.33
10	LLWRAARPG	205	2.7000	30.00
11	LVLVSALRA	298	2.6000	28.89
12	FWSQQVLDE	328	2.6000	28.89
13	LRLYDSADR	18	2.5000	27.78
14	VEPSAVRLG	309	2.5000	27.78
15	LWRAARPGE	206	2.4000	26.67
16	MIGWDGHKM	283	2.3000	25.56
17	VELIEKMLA	136	1.8000	20.00
18	IFPHHEFTA	254	1.8000	20.00
19	VRRYLADDL	363	1.8000	20.00
20	LAGHYRADR	319	1.7000	18.89
21	WRTATALPA	344	1.6000	17.78
22	YVQNITDID	77	1.5000	16.67
23	VECAAIALS	230	1.5000	16.67
24	MYVCGITPY	39	1.3000	14.44
25	MQSWYCPPV	0	1.2000	13.33
26	LIEKMLACG	138	1.2000	13.33
27	LAQAEVALF	102	1.1000	12.22
28	MAALRVLPP	114	1.1000	12.22
29	YVIDREMGE	149	1.1000	12.22
30	LGHAATYVT	52	1.0000	11.11
31	YVCGITPYD	40	0.9000	10.00

32	IHRLWLDLG	64	0.9000	10.00
33	IEKMLACGA	139	0.9000	10.00
34	YFRADATLQ	162	0.9000	10.00
35	FRADATLQF	163	0.9000	10.00
36	VAPGSKATM	31	0.8000	8.89
37	YVTFDLIHR	58	0.6000	6.67
38	LGHELHYVQ	71	0.6000	6.67
39	LHYVQNITD	75	0.6000	6.67
40	MLACGAAYV	142	0.6000	6.67
41	VARVRRYLA	360	0.6000	6.67

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	YVTFDLIHR	58	4.0000	45.98
2	LVLVSALRA	298	4.0000	45.98
3	FRADATLQF	163	3.7000	42.53
4	WRTATALPA	344	3.7000	42.53
5	VELIEKMLA	136	3.6000	41.38
6	FDLIHRLWL	61	3.0600	35.17
7	MAALRVLPP	114	2.5000	28.74
8	LRVLPPQDY	117	2.5000	28.74
9	FWSQQVLDE	328	2.1000	24.14
10	WRDLAQAEV	99	2.0000	22.99
11	WRAARPGEP	207	2.0000	22.99
12	LRLYDSADR	18	1.9000	21.84
13	VRPVAPGSK	28	1.8000	20.69
14	LRAQDVEPS	304	1.8000	20.69
15	LVSALRAQD	300	1.7000	19.54
16	YVIDREMGE	149	1.5000	17.24
17	FARHYVHAG	274	1.5000	17.24
18	YVHAGMIGW	278	1.2000	13.79
19	LGLLAGHYR	316	1.2000	13.79

20	LHRWRTATA	341	1.2000	13.79
21	LAQAEVALF	102	1.1000	12.64
22	VVARVRRYL	359	0.9600	11.03
23	YVGATEAIA	125	0.9000	10.34
24	VECAAIALS	230	0.9000	10.34
25	LRLCEERGG	183	0.8000	9.20
26	VARVRRYLA	360	0.7000	8.05
27	WVTDAVEYG	383	0.7000	8.05
28	LHYVQNITD	75	0.6000	6.90
29	MQSWYCPPV	0	0.5500	6.32
30	YVCGITPYD	40	0.5500	6.32
31	MIGWDGHKM	283	0.4000	4.60
32	WYCPPVPVL	3	0.3100	3.56
33	MLACGAAYV	142	0.3000	3.45
34	LWRAARPGE	206	0.2500	2.87
35	VCGITPYDA	41	0.2000	2.30
36	VRLGLLAGH	314	0.2000	2.30
37	MYVCGITPY	39	0.1000	1.15
38	IEKMLACGA	139	0.1000	1.15
39	LAGHYRADR	319	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	LVLVSALRA	298	2.2000	32.35
2	VELIEKMLA	136	2.0000	29.41
3	WRTATALPA	344	1.9000	27.94
4	VRPVAPGSK	28	1.6000	23.53
5	LHRWRTATA	341	1.2000	17.65
6	LRVLPPQDY	117	1.1000	16.18
7	WRDLAQAEV	99	1.0000	14.71
8	YVTFDLIHR	58	0.9000	13.24
9	YVGATEAIA	125	0.9000	13.24

10	WRAARPGEP	207	0.9000	13.24
11	VRLGLLAGH	314	0.7800	11.47
12	LVSALRAQD	300	0.6000	8.82
13	VECAAIALS	230	0.5000	7.35
14	LRLYDSADR	18	0.4000	5.88
15	FDLIHRLWL	61	0.3000	4.41
16	LRAQDVEPS	304	0.3000	4.41
17	IEKMLACGA	139	0.1000	1.47
18	VLVSALRAQ	299	-0.1000	0
19	VVARVRRYL	359	-0.2000	0
20	MAALRVLPP	114	-0.3000	0
21	YFRADATLQ	162	-0.4000	0
22	WHVECAAIA	228	-0.4000	0
23	YVHAGMIGW	278	-0.4000	0
24	VCGITPYDA	41	-0.5000	0
25	FARHYVHAG	274	-0.6000	0
26	MLACGAAYV	142	-0.7000	0
27	LAQAEVALF	102	-0.8000	0
28	LRLCEERGG	183	-0.8000	0
29	FGPGRPGWH	221	-0.8200	0
30	LGLLAGHYR	316	-1.0000	0
31	FWSQQVLDE	328	-1.1000	0
32	YVQNITDID	77	-1.2000	0
33	FERADRDGV	89	-1.3000	0
34	LAGHYRADR	319	-1.4000	0
35	VAPGSKATM	31	-1.5000	0
36	YVIDREMGE	149	-1.5000	0
37	IALSRIGSG	235	-1.5000	0
38	MQSWYCPPV	0	-1.6000	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	LVLVSALRA	298	5.0000	60.24
2	VELIEKMLA	136	4.6000	55.42
3	VRPVAPGSK	28	2.7000	32.53
4	WRTATALPA	344	2.7000	32.53
5	MAALRVLPP	114	2.5000	30.12
6	LRAQDVEPS	304	2.4000	28.92
7	LRVLPPQDY	117	2.2000	26.51
8	LHRWRTATA	341	2.2000	26.51
9	VRLGLLAGH	314	1.7800	21.45
10	VARVRRYLA	360	1.7000	20.48
11	LVSALRAQD	300	1.6000	19.28
12	YVTFDLIHR	58	1.5000	18.07
13	VECAAIALS	230	1.5000	18.07
14	LRLYDSADR	18	1.4000	16.87
15	VCGITPYDA	41	1.2000	14.46
16	FDLIHRLWL	61	1.1000	13.25
17	IEKMLACGA	139	1.1000	13.25
18	VLVSALRAQ	299	1.1000	13.25
19	VVARVRRYL	359	1.0000	12.05
20	FRADATLQF	163	0.8000	9.64
21	LGLLAGHYR	316	0.7000	8.43
22	MQSWYCPPV	0	0.5500	6.63
23	LHYVQNITD	75	0.5000	6.02
24	LRLCEERGG	183	0.4000	4.82
25	MLACGAAYV	142	0.3000	3.61
26	LAQAEVALF	102	0.2000	2.41
27	YVHAGMIGW	278	0.2000	2.41
28	LGHAATYVT	52	-0.1000	0
29	YVGATEAIA	125	-0.1000	0
30	MIGWDGHKM	283	-0.1000	0
31	LWRAARPGE	206	-0.1500	0
32	MYVCGITPY	39	-0.2000	0
33	LIHRLWLDL	63	-0.3000	0
34	YFRADATLQ	162	-0.3000	0

35	FWSQQVLDE	328	-0.3000	0
36	IALSRIGSG	235	-0.4000	0
37	LAGHYRADR	319	-0.4000	0
38	VAPGSKATM	31	-0.5000	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	LVLVSALRA	298	4.0000	44.94
2	FWSQQVLDE	328	3.7000	41.57
3	WRTATALPA	344	3.7000	41.57
4	VELIEKMLA	136	3.6000	40.45
5	LVSALRAQD	300	3.3000	37.08
6	FDLIHRLWL	61	3.1000	34.83
7	YVIDREMGE	149	3.1000	34.83
8	FRADATLQF	163	2.7000	30.34
9	YVTFDLIHR	58	2.5000	28.09
10	LRVLPPQDY	117	2.3000	25.84
11	LHYVQNITD	75	2.2000	24.72
12	YVCGITPYD	40	2.1500	24.16
13	YVHAGMIGW	278	2.1000	23.60
14	VRLGLLAGH	314	2.0000	22.47
15	MAALRVLPP	114	1.9000	21.35
16	LWRAARPGE	206	1.8500	20.79
17	YFRADATLQ	162	1.5000	16.85
18	WRAARPGEP	207	1.4000	15.73
19	FARHYVHAG	274	1.4000	15.73
20	LRAQDVEPS	304	1.4000	15.73
21	WRDLAQAEV	99	1.3000	14.61
22	YVQNITDID	77	1.2000	13.48
23	LHRWRTATA	341	1.2000	13.48
24	VRPVAPGSK	28	1.0000	11.24
25	VQNITDIDD	78	1.0000	11.24

26	VGATEAIAE	126	1.0000	11.24
27	VVARVRRYL	359	1.0000	11.24
28	YVGATEAIA	125	0.9000	10.11
29	VLVSALRAQ	299	0.9000	10.11
30	LSRIGSGLD	237	0.8000	8.99
31	WLDLGHELH	68	0.7000	7.87
32	LRLCEERGG	183	0.7000	7.87
33	VARVRRYLA	360	0.7000	7.87
34	WVTDAVEYG	383	0.6000	6.74
35	FGPGRPGWH	221	0.5000	5.62
36	VECAAIALS	230	0.5000	5.62
37	LRLYDSADR	18	0.4000	4.49
38	WYCPPVPVL	3	0.3500	3.93
39	VCGITPYDA	41	0.2000	2.25
40	IAEMVELIE	132	0.2000	2.25
41	LAQAEVALF	102	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	LRAQDVEPS	304	3.7000	44.05
2	VVARVRRYL	359	3.5000	41.67
3	LHRWRTATA	341	3.0000	35.71
4	VLVSALRAQ	299	2.8000	33.33
5	LVLVSALRA	298	2.6000	30.95
6	LRLYDSADR	18	2.5000	29.76
7	LRVLPPQDY	117	2.2000	26.19
8	LRLCEERGG	183	2.0000	23.81
9	VRLGLLAGH	314	1.9800	23.57
10	VELIEKMLA	136	1.8000	21.43
11	IFPHHEFTA	254	1.8000	21.43
12	FARHYVHAG	274	1.7000	20.24
13	LAGHYRADR	319	1.7000	20.24

14	LVSALRAQD	300	1.6000	19.05
15	WRTATALPA	344	1.6000	19.05
16	VECAAIALS	230	1.5000	17.86
17	LLWRAARPG	205	1.4000	16.67
18	MIGWDGHKM	283	1.2000	14.29
19	VEPSAVRLG	309	1.2000	14.29
20	MQSWYCPPV	0	0.9000	10.71
21	IEKMLACGA	139	0.9000	10.71
22	VRRYLADDL	363	0.8000	9.52
23	MAALRVLPP	114	0.7000	8.33
24	YVTFDLIHR	58	0.6000	7.14
25	VARVRRYLA	360	0.6000	7.14
26	LGLLAGHYR	316	0.5000	5.95
27	VRPVAPGSK	28	0.3000	3.57
28	MLACGAAYV	142	0.3000	3.57
29	MYVCGITPY	39	0.2000	2.38
30	LAQAEVALF	102	0.2000	2.38
31	LGHAATYVT	52	0.1000	1.19
32	YFRADATLQ	162	0.1000	1.19
33	VCGITPYDA	41	-0.1000	0
34	YVGATEAIA	125	-0.1000	0
35	LIEKMLACG	138	-0.1000	0
36	LGHELHYVQ	71	-0.2000	0
37	VAPGSKATM	31	-0.3000	0
38	IGWDGHKMS	284	-0.3000	0
39	VPVLPGRGP	8	-0.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FARHYVHAG	274	2.7000	32.14
2	LRAQDVEPS	304	2.7000	32.14
3	WRTATALPA	344	2.6000	30.95

4	VVARVRRYL	359	2.5000	29.76
5	LHRWRTATA	341	2.0000	23.81
6	VLVSALRAQ	299	1.8000	21.43
7	YVTFDLIHR	58	1.6000	19.05
8	LVLVSALRA	298	1.6000	19.05
9	LRLYDSADR	18	1.5000	17.86
10	LRVLPPQDY	117	1.2000	14.29
11	YFRADATLQ	162	1.1000	13.10
12	FRADATLQF	163	1.0000	11.90
13	LRLCEERGG	183	1.0000	11.90
14	VRLGLLAGH	314	0.9800	11.67
15	YVGATEAIA	125	0.9000	10.71
16	VELIEKMLA	136	0.8000	9.52
17	IFPHHEFTA	254	0.8000	9.52
18	LAGHYRADR	319	0.7000	8.33
19	LVSALRAQD	300	0.6000	7.14
20	FWSQQVLDE	328	0.6000	7.14
21	VECAAIALS	230	0.5000	5.95
22	LLWRAARPG	205	0.4000	4.76
23	WRDLAQAEV	99	0.3000	3.57
24	YRADRFWSQ	323	0.3000	3.57
25	WHVECAAIA	228	0.2000	2.38
26	MIGWDGHKM	283	0.2000	2.38
27	VEPSAVRLG	309	0.2000	2.38
28	MQSWYCPPV	0	-0.1000	0
29	IEKMLACGA	139	-0.1000	0
30	WRAARPGEP	207	-0.1000	0
31	YVHAGMIGW	278	-0.1000	0
32	WVTDAVEYG	383	-0.1000	0
33	YVQNITDID	77	-0.2000	0
34	VRRYLADDL	363	-0.2000	0
35	MAALRVLPP	114	-0.3000	0
36	FERADRDGV	89	-0.4000	0
37	VARVRRYLA	360	-0.4000	0

38	FDLIHRLWL	61	-0.5000	0
39	LGLLAGHYR	316	-0.5000	0
40	YGGHDAGAP	390	-0.6000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVARVRRYL	359	4.4600	50.68
2	LRAQDVEPS	304	4.1000	46.59
3	LRLYDSADR	18	4.0000	45.45
4	LRVLPPQDY	117	3.5000	39.77
5	LRLCEERGG	183	3.4000	38.64
6	LAGHYRADR	319	3.2000	36.36
7	FARHYVHAG	274	3.1000	35.23
8	LHRWRTATA	341	3.0000	34.09
9	LLWRAARPG	205	2.8000	31.82
10	MIGWDGHKM	283	2.7000	30.68
11	LVSALRAQD	300	2.7000	30.68
12	LVLVSALRA	298	2.6000	29.55
13	VEPSAVRLG	309	2.6000	29.55
14	YVTFDLIHR	58	2.1000	23.86
15	LAQAEVALF	102	2.1000	23.86
16	VLVSALRAQ	299	2.1000	23.86
17	LGLLAGHYR	316	2.0000	22.73
18	MQSWYCPPV	0	1.9000	21.59
19	FRADATLQF	163	1.9000	21.59
20	VECAAIALS	230	1.9000	21.59
21	VELIEKMLA	136	1.8000	20.45
22	IFPHHEFTA	254	1.8000	20.45
23	VRRYLADDL	363	1.7600	20.00
24	MAALRVLPP	114	1.7000	19.32
25	WRTATALPA	344	1.6000	18.18
26	MYVCGITPY	39	1.5000	17.05

27	VRLGLLAGH	314	1.4000	15.91
28	LIEKMLACG	138	1.3000	14.77
29	MLACGAAYV	142	1.3000	14.77
30	VAPGSKATM	31	1.2000	13.64
31	IHRLWLDLG	64	1.0000	11.36
32	FWSQQVLDE	328	1.0000	11.36
33	IEKMLACGA	139	0.9000	10.23
34	VSGERRFAR	268	0.9000	10.23
35	LGHAATYVT	52	0.8000	9.09
36	LWRAARPGE	206	0.8000	9.09
37	VPVLPGRGP	8	0.6000	6.82
38	VARVRRYLA	360	0.6000	6.82
39	LPGRGPQLR	11	0.5000	5.68
40	LIHRLWLDL	63	0.4600	5.23
41	VRPVAPGSK	28	0.4000	4.55

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	VVARVRRYL	359	4.4600	50.68
2	LRAQDVEPS	304	4.1000	46.59
3	LRLYDSADR	18	4.0000	45.45
4	LRVLPPQDY	117	3.5000	39.77
5	LRLCEERGG	183	3.4000	38.64
6	LAGHYRADR	319	3.2000	36.36
7	FARHYVHAG	274	3.1000	35.23
8	LHRWRTATA	341	3.0000	34.09
9	LLWRAARPG	205	2.8000	31.82
10	MIGWDGHKM	283	2.7000	30.68
11	LVSALRAQD	300	2.7000	30.68
12	LVLVSALRA	298	2.6000	29.55
13	VEPSAVRLG	309	2.6000	29.55
14	YVTFDLIHR	58	2.1000	23.86

15	LAQAEVALF	102	2.1000	23.86
16	VLVSALRAQ	299	2.1000	23.86
17	LGLLAGHYR	316	2.0000	22.73
18	MQSWYCPPV	0	1.9000	21.59
19	FRADATLQF	163	1.9000	21.59
20	VECAAIALS	230	1.9000	21.59
21	VELIEKMLA	136	1.8000	20.45
22	IFPHHEFTA	254	1.8000	20.45
23	VRRYLADDL	363	1.7600	20.00
24	MAALRVLPP	114	1.7000	19.32
25	WRTATALPA	344	1.6000	18.18
26	MYVCGITPY	39	1.5000	17.05
27	VRLGLLAGH	314	1.4000	15.91
28	LIEKMLACG	138	1.3000	14.77
29	MLACGAAYV	142	1.3000	14.77
30	VAPGSKATM	31	1.2000	13.64
31	IHRLWLDLG	64	1.0000	11.36
32	FWSQQVLDE	328	1.0000	11.36
33	IEKMLACGA	139	0.9000	10.23
34	VSGERRFAR	268	0.9000	10.23
35	LGHAATYVT	52	0.8000	9.09
36	LWRAARPGE	206	0.8000	9.09
37	VPVLPGRGP	8	0.6000	6.82
38	VARVRRYLA	360	0.6000	6.82
39	LPGRGPQLR	11	0.5000	5.68
40	LIHRLWLDL	63	0.4600	5.23
41	VRPVAPGSK	28	0.4000	4.55

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	LRLYDSADR	18	5.3000	54.08
2	LVLVSALRA	298	5.2000	53.06

3	VRRYLADDL	363	5.2000	53.06
4	YVTFDLIHR	58	4.2000	42.86
5	ITPYDATHL	44	3.5000	35.71
6	LIHRLWLDL	63	3.5000	35.71
7	VVARVRRYL	359	3.3000	33.67
8	VELIEKMLA	136	3.1000	31.63
9	WRTATALPA	344	3.1000	31.63
10	MIGWDGHKM	283	2.8800	29.39
11	FDLIHRLWL	61	2.7000	27.55
12	VLPGRGPQL	10	2.6000	26.53
13	IFPHHEFTA	254	2.6000	26.53
14	VARVRRYLA	360	2.6000	26.53
15	MGEYQDIYF	155	2.5000	25.51
16	MQSWYCPPV	0	2.4000	24.49
17	VRLGLLAGH	314	2.3000	23.47
18	FRADATLQF	163	2.2600	23.06
19	LWLDLGHEL	67	2.1000	21.43
20	LHYVQNITD	75	2.1000	21.43
21	LGLLAGHYR	316	2.1000	21.43
22	IYFRADATL	161	2.0000	20.41
23	IQGGGSDLI	246	2.0000	20.41
24	LHRWRTATA	341	1.8600	18.98
25	LRVLPPQDY	117	1.8000	18.37
26	VALFCEDMA	107	1.7000	17.35
27	LVATAIDAL	400	1.6500	16.84
28	VTFDLIHRL	59	1.5500	15.82
29	VQNITDIDD	78	1.5000	15.31
30	YVHAGMIGW	278	1.5000	15.31
31	LACGAAYVI	143	1.4000	14.29
32	LVSALRAQD	300	1.4000	14.29
33	IAALDGWVT	377	1.4000	14.29
34	VCGITPYDA	41	1.3000	13.27
35	MLACGAAYV	142	1.3000	13.27
36	LAGHYRADR	319	1.3000	13.27

37	LGHAATYVT	52	1.1600	11.84
38	IEKMLACGA	139	1.1000	11.22
39	MAALRVLPP	114	1.0000	10.20
40	YVIDREMGE	149	1.0000	10.20
41	IGSGLDIQG	240	1.0000	10.20

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	YVTFDLIHR	58	5.2000	53.06
2	LRLYDSADR	18	4.3000	43.88
3	LVLVSALRA	298	4.2000	42.86
4	VRRYLADDL	363	4.2000	42.86
5	WRTATALPA	344	4.1000	41.84
6	FDLIHRLWL	61	3.7000	37.76
7	FRADATLQF	163	3.2600	33.27
8	ITPYDATHL	44	2.5000	25.51
9	LIHRLWLDL	63	2.5000	25.51
10	YVHAGMIGW	278	2.5000	25.51
11	VVARVRRYL	359	2.3000	23.47
12	VELIEKMLA	136	2.1000	21.43
13	YVIDREMGE	149	2.0000	20.41
14	MIGWDGHKM	283	1.8800	19.18
15	VLPGRGPQL	10	1.6000	16.33
16	IFPHHEFTA	254	1.6000	16.33
17	VARVRRYLA	360	1.6000	16.33
18	MGEYQDIYF	155	1.5000	15.31
19	YDRDTMLRL	177	1.5000	15.31
20	MQSWYCPPV	0	1.4000	14.29
21	FERADRDGV	89	1.4000	14.29
22	YVGATEAIA	125	1.3000	13.27
23	FARHYVHAG	274	1.3000	13.27
24	VRLGLLAGH	314	1.3000	13.27

25	WYCPPVPVL	3	1.1000	11.22
26	LWLDLGHEL	67	1.1000	11.22
27	LHYVQNITD	75	1.1000	11.22
28	LGLLAGHYR	316	1.1000	11.22
29	IYFRADATL	161	1.0000	10.20
30	IQGGGSDLI	246	1.0000	10.20
31	WRDLAQAEV	99	0.9000	9.18
32	FGYESGYDR	171	0.9000	9.18
33	WRAARPGEP	207	0.9000	9.18
34	LHRWRTATA	341	0.8600	8.78
35	LRVLPPQDY	117	0.8000	8.16
36	VALFCEDMA	107	0.7000	7.14
37	WHVECAAIA	228	0.7000	7.14
38	FPHHEFTAA	255	0.7000	7.14
39	YGGHDAGAP	390	0.7000	7.14
40	LVATAIDAL	400	0.6500	6.63
41	VTFDLIHRL	59	0.5500	5.61

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	LRLYDSADR	18	5.3000	54.08
2	LVLVSALRA	298	5.2000	53.06
3	VRRYLADDL	363	5.2000	53.06
4	YVTFDLIHR	58	4.2000	42.86
5	ITPYDATHL	44	3.5000	35.71
6	LIHRLWLDL	63	3.5000	35.71
7	VVARVRRYL	359	3.3000	33.67
8	VELIEKMLA	136	3.1000	31.63
9	WRTATALPA	344	3.1000	31.63
10	MIGWDGHKM	283	2.8800	29.39
11	FDLIHRLWL	61	2.7000	27.55
12	VLPGRGPQL	10	2.6000	26.53

13	IFPHHEFTA	254	2.6000	26.53
14	VARVRRYLA	360	2.6000	26.53
15	MGEYQDIYF	155	2.5000	25.51
16	MQSWYCPPV	0	2.4000	24.49
17	VRLGLLAGH	314	2.3000	23.47
18	FRADATLQF	163	2.2600	23.06
19	LWLDLGHEL	67	2.1000	21.43
20	LHYVQNITD	75	2.1000	21.43
21	LGLLAGHYR	316	2.1000	21.43
22	IYFRADATL	161	2.0000	20.41
23	IQGGGSDLI	246	2.0000	20.41
24	LHRWRTATA	341	1.8600	18.98
25	LRVLPPQDY	117	1.8000	18.37
26	VALFCEDMA	107	1.7000	17.35
27	LVATAIDAL	400	1.6500	16.84
28	VTFDLIHRL	59	1.5500	15.82
29	VQNITDIDD	78	1.5000	15.31
30	YVHAGMIGW	278	1.5000	15.31
31	LACGAAYVI	143	1.4000	14.29
32	LVSALRAQD	300	1.4000	14.29
33	IAALDGWVT	377	1.4000	14.29
34	VCGITPYDA	41	1.3000	13.27
35	MLACGAAYV	142	1.3000	13.27
36	LAGHYRADR	319	1.3000	13.27
37	LGHAATYVT	52	1.1600	11.84
38	IEKMLACGA	139	1.1000	11.22
39	MAALRVLPP	114	1.0000	10.20
40	YVIDREMGE	149	1.0000	10.20
41	IGSGLDIQG	240	1.0000	10.20

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	VRPVAPGSK	28	6.1000	62.24
2	LRVLPPQDY	117	4.5000	45.92
3	LGLLAGHYR	316	4.5000	45.92
4	YVTFDLIHR	58	4.2000	42.86
5	LVLVSALRA	298	3.8000	38.78
6	LRLYDSADR	18	3.6000	36.73
7	FGYESGYDR	171	3.4000	34.69
8	WRTATALPA	344	2.8000	28.57
9	YFRADATLQ	162	2.5000	25.51
10	WRAARPGEP	207	2.2000	22.45
11	VCGITPYDA	41	1.9000	19.39
12	LRLCEERGG	183	1.9000	19.39
13	FDLIHRLWL	61	1.6000	16.33
14	FRADATLQF	163	1.3000	13.27
15	YVHAGMIGW	278	1.3000	13.27
16	VRRYLADDL	363	1.1000	11.22
17	FGPGRPGWH	221	1.0000	10.20
18	VLVSALRAQ	299	1.0000	10.20
19	YDSADRQVR	21	0.8000	8.16
20	IEKMLACGA	139	0.8000	8.16
21	MVELIEKML	135	0.7000	7.14
22	VVARVRRYL	359	0.7000	7.14
23	VARVRRYLA	360	0.7000	7.14
24	MYVCGITPY	39	0.6000	6.12
25	VRLGLLAGH	314	0.6000	6.12
26	LPGRGPQLR	11	0.4000	4.08
27	VGATEAIAE	126	0.4000	4.08
28	ITPYDATHL	44	0.3000	3.06
29	YVGATEAIA	125	0.3000	3.06
30	VELIEKMLA	136	0.3000	3.06
31	VSGERRFAR	268	0.3000	3.06
32	MIGWDGHKM	283	0.3000	3.06
33	LWLDLGHEL	67	0.2000	2.04
34	VDVVARVRR	357	0.2000	2.04

35	LHYVQNITD	75	0.1000	1.02
36	LGHAATYVT	52	-0.1000	0
37	WRDLAQAEV	99	-0.1000	0
38	VPVLPGRGP	8	-0.2000	0

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	VRPVAPGSK	28	6.1000	62.24
2	LRVLPPQDY	117	4.5000	45.92
3	LGLLAGHYR	316	4.5000	45.92
4	YVTFDLIHR	58	4.2000	42.86
5	LVLVSALRA	298	3.8000	38.78
6	LRLYDSADR	18	3.6000	36.73
7	FGYESGYDR	171	3.4000	34.69
8	WRTATALPA	344	2.8000	28.57
9	YFRADATLQ	162	2.5000	25.51
10	WRAARPGEP	207	2.2000	22.45
11	VCGITPYDA	41	1.9000	19.39
12	LRLCEERGG	183	1.9000	19.39
13	FDLIHRLWL	61	1.6000	16.33
14	FRADATLQF	163	1.3000	13.27
15	YVHAGMIGW	278	1.3000	13.27
16	VRRYLADDL	363	1.1000	11.22
17	FGPGRPGWH	221	1.0000	10.20
18	VLVSALRAQ	299	1.0000	10.20
19	YDSADRQVR	21	0.8000	8.16
20	IEKMLACGA	139	0.8000	8.16
21	MVELIEKML	135	0.7000	7.14
22	VVARVRRYL	359	0.7000	7.14
23	VARVRRYLA	360	0.7000	7.14
24	MYVCGITPY	39	0.6000	6.12
25	VRLGLLAGH	314	0.6000	6.12

26	LPGRGPQLR	11	0.4000	4.08
27	VGATEAIAE	126	0.4000	4.08
28	ITPYDATHL	44	0.3000	3.06
29	YVGATEAIA	125	0.3000	3.06
30	VELIEKMLA	136	0.3000	3.06
31	VSGERRFAR	268	0.3000	3.06
32	MIGWDGHKM	283	0.3000	3.06
33	LWLDLGHEL	67	0.2000	2.04
34	VDVVARVRR	357	0.2000	2.04
35	LHYVQNITD	75	0.1000	1.02
36	LGHAATYVT	52	-0.1000	0
37	WRDLAQAEV	99	-0.1000	0
38	VPVLPGRGP	8	-0.2000	0