MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sat Mar 13 00:42:50 2010
Length of input sequence	291 amino acids
Number of nanomers from input sequence	283
Number of nanomers with obligatory P1 anchor residue	88
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	29

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	FARLYAVEL	111	2.8000	46.67
2	MQGLLALPL	151	2.1000	35.00
3	VRGIFPTAV	243	2.0900	34.83
4	YEKLEGVPL	122	1.9000	31.67
5	LRRQAPELL	28	1.7000	28.33
6	VRGNLAAAM	143	1.5200	25.33
7	LPLLAGYDI	157	1.3000	21.67
8	INSLSGTPA	10	0.6900	11.50

9	IVSFDAAGG	176	0.5800	9.67
10	MKKLYSQVT	206	0.4000	6.67
11	FLRRQAPEL	27	0.1700	2.83
12	YQAVGSGSL	192	-0.0500	0
13	VVMAGDRRS	68	-0.4100	0
14	LKYPGGVVM	62	-0.5200	0
15	IVALKYPGG	59	-0.7300	0
16	IAGTAAVAV	101	-0.8000	0
17	LSGTPAVDL	13	-0.9000	0
18	MVRGNLAAA	142	-0.9000	0
19	IHASDPQSA	165	-0.9000	0
20	LVRGIFPTA	242	-0.9300	0
21	FDAAGGWNI	179	-0.9800	0
22	LAIMVRGNL	139	-1.1000	0
23	VEFARLYAV	109	-1.3000	0
24	INRLAIMVR	136	-1.4100	0
25	LLALPLLAG	154	-1.6000	0
26	LRVAVEALY	220	-1.6000	0
27	VAVEFARLY	107	-1.7100	0
28	VYITDDYTA	90	-1.8000	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	MQGLLALPL	151	3.1000	51.67
2	VRGIFPTAV	243	3.0900	51.50
3	FARLYAVEL	111	2.8000	46.67
4	LRRQAPELL	28	2.7000	45.00
5	VRGNLAAAM	143	2.5200	42.00
6	LPLLAGYDI	157	2.3000	38.33
7	INSLSGTPA	10	1.6900	28.17
8	IVSFDAAGG	176	1.5800	26.33
9	MKKLYSQVT	206	1.4000	23.33

10	YEKLEGVPL	122	0.9000	15.00
11	VVMAGDRRS	68	0.5900	9.83
12	LKYPGGVVM	62	0.4800	8.00
13	IVALKYPGG	59	0.2700	4.50
14	IAGTAAVAV	101	0.2000	3.33
15	FLRRQAPEL	27	0.1700	2.83
16	LSGTPAVDL	13	0.1000	1.67
17	MVRGNLAAA	142	0.1000	1.67
18	IHASDPQSA	165	0.1000	1.67
19	LVRGIFPTA	242	0.0700	1.17
20	LAIMVRGNL	139	-0.1000	0
21	VEFARLYAV	109	-0.3000	0
22	INRLAIMVR	136	-0.4100	0
23	LLALPLLAG	154	-0.6000	0
24	LRVAVEALY	220	-0.6000	0
25	VAVEFARLY	107	-0.7100	0
26	VYITDDYTA	90	-0.8000	0
27	VPLTFAGKI	128	-0.9000	0
28	FDAAGGWNI	179	-0.9800	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	INRLAIMVR	136	3.8000	40.00
2	VRGNLAAAM	143	3.7000	38.95
3	VRGIFPTAV	243	3.6000	37.89
4	MVRGNLAAA	142	3.5000	36.84
5	MAGDRRSTQ	70	3.3700	35.47
6	LRRQAPELL	28	3.1600	33.26
7	LTFAGKINR	130	3.0000	31.58
8	VIIDADGAV	251	2.9000	30.53
9	LVRGIFPTA	242	2.6000	27.37
10	LAIMVRGNL	139	2.5600	26.95

11	LLPASISGG	35	2.4700	26.00
12	VRKVYITDD	87	2.2000	23.16
13	ITDDYTATG	92	2.2000	23.16
14	YPGGVVMAG	64	1.9000	20.00
15	IHASDPQSA	165	1.9000	20.00
16	VSFDAAGGW	177	1.9000	20.00
17	IVALKYPGG	59	1.8000	18.95
18	LLALPLLAG	154	1.8000	18.95
19	IVSFDAAGG	176	1.7000	17.89
20	VGSGSLFAK	195	1.7000	17.89
21	LARAIIESR	269	1.7000	17.89
22	LRVAVEALY	220	1.6000	16.84
23	MQGLLALPL	151	1.5600	16.42
24	ISGGAPLAG	40	1.5000	15.79
25	LKYPGGVVM	62	1.5000	15.79
26	IDADGAVDV	253	1.5000	15.79
27	LPHGTTIVA	53	1.4000	14.74
28	VEFARLYAV	109	1.3500	14.21
29	VVMAGDRRS	68	1.3000	13.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MAGDRRSTQ	70	3.0700	33.74
2	MVRGNLAAA	142	2.5000	27.47
3	LVRGIFPTA	242	1.6000	17.58
4	VRGIFPTAV	243	1.6000	17.58
5	YPGGVVMAG	64	1.5000	16.48
6	INRLAIMVR	136	1.3000	14.29
7	LRRQAPELL	28	1.2000	13.19
8	VRGNLAAAM	143	1.2000	13.19
9	IHASDPQSA	165	0.9000	9.89
10	VSFDAAGGW	177	0.9000	9.89

11	VIIDADGAV	251	0.9000	9.89
12	YITDDYTAT	91	0.7000	7.69
13	LAIMVRGNL	139	0.6000	6.59
14	VGSGSLFAK	195	0.6000	6.59
15	FPTAVIIDA	247	0.6000	6.59
16	LTFAGKINR	130	0.5000	5.49
17	WNIEEEGYQ	185	0.5000	5.49
18	WPLPDRLSI	2	0.4000	4.40
19	FLRRQAPEL	27	0.4000	4.40
20	LPHGTTIVA	53	0.4000	4.40
21	YQAVGSGSL	192	0.2000	2.20
22	VRKVYITDD	87	0.1000	1.10
23	LLPASISGG	35	0.0700	0.77
24	VVMAGDRRS	68	-0.1000	0
25	FARLYAVEL	111	-0.1000	0
26	ITDDYTATG	92	-0.2000	0
27	MQGLLALPL	151	-0.4000	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	MAGDRRSTQ	70	3.8000	43.18
2	MVRGNLAAA	142	3.5000	39.77
3	LRRQAPELL	28	2.6000	29.55
4	VRGIFPTAV	243	2.6000	29.55
5	VRGNLAAAM	143	2.2000	25.00
6	INRLAIMVR	136	2.0000	22.73
7	IHASDPQSA	165	2.0000	22.73
8	LVRGIFPTA	242	1.2000	13.64
9	LTFAGKINR	130	1.1800	13.41
10	VRKVYITDD	87	1.1000	12.50
11	MQGLLALPL	151	1.1000	12.50
12	LPHGTTIVA	53	1.0800	12.27

13	LLALPLLAG	154	0.9000	10.23
14	LLPASISGG	35	0.8000	9.09
15	ITDDYTATG	92	0.8000	9.09
16	IMVRGNLAA	141	0.7000	7.95
17	ISGGAPLAG	40	0.6000	6.82
18	VVMAGDRRS	68	0.6000	6.82
19	LAGYDIHAS	160	0.6000	6.82
20	LARAIIESR	269	0.6000	6.82
21	VSFDAAGGW	177	0.5000	5.68
22	VIIDADGAV	251	0.5000	5.68
23	LEGVPLTFA	125	0.4000	4.55
24	IDADGAVDV	253	0.3800	4.32
25	LYAVELEHY	114	0.3000	3.41
26	LEHYEKLEG	119	0.3000	3.41
27	IVSFDAAGG	176	0.3000	3.41
28	LRVAVEALY	220	0.3000	3.41
29	LSINSLSGT	8	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MAGDRRSTQ	70	3.8000	43.18
2	MVRGNLAAA	142	3.5000	39.77
3	LRRQAPELL	28	2.6000	29.55
4	VRGIFPTAV	243	2.6000	29.55
5	VRGNLAAAM	143	2.2000	25.00
6	INRLAIMVR	136	2.0000	22.73
7	IHASDPQSA	165	2.0000	22.73
8	LVRGIFPTA	242	1.2000	13.64
9	LTFAGKINR	130	1.1800	13.41
10	VRKVYITDD	87	1.1000	12.50
11	MQGLLALPL	151	1.1000	12.50
12	LPHGTTIVA	53	1.0800	12.27

13	LLALPLLAG	154	0.9000	10.23
14	LLPASISGG	35	0.8000	9.09
15	ITDDYTATG	92	0.8000	9.09
16	IMVRGNLAA	141	0.7000	7.95
17	ISGGAPLAG	40	0.6000	6.82
18	VVMAGDRRS	68	0.6000	6.82
19	LAGYDIHAS	160	0.6000	6.82
20	LARAIIESR	269	0.6000	6.82
21	VSFDAAGGW	177	0.5000	5.68
22	VIIDADGAV	251	0.5000	5.68
23	LEGVPLTFA	125	0.4000	4.55
24	IDADGAVDV	253	0.3800	4.32
25	LYAVELEHY	114	0.3000	3.41
26	LEHYEKLEG	119	0.3000	3.41
27	IVSFDAAGG	176	0.3000	3.41
28	LRVAVEALY	220	0.3000	3.41
29	LSINSLSGT	8	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MAGDRRSTQ	70	3.8000	43.18
2	MVRGNLAAA	142	3.5000	39.77
3	LRRQAPELL	28	2.6000	29.55
4	VRGIFPTAV	243	2.6000	29.55
5	VRGNLAAAM	143	2.2000	25.00
6	INRLAIMVR	136	2.0000	22.73
7	IHASDPQSA	165	2.0000	22.73
8	LVRGIFPTA	242	1.2000	13.64
9	LTFAGKINR	130	1.1800	13.41
10	VRKVYITDD	87	1.1000	12.50
11	MQGLLALPL	151	1.1000	12.50
12	LPHGTTIVA	53	1.0800	12.27

13	LLALPLLAG	154	0.9000	10.23
14	LLPASISGG	35	0.8000	9.09
15	ITDDYTATG	92	0.8000	9.09
16	IMVRGNLAA	141	0.7000	7.95
17	ISGGAPLAG	40	0.6000	6.82
18	VVMAGDRRS	68	0.6000	6.82
19	LAGYDIHAS	160	0.6000	6.82
20	LARAIIESR	269	0.6000	6.82
21	VSFDAAGGW	177	0.5000	5.68
22	VIIDADGAV	251	0.5000	5.68
23	LEGVPLTFA	125	0.4000	4.55
24	IDADGAVDV	253	0.3800	4.32
25	LYAVELEHY	114	0.3000	3.41
26	LEHYEKLEG	119	0.3000	3.41
27	IVSFDAAGG	176	0.3000	3.41
28	LRVAVEALY	220	0.3000	3.41
29	LSINSLSGT	8	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YPGGVVMAG	64	2.9000	30.53
2	INRLAIMVR	136	2.8000	29.47
3	VRGNLAAAM	143	2.7000	28.42
4	VRGIFPTAV	243	2.6000	27.37
5	MVRGNLAAA	142	2.5000	26.32
6	MAGDRRSTQ	70	2.3700	24.95
7	LRRQAPELL	28	2.1600	22.74
8	LTFAGKINR	130	2.0000	21.05
9	VIIDADGAV	251	1.9000	20.00
10	LVRGIFPTA	242	1.6000	16.84
11	LAIMVRGNL	139	1.5600	16.42
12	LLPASISGG	35	1.4700	15.47

13	YITDDYTAT	91	1.4000	14.74
14	FLRRQAPEL	27	1.3600	14.32
15	WPLPDRLSI	2	1.3000	13.68
16	VRKVYITDD	87	1.2000	12.63
17	ITDDYTATG	92	1.2000	12.63
18	YQAVGSGSL	192	1.1600	12.21
19	IHASDPQSA	165	0.9000	9.47
20	VSFDAAGGW	177	0.9000	9.47
21	FARLYAVEL	111	0.8600	9.05
22	IVALKYPGG	59	0.8000	8.42
23	LLALPLLAG	154	0.8000	8.42
24	IVSFDAAGG	176	0.7000	7.37
25	VGSGSLFAK	195	0.7000	7.37
26	LARAIIESR	269	0.7000	7.37
27	LRVAVEALY	220	0.6000	6.32
28	FPTAVIIDA	247	0.6000	6.32
29	MQGLLALPL	151	0.5600	5.89

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	MAGDRRSTQ	70	3.8000	43.18
2	MVRGNLAAA	142	3.5000	39.77
3	LRRQAPELL	28	2.6000	29.55
4	VRGIFPTAV	243	2.6000	29.55
5	VRGNLAAAM	143	2.2000	25.00
6	INRLAIMVR	136	2.0000	22.73
7	IHASDPQSA	165	2.0000	22.73
8	LVRGIFPTA	242	1.2000	13.64
9	LTFAGKINR	130	1.1800	13.41
10	VRKVYITDD	87	1.1000	12.50
11	MQGLLALPL	151	1.1000	12.50
12	LPHGTTIVA	53	1.0800	12.27

13	LLALPLLAG	154	0.9000	10.23
14	LLPASISGG	35	0.8000	9.09
15	ITDDYTATG	92	0.8000	9.09
16	IMVRGNLAA	141	0.7000	7.95
17	ISGGAPLAG	40	0.6000	6.82
18	VVMAGDRRS	68	0.6000	6.82
19	LAGYDIHAS	160	0.6000	6.82
20	LARAIIESR	269	0.6000	6.82
21	VSFDAAGGW	177	0.5000	5.68
22	VIIDADGAV	251	0.5000	5.68
23	LEGVPLTFA	125	0.4000	4.55
24	IDADGAVDV	253	0.3800	4.32
25	LYAVELEHY	114	0.3000	3.41
26	LEHYEKLEG	119	0.3000	3.41
27	IVSFDAAGG	176	0.3000	3.41
28	LRVAVEALY	220	0.3000	3.41
29	LSINSLSGT	8	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YDIHASDPQ	163	2.5000	29.07
2	LRRQAPELL	28	1.9000	22.09
3	VRGNLAAAM	143	1.9000	22.09
4	VRGIFPTAV	243	1.4000	16.28
5	INRLAIMVR	136	1.0000	11.63
6	VVMAGDRRS	68	0.9000	10.47
7	MQGLLALPL	151	0.9000	10.47
8	LYSQVTDGD	209	0.8000	9.30
9	IMVRGNLAA	141	0.7000	8.14
10	MKKLYSQVT	206	0.7000	8.14
11	IHASDPQSA	165	0.6000	6.98
12	WNIEEEGYQ	185	0.6000	6.98

13	FARLYAVEL	111	0.5800	6.74
14	IFPTAVIID	246	0.0800	0.93
15	VIIDADGAV	251	-0.1000	0
16	VYITDDYTA	90	-0.2000	0
17	YITDDYTAT	91	-0.3000	0
18	LFAKSSMKK	200	-0.4000	0
19	FPTAVIIDA	247	-0.5200	0
20	YTATGIAGT	96	-0.6000	0
21	LLALPLLAG	154	-0.6000	0
22	IVSFDAAGG	176	-0.6000	0
23	VELEHYEKL	117	-0.7000	0
24	IAGTAAVAV	101	-0.7200	0
25	INSLSGTPA	10	-0.8000	0
26	MVRGNLAAA	142	-0.9000	0
27	LPHGTTIVA	53	-0.9200	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	IMVRGNLAA	141	4.9000	51.04
2	VVMAGDRRS	68	4.8000	50.00
3	ISGRDVRKV	82	2.8000	29.17
4	LFAKSSMKK	200	2.4000	25.00
5	FAGKINRLA	132	2.3000	23.96
6	VRGIFPTAV	243	1.8800	19.58
7	VYITDDYTA	90	1.7000	17.71
8	VRGNLAAAM	143	1.6000	16.67
9	IVSFDAAGG	176	1.6000	16.67
10	LPDRLSINS	4	1.4000	14.58
11	LPHGTTIVA	53	1.4000	14.58
12	MKKLYSQVT	206	1.4000	14.58
13	MVRGNLAAA	142	1.0000	10.42
14	LAGYDIHAS	160	0.9000	9.38

15	IHASDPQSA	165	0.9000	9.38
16	MQGLLALPL	151	0.8000	8.33
17	INRLAIMVR	136	0.6000	6.25
18	VDVPESRIA	259	0.6000	6.25
19	LRRQAPELL	28	0.3000	3.12
20	IFPTAVIID	246	0.3000	3.12
21	LLPASISGG	35	-0.2000	0
22	VRKVYITDD	87	-0.2000	0
23	YDIHASDPQ	163	-0.2000	0
24	FLRRQAPEL	27	-0.3000	0
25	LLAGYDIHA	159	-0.3000	0
26	MISGRDVRK	81	-0.6000	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	VRGIFPTAV	243	3.2000	36.36
2	IVSFDAAGG	176	2.3000	26.14
3	VVMAGDRRS	68	2.2000	25.00
4	INRLAIMVR	136	2.1000	23.86
5	MQGLLALPL	151	1.7000	19.32
6	MKKLYSQVT	206	1.7000	19.32
7	VRKVYITDD	87	1.3000	14.77
8	VRGNLAAAM	143	1.3000	14.77
9	LRRQAPELL	28	1.2000	13.64
10	INSLSGTPA	10	0.9000	10.23
11	IMVRGNLAA	141	0.8000	9.09
12	LLPASISGG	35	0.7000	7.95
13	LFAKSSMKK	200	0.7000	7.95
14	VYITDDYTA	90	0.2000	2.27
15	LLALPLLAG	154	0.2000	2.27
16	LEGVPLTFA	125	0.1000	1.14
17	LYSQVTDGD	209	0.1000	1.14

18	IHASDPQSA	165	-0.1000	0
19	IVALKYPGG	59	-0.4000	0
20	FARLYAVEL	111	-0.4000	0
21	LPLLAGYDI	157	-0.5000	0
22	YQAVGSGSL	192	-0.5000	0
23	IFPTAVIID	246	-0.5200	0
24	MVRGNLAAA	142	-0.7000	0
25	LRVAVEALY	220	-0.7000	0
26	LPHGTTIVA	53	-0.7200	0
27	VEFARLYAV	109	-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	VRKVYITDD	87	3.0000	31.91
2	IVSFDAAGG	176	2.6000	27.66
3	VRGIFPTAV	243	2.5000	26.60
4	LYSQVTDGD	209	1.8000	19.15
5	MQGLLALPL	151	1.7000	18.09
6	FARLYAVEL	111	1.6000	17.02
7	MKKLYSQVT	206	1.6000	17.02
8	YQAVGSGSL	192	1.5000	15.96
9	VRGNLAAAM	143	1.4000	14.89
10	LRRQAPELL	28	1.2000	12.77
11	VVMAGDRRS	68	1.2000	12.77
12	IFPTAVIID	246	1.1800	12.55
13	INRLAIMVR	136	1.1000	11.70
14	LLPASISGG	35	1.0000	10.64
15	LLALPLLAG	154	0.5000	5.32
16	YDIHASDPQ	163	0.3000	3.19
17	INSLSGTPA	10	-0.1000	0
18	IVALKYPGG	59	-0.1000	0
19	IMVRGNLAA	141	-0.2000	0

20	YEKLEGVPL	122	-0.5000	0
21	FPTAVIIDA	247	-0.5200	0
22	LRVAVEALY	220	-0.6000	0
23	YPGGVVMAG	64	-0.8000	0
24	VYITDDYTA	90	-0.8000	0
25	LEGVPLTFA	125	-0.9000	0
26	FAGKINRLA	132	-0.9000	0
27	LAGYDIHAS	160	-1.0000	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	VRGIFPTAV	243	2.2000	25.00
2	IVSFDAAGG	176	1.3000	14.77
3	VVMAGDRRS	68	1.2000	13.64
4	INRLAIMVR	136	1.1000	12.50
5	MQGLLALPL	151	0.7000	7.95
6	MKKLYSQVT	206	0.7000	7.95
7	FARLYAVEL	111	0.6000	6.82
8	YQAVGSGSL	192	0.5000	5.68
9	VRKVYITDD	87	0.3000	3.41
10	VRGNLAAAM	143	0.3000	3.41
11	LRRQAPELL	28	0.2000	2.27
12	INSLSGTPA	10	-0.1000	0
13	IMVRGNLAA	141	-0.2000	0
14	LLPASISGG	35	-0.3000	0
15	LFAKSSMKK	200	-0.3000	0
16	YDIHASDPQ	163	-0.5000	0
17	FPTAVIIDA	247	-0.5200	0
18	VYITDDYTA	90	-0.8000	0
19	LLALPLLAG	154	-0.8000	0
20	LEGVPLTFA	125	-0.9000	0
21	FAGKINRLA	132	-0.9000	0

22	LYSQVTDGD	209	-0.9000	0
23	LAGYDIHAS	160	-1.0000	0
24	IHASDPQSA	165	-1.1000	0
25	IVALKYPGG	59	-1.4000	0
26	YSQVTDGDS	210	-1.4000	0
27	YEKLEGVPL	122	-1.5000	0
28	LPLLAGYDI	157	-1.5000	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	VRKVYITDD	87	4.0000	42.55
2	IVSFDAAGG	176	3.6000	38.30
3	VRGIFPTAV	243	3.5000	37.23
4	LYSQVTDGD	209	2.8000	29.79
5	MQGLLALPL	151	2.7000	28.72
6	MKKLYSQVT	206	2.6000	27.66
7	VRGNLAAAM	143	2.4000	25.53
8	LRRQAPELL	28	2.2000	23.40
9	VVMAGDRRS	68	2.2000	23.40
10	IFPTAVIID	246	2.1800	23.19
11	INRLAIMVR	136	2.1000	22.34
12	LLPASISGG	35	2.0000	21.28
13	LLALPLLAG	154	1.5000	15.96
14	VEALYDAAD	224	1.0000	10.64
15	INSLSGTPA	10	0.9000	9.57
16	IVALKYPGG	59	0.9000	9.57
17	IMVRGNLAA	141	0.8000	8.51
18	FARLYAVEL	111	0.6000	6.38
19	YQAVGSGSL	192	0.5000	5.32
20	LRVAVEALY	220	0.4000	4.26
21	VYITDDYTA	90	0.2000	2.13
22	LEGVPLTFA	125	0.1000	1.06

23	IHASDPQSA	165	-0.1000	0
24	ITDDYTATG	92	-0.2000	0
25	LKYPGGVVM	62	-0.3000	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	VRGNLAAAM	143	3.4000	37.78
2	LRRQAPELL	28	2.8600	31.78
3	INRLAIMVR	136	2.5000	27.78
4	VRGIFPTAV	243	2.4000	26.67
5	LYSQVTDGD	209	1.9000	21.11
6	MQGLLALPL	151	1.8600	20.67
7	YDIHASDPQ	163	1.8000	20.00
8	FARLYAVEL	111	1.5400	17.11
9	ITDDYTATG	92	1.4000	15.56
10	MKKLYSQVT	206	1.4000	15.56
11	VVMAGDRRS	68	1.3000	14.44
12	IFPTAVIID	246	1.1800	13.11
13	VIIDADGAV	251	0.9000	10.00
14	LLALPLLAG	154	0.8000	8.89
15	IVSFDAAGG	176	0.8000	8.89
16	IMVRGNLAA	141	0.7000	7.78
17	IHASDPQSA	165	0.6000	6.67
18	LLPASISGG	35	0.4000	4.44
19	YITDDYTAT	91	0.4000	4.44
20	LARAIIESR	269	0.3000	3.33
21	IAGTAAVAV	101	0.2800	3.11
22	VELEHYEKL	117	0.2600	2.89
23	YPGGVVMAG	64	0.2000	2.22
24	IVALKYPGG	59	0.1000	1.11
25	YTATGIAGT	96	0.1000	1.11
26	VAVEFARLY	107	0.1000	1.11

27	YQAVGSGSL	192	-0.0400	0
28	WNIEEEGYQ	185	-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	VRGIFPTAV	243	3.2000	36.36
2	IVSFDAAGG	176	2.3000	26.14
3	VVMAGDRRS	68	2.2000	25.00
4	INRLAIMVR	136	2.1000	23.86
5	MQGLLALPL	151	1.7000	19.32
6	MKKLYSQVT	206	1.7000	19.32
7	VRKVYITDD	87	1.3000	14.77
8	VRGNLAAAM	143	1.3000	14.77
9	LRRQAPELL	28	1.2000	13.64
10	INSLSGTPA	10	0.9000	10.23
11	IMVRGNLAA	141	0.8000	9.09
12	LLPASISGG	35	0.7000	7.95
13	LFAKSSMKK	200	0.7000	7.95
14	VYITDDYTA	90	0.2000	2.27
15	LLALPLLAG	154	0.2000	2.27
16	LEGVPLTFA	125	0.1000	1.14
17	LYSQVTDGD	209	0.1000	1.14
18	IHASDPQSA	165	-0.1000	0
19	IVALKYPGG	59	-0.4000	0
20	FARLYAVEL	111	-0.4000	0
21	LPLLAGYDI	157	-0.5000	0
22	YQAVGSGSL	192	-0.5000	0
23	IFPTAVIID	246	-0.5200	0
24	MVRGNLAAA	142	-0.7000	0
25	LRVAVEALY	220	-0.7000	0
26	LPHGTTIVA	53	-0.7200	0
27	VEFARLYAV	109	-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	YDIHASDPQ	163	2.5000	29.07
2	LRRQAPELL	28	1.9000	22.09
3	VRGNLAAAM	143	1.9000	22.09
4	VRGIFPTAV	243	1.4000	16.28
5	INRLAIMVR	136	1.0000	11.63
6	VVMAGDRRS	68	0.9000	10.47
7	MQGLLALPL	151	0.9000	10.47
8	LYSQVTDGD	209	0.8000	9.30
9	IMVRGNLAA	141	0.7000	8.14
10	MKKLYSQVT	206	0.7000	8.14
11	IHASDPQSA	165	0.6000	6.98
12	WNIEEEGYQ	185	0.6000	6.98
13	FARLYAVEL	111	0.5800	6.74
14	IFPTAVIID	246	0.0800	0.93
15	VIIDADGAV	251	-0.1000	0
16	VYITDDYTA	90	-0.2000	0
17	YITDDYTAT	91	-0.3000	0
18	LFAKSSMKK	200	-0.4000	0
19	FPTAVIIDA	247	-0.5200	0
20	YTATGIAGT	96	-0.6000	0
21	LLALPLLAG	154	-0.6000	0
22	IVSFDAAGG	176	-0.6000	0
23	VELEHYEKL	117	-0.7000	0
24	IAGTAAVAV	101	-0.7200	0
25	INSLSGTPA	10	-0.8000	0
26	MVRGNLAAA	142	-0.9000	0
27	LPHGTTIVA	53	-0.9200	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	YQAVGSGSL	192	6.1000	52.59
2	LSGTPAVDL	13	5.3000	45.69
3	MQGLLALPL	151	5.2000	44.83
4	FARLYAVEL	111	4.9000	42.24
5	VRGIFPTAV	243	4.9000	42.24
6	FAKSSMKKL	201	4.6000	39.66
7	VPLTFAGKI	128	4.3000	37.07
8	LRRQAPELL	28	4.2000	36.21
9	IAGTAAVAV	101	4.2000	36.21
10	WPLPDRLSI	2	3.8000	32.76
11	FLRRQAPEL	27	3.8000	32.76
12	YEKLEGVPL	122	3.7000	31.90
13	LPLLAGYDI	157	3.2000	27.59
14	FDAAGGWNI	179	2.9000	25.00
15	IFPTAVIID	246	2.8000	24.14
16	LKYPGGVVM	62	2.7000	23.28
17	VEFARLYAV	109	2.7000	23.28
18	VDLSSFTDF	19	2.4000	20.69
19	LAIMVRGNL	139	2.4000	20.69
20	VRGNLAAAM	143	2.3000	19.83
21	VYITDDYTA	90	2.0000	17.24
22	VELEHYEKL	117	2.0000	17.24
23	LYAVELEHY	114	1.9000	16.38
24	IHASDPQSA	165	1.9000	16.38
25	VPESRIAEL	261	1.7000	14.66
26	MKKLYSQVT	206	1.4000	12.07
27	FPTAVIIDA	247	1.4000	12.07
28	VRKVYITDD	87	1.3000	11.21
29	YTATGIAGT	96	1.3000	11.21

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	YQAVGSGSL	192	6.1000	52.59
2	LSGTPAVDL	13	5.3000	45.69
3	MQGLLALPL	151	5.2000	44.83
4	FARLYAVEL	111	4.9000	42.24
5	VRGIFPTAV	243	4.9000	42.24
6	FAKSSMKKL	201	4.6000	39.66
7	VPLTFAGKI	128	4.3000	37.07
8	LRRQAPELL	28	4.2000	36.21
9	IAGTAAVAV	101	4.2000	36.21
10	WPLPDRLSI	2	3.8000	32.76
11	FLRRQAPEL	27	3.8000	32.76
12	YEKLEGVPL	122	3.7000	31.90
13	LPLLAGYDI	157	3.2000	27.59
14	FDAAGGWNI	179	2.9000	25.00
15	IFPTAVIID	246	2.8000	24.14
16	LKYPGGVVM	62	2.7000	23.28
17	VEFARLYAV	109	2.7000	23.28
18	VDLSSFTDF	19	2.4000	20.69
19	LAIMVRGNL	139	2.4000	20.69
20	VRGNLAAAM	143	2.3000	19.83
21	VYITDDYTA	90	2.0000	17.24
22	VELEHYEKL	117	2.0000	17.24
23	LYAVELEHY	114	1.9000	16.38
24	IHASDPQSA	165	1.9000	16.38
25	VPESRIAEL	261	1.7000	14.66
26	MKKLYSQVT	206	1.4000	12.07
27	FPTAVIIDA	247	1.4000	12.07
28	VRKVYITDD	87	1.3000	11.21
29	YTATGIAGT	96	1.3000	11.21

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	FLRRQAPEL	27	2.8000	32.56
2	LEHYEKLEG	119	2.8000	32.56
3	LAIMVRGNL	139	2.4000	27.91
4	VRGNLAAAM	143	2.1000	24.42
5	IVSFDAAGG	176	2.1000	24.42
6	IMVRGNLAA	141	2.0000	23.26
7	VALKYPGGV	60	1.9000	22.09
8	LAGYDIHAS	160	1.9000	22.09
9	ISGRDVRKV	82	1.4000	16.28
10	FAGKINRLA	132	1.3000	15.12
11	MVRGNLAAA	142	1.0000	11.63
12	LLALPLLAG	154	0.9000	10.47
13	YQAVGSGSL	192	0.9000	10.47
14	VRKVYITDD	87	0.8000	9.30
15	MQGLLALPL	151	0.8000	9.30
16	WNIEEEGYQ	185	0.7000	8.14
17	LFAKSSMKK	200	0.7000	8.14
18	INRLAIMVR	136	0.6000	6.98
19	IESRSGADT	274	0.6000	6.98
20	IFPTAVIID	246	0.5000	5.81
21	LRVAVEALY	220	0.4000	4.65
22	FARLYAVEL	111	0.3000	3.49
23	VVMAGDRRS	68	0.2000	2.33
24	WPLPDRLSI	2	0.1000	1.16
25	YPGGVVMAG	64	-0.1000	0
26	FTDFLRRQA	24	-0.4000	0
27	IVALKYPGG	59	-0.5000	0

ALLELE: DRB1_0802	Threshold for 3 % with score: 1.0	Highest Score achievable by any peptide: 8

Rank	Sequence	At Position	Score	% of Highest Score
1	IMVRGNLAA	141	2.0000	25.00
2	LAGYDIHAS	160	1.9000	23.75
3	FLRRQAPEL	27	1.8000	22.50
4	VALKYPGGV	60	1.6000	20.00
5	LEHYEKLEG	119	1.5000	18.75
6	LAIMVRGNL	139	1.4000	17.50
7	LFAKSSMKK	200	1.4000	17.50
8	FAGKINRLA	132	1.3000	16.25
9	ISGRDVRKV	82	1.1000	13.75
10	MVRGNLAAA	142	1.0000	12.50
11	VRGNLAAAM	143	1.0000	12.50
12	IVSFDAAGG	176	0.8000	10.00
13	INRLAIMVR	136	0.6000	7.50
14	VVMAGDRRS	68	0.2000	2.50
15	WPLPDRLSI	2	-0.1000	0
16	WNIEEEGYQ	185	-0.1000	0
17	YQAVGSGSL	192	-0.1000	0
18	MQGLLALPL	151	-0.2000	0
19	IESRSGADT	274	-0.3000	0
20	FTDFLRRQA	24	-0.4000	0
21	LLALPLLAG	154	-0.4000	0
22	FPTAVIIDA	247	-0.6000	0
23	LPDRLSINS	4	-0.7000	0
24	FARLYAVEL	111	-0.7000	0
25	LTFAGKINR	130	-0.7000	0
26	LRVAVEALY	220	-0.7000	0
27	IAELARAII	266	-0.8000	0
28	VRGIFPTAV	243	-0.9000	0

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

Rank	Sequence	At Position	Score	% of Highest Score

1	IMVRGNLAA	141	3.0000	37.50
2	LAGYDIHAS	160	2.9000	36.25
3	VALKYPGGV	60	2.6000	32.50
4	LEHYEKLEG	119	2.5000	31.25
5	LAIMVRGNL	139	2.4000	30.00
6	LFAKSSMKK	200	2.4000	30.00
7	ISGRDVRKV	82	2.1000	26.25
8	MVRGNLAAA	142	2.0000	25.00
9	VRGNLAAAM	143	2.0000	25.00
10	IVSFDAAGG	176	1.8000	22.50
11	INRLAIMVR	136	1.6000	20.00
12	VVMAGDRRS	68	1.2000	15.00
13	FLRRQAPEL	27	0.8000	10.00
14	MQGLLALPL	151	0.8000	10.00
15	IESRSGADT	274	0.7000	8.75
16	LLALPLLAG	154	0.6000	7.50
17	LPDRLSINS	4	0.3000	3.75
18	LTFAGKINR	130	0.3000	3.75
19	FAGKINRLA	132	0.3000	3.75
20	LRVAVEALY	220	0.3000	3.75
21	IAELARAII	266	0.2000	2.50
22	VRGIFPTAV	243	0.1000	1.25
23	LLPASISGG	35	-0.3000	0
24	MAGDRRSTQ	70	-0.6000	0
25	VMAGDRRST	69	-0.7000	0
26	VEFARLYAV	109	-0.7000	0
27	MKKLYSQVT	206	-0.7000	0
28	IVALKYPGG	59	-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	LEHYEKLEG	119	3.8000	44.19

2	LAIMVRGNL	139	3.4000	39.53
3	VRGNLAAAM	143	3.1000	36.05
4	IVSFDAAGG	176	3.1000	36.05
5	IMVRGNLAA	141	3.0000	34.88
6	VALKYPGGV	60	2.9000	33.72
7	LAGYDIHAS	160	2.9000	33.72
8	ISGRDVRKV	82	2.4000	27.91
9	MVRGNLAAA	142	2.0000	23.26
10	LLALPLLAG	154	1.9000	22.09
11	FLRRQAPEL	27	1.8000	20.93
12	VRKVYITDD	87	1.8000	20.93
13	MQGLLALPL	151	1.8000	20.93
14	LFAKSSMKK	200	1.7000	19.77
15	INRLAIMVR	136	1.6000	18.60
16	IESRSGADT	274	1.6000	18.60
17	IFPTAVIID	246	1.5000	17.44
18	LRVAVEALY	220	1.4000	16.28
19	VVMAGDRRS	68	1.2000	13.95
20	LLPASISGG	35	1.0000	11.63
21	IVALKYPGG	59	0.5000	5.81
22	VRGIFPTAV	243	0.4000	4.65
23	IAELARAII	266	0.4000	4.65
24	LPDRLSINS	4	0.3000	3.49
25	LTFAGKINR	130	0.3000	3.49
26	FAGKINRLA	132	0.3000	3.49
27	LALPLLAGY	155	0.3000	3.49
28	VMAGDRRST	69	0.2000	2.33
29	MAGDRRSTQ	70	0.2000	2.33

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	IMVRGNLAA	141	2.6000	29.89

2	LAGYDIHAS	160	2.4000	27.59
3	LFAKSSMKK	200	2.4000	27.59
4	LEHYEKLEG	119	2.1000	24.14
5	FLRRQAPEL	27	2.0000	22.99
6	VRGIFPTAV	243	1.9000	21.84
7	INRLAIMVR	136	1.6000	18.39
8	FAGKINRLA	132	1.0000	11.49
9	MVRGNLAAA	142	1.0000	11.49
10	VRGNLAAAM	143	1.0000	11.49
11	VALKYPGGV	60	0.9000	10.34
12	VRKVYITDD	87	0.9000	10.34
13	ISGRDVRKV	82	0.8000	9.20
14	IVSFDAAGG	176	0.8000	9.20
15	LAIMVRGNL	139	0.7000	8.05
16	WPLPDRLSI	2	0.5000	5.75
17	LLPASISGG	35	0.5000	5.75
18	INSLSGTPA	10	0.4000	4.60
19	MQGLLALPL	151	0.4000	4.60
20	FARLYAVEL	111	0.3000	3.45
21	FPTAVIIDA	247	0.2800	3.22
22	MAGDRRSTQ	70	0.2000	2.30
23	LEGVPLTFA	125	0.2000	2.30
24	LLALPLLAG	154	0.2000	2.30
25	LPDRLSINS	4	0.1800	2.07
26	LTFAGKINR	130	0.1800	2.07
27	VVMAGDRRS	68	-0.1000	0
28	LSINSLSGT	8	-0.3000	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	LEHYEKLEG	119	4.6000	45.54
2	FLRRQAPEL	27	3.9500	39.11

3	IMVRGNLAA	141	3.8000	37.62
4	LLALPLLAG	154	2.7000	26.73
5	MQGLLALPL	151	2.6000	25.74
6	LAGYDIHAS	160	2.6000	25.74
7	LAIMVRGNL	139	2.5000	24.75
8	LFAKSSMKK	200	2.3000	22.77
9	INRLAIMVR	136	2.2000	21.78
10	VRGNLAAAM	143	2.1000	20.79
11	IVSFDAAGG	176	2.1000	20.79
12	IFPTAVIID	246	2.1000	20.79
13	VALKYPGGV	60	2.0000	19.80
14	WPLPDRLSI	2	1.9000	18.81
15	VRKVYITDD	87	1.9000	18.81
16	ISGRDVRKV	82	1.6000	15.84
17	YPGGVVMAG	64	1.5000	14.85
18	FAGKINRLA	132	1.5000	14.85
19	MVRGNLAAA	142	1.0000	9.90
20	YQAVGSGSL	192	1.0000	9.90
21	FPTAVIIDA	247	1.0000	9.90
22	LPDRLSINS	4	0.9000	8.91
23	LTFAGKINR	130	0.9000	8.91
24	FARLYAVEL	111	0.8000	7.92
25	WNIEEEGYQ	185	0.8000	7.92
26	IVALKYPGG	59	0.6500	6.44
27	IESRSGADT	274	0.6000	5.94
28	VRGIFPTAV	243	0.5000	4.95
29	VVMAGDRRS	68	0.4000	3.96

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	INRLAIMVR	136	2.6000	31.33
2	MQGLLALPL	151	2.0000	24.10

3	LLALPLLAG	154	1.8000	21.69
4	LAIMVRGNL	139	1.1000	13.25
5	WPLPDRLSI	2	1.0000	12.05
6	VRGNLAAAM	143	1.0000	12.05
7	FPTAVIIDA	247	1.0000	12.05
8	LTFAGKINR	130	0.9000	10.84
9	IMVRGNLAA	141	0.8000	9.64
10	VRGIFPTAV	243	0.8000	9.64
11	IVSFDAAGG	176	0.7000	8.43
12	VVMAGDRRS	68	0.4000	4.82
13	LEHYEKLEG	119	0.4000	4.82
14	MVRGNLAAA	142	0.3000	3.61
15	FARLYAVEL	111	0.2000	2.41
16	LFAKSSMKK	200	0.2000	2.41
17	YQAVGSGSL	192	0.1000	1.20
18	FLRRQAPEL	27	-0.0500	0
19	IFPTAVIID	246	-0.2000	0
20	IVALKYPGG	59	-0.2500	0
21	FTDFLRRQA	24	-0.3000	0
22	LRRQAPELL	28	-0.3000	0
23	LAGYDIHAS	160	-0.3000	0
24	IAELARAII	266	-0.4000	0
25	YPGGVVMAG	64	-0.5000	0
26	VRKVYITDD	87	-0.7000	0
27	WNIEEEGYQ	185	-0.7000	0
28	LRVAVEALY	220	-0.7000	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	VVMAGDRRS	68	3.0000	35.71
2	LAGYDIHAS	160	2.3000	27.38
3	VRGNLAAAM	143	2.1000	25.00

4	IVSFDAAGG	176	2.1000	25.00
5	LRRQAPELL	28	2.0000	23.81
6	ISGRDVRKV	82	1.8000	21.43
7	INRLAIMVR	136	1.6000	19.05
8	IMVRGNLAA	141	1.6000	19.05
9	MVRGNLAAA	142	1.5000	17.86
10	LEHYEKLEG	119	1.4000	16.67
11	MQGLLALPL	151	1.2000	14.29
12	LFAKSSMKK	200	1.2000	14.29
13	LLALPLLAG	154	1.0000	11.90
14	LAIMVRGNL	139	0.8000	9.52
15	FTDFLRRQA	24	0.7000	8.33
16	VRGIFPTAV	243	0.7000	8.33
17	VMAGDRRST	69	0.6000	7.14
18	LTFAGKINR	130	0.6000	7.14
19	FAGKINRLA	132	0.6000	7.14
20	IHASDPQSA	165	0.3000	3.57
21	LRVAVEALY	220	0.3000	3.57
22	VEFARLYAV	109	0.2000	2.38
23	LLPASISGG	35	0.1000	1.19
24	VALKYPGGV	60	0.1000	1.19
25	IAELARAII	266	-0.1000	0
26	INSLSGTPA	10	-0.2000	0
27	MKKLYSQVT	206	-0.2000	0
28	LPLLAGYDI	157	-0.3000	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	INRLAIMVR	136	3.6000	43.37
2	MQGLLALPL	151	3.0000	36.14
3	LLALPLLAG	154	2.8000	33.73
4	LAIMVRGNL	139	2.1000	25.30

5	VRGNLAAAM	143	2.0000	24.10
6	LTFAGKINR	130	1.9000	22.89
7	IMVRGNLAA	141	1.8000	21.69
8	VRGIFPTAV	243	1.8000	21.69
9	IVSFDAAGG	176	1.7000	20.48
10	VVMAGDRRS	68	1.4000	16.87
11	LEHYEKLEG	119	1.4000	16.87
12	MVRGNLAAA	142	1.3000	15.66
13	LFAKSSMKK	200	1.2000	14.46
14	IFPTAVIID	246	0.8000	9.64
15	IVALKYPGG	59	0.7500	9.04
16	LRRQAPELL	28	0.7000	8.43
17	LAGYDIHAS	160	0.7000	8.43
18	IAELARAII	266	0.6000	7.23
19	VRKVYITDD	87	0.3000	3.61
20	LRVAVEALY	220	0.3000	3.61
21	LPLLAGYDI	157	0.2000	2.41
22	INSLSGTPA	10	0.1000	1.20
23	VALKYPGGV	60	-0.1000	0
24	MKKLYSQVT	206	-0.2000	0
25	LLPASISGG	35	-0.3000	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	INRLAIMVR	136	3.6000	43.37
2	MQGLLALPL	151	3.0000	36.14
3	LLALPLLAG	154	2.8000	33.73
4	LAIMVRGNL	139	2.1000	25.30
5	VRGNLAAAM	143	2.0000	24.10
6	LTFAGKINR	130	1.9000	22.89
7	IMVRGNLAA	141	1.8000	21.69
8	VRGIFPTAV	243	1.8000	21.69

9	IVSFDAAGG	176	1.7000	20.48
10	VVMAGDRRS	68	1.4000	16.87
11	LEHYEKLEG	119	1.4000	16.87
12	MVRGNLAAA	142	1.3000	15.66
13	LFAKSSMKK	200	1.2000	14.46
14	IFPTAVIID	246	0.8000	9.64
15	IVALKYPGG	59	0.7500	9.04
16	LRRQAPELL	28	0.7000	8.43
17	LAGYDIHAS	160	0.7000	8.43
18	IAELARAII	266	0.6000	7.23
19	VRKVYITDD	87	0.3000	3.61
20	LRVAVEALY	220	0.3000	3.61
21	LPLLAGYDI	157	0.2000	2.41
22	INSLSGTPA	10	0.1000	1.20
23	VALKYPGGV	60	-0.1000	0
24	MKKLYSQVT	206	-0.2000	0
25	LLPASISGG	35	-0.3000	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	MAGDRRSTQ	70	4.0700	44.73
2	MVRGNLAAA	142	3.5000	38.46
3	LVRGIFPTA	242	2.6000	28.57
4	VRGIFPTAV	243	2.6000	28.57
5	INRLAIMVR	136	2.3000	25.27
6	LRRQAPELL	28	2.2000	24.18
7	VRGNLAAAM	143	2.2000	24.18
8	IHASDPQSA	165	1.9000	20.88
9	VSFDAAGGW	177	1.9000	20.88
10	VIIDADGAV	251	1.9000	20.88
11	LAIMVRGNL	139	1.6000	17.58
12	VGSGSLFAK	195	1.6000	17.58

13	LTFAGKINR	130	1.5000	16.48
14	LPHGTTIVA	53	1.4000	15.38
15	VRKVYITDD	87	1.1000	12.09
16	LLPASISGG	35	1.0700	11.76
17	VVMAGDRRS	68	0.9000	9.89
18	ITDDYTATG	92	0.8000	8.79
19	MQGLLALPL	151	0.6000	6.59
20	YPGGVVMAG	64	0.5000	5.49
21	VMAGDRRST	69	0.5000	5.49
22	LFAKSSMKK	200	0.5000	5.49
23	IDADGAVDV	253	0.5000	5.49
24	LSINSLSGT	8	0.4700	5.16
25	IVALKYPGG	59	0.4000	4.40
26	LEGVPLTFA	125	0.4000	4.40
27	LLALPLLAG	154	0.4000	4.40
28	VEFARLYAV	109	0.3500	3.85
29	IVSFDAAGG	176	0.3000	3.30

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	VVMAGDRRS	68	2.0000	23.81
2	FTDFLRRQA	24	1.7000	20.24
3	FAGKINRLA	132	1.6000	19.05
4	LAGYDIHAS	160	1.3000	15.48
5	VRGNLAAAM	143	1.1000	13.10
6	IVSFDAAGG	176	1.1000	13.10
7	LRRQAPELL	28	1.0000	11.90
8	ISGRDVRKV	82	0.8000	9.52
9	INRLAIMVR	136	0.6000	7.14
10	IMVRGNLAA	141	0.6000	7.14
11	YDIHASDPQ	163	0.6000	7.14
12	MVRGNLAAA	142	0.5000	5.95

13	FLRRQAPEL	27	0.4000	4.76
14	LEHYEKLEG	119	0.4000	4.76
15	MQGLLALPL	151	0.2000	2.38
16	LFAKSSMKK	200	0.2000	2.38
17	WPLPDRLSI	2	0.1000	1.19
18	LAIMVRGNL	139	-0.2000	0
19	VRGIFPTAV	243	-0.3000	0
20	FPTAVIIDA	247	-0.3000	0
21	VMAGDRRST	69	-0.4000	0
22	LTFAGKINR	130	-0.4000	0
23	IHASDPQSA	165	-0.7000	0
24	LRVAVEALY	220	-0.7000	0
25	VEFARLYAV	109	-0.8000	0
26	LLPASISGG	35	-0.9000	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	VRGNLAAAM	143	2.6000	29.55
2	IVSFDAAGG	176	2.5000	28.41
3	VVMAGDRRS	68	2.4000	27.27
4	INRLAIMVR	136	2.1000	23.86
5	LRRQAPELL	28	1.9600	22.27
6	ISGRDVRKV	82	1.8000	20.45
7	LEHYEKLEG	119	1.8000	20.45
8	FTDFLRRQA	24	1.7000	19.32
9	LAGYDIHAS	160	1.7000	19.32
10	FAGKINRLA	132	1.6000	18.18
11	LLALPLLAG	154	1.4000	15.91
12	FLRRQAPEL	27	1.3600	15.45
13	MQGLLALPL	151	1.1600	13.18
14	LTFAGKINR	130	1.1000	12.50
15	WPLPDRLSI	2	1.0000	11.36

16	FARLYAVEL	111	0.9600	10.91
17	LAIMVRGNL	139	0.7600	8.64
18	VRGIFPTAV	243	0.7000	7.95
19	IMVRGNLAA	141	0.6000	6.82
20	LRVAVEALY	220	0.6000	6.82
21	LLPASISGG	35	0.5000	5.68
22	MVRGNLAAA	142	0.5000	5.68
23	VMAGDRRST	69	0.3000	3.41
24	LFAKSSMKK	200	0.3000	3.41
25	VEFARLYAV	109	0.2000	2.27
26	VALKYPGGV	60	0.1000	1.14
27	VAVEFARLY	107	-0.1000	0

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	VVMAGDRRS	68	3.0000	35.71
2	LAGYDIHAS	160	2.3000	27.38
3	VRGNLAAAM	143	2.1000	25.00
4	IVSFDAAGG	176	2.1000	25.00
5	LRRQAPELL	28	2.0000	23.81
6	ISGRDVRKV	82	1.8000	21.43
7	INRLAIMVR	136	1.6000	19.05
8	IMVRGNLAA	141	1.6000	19.05
9	MVRGNLAAA	142	1.5000	17.86
10	LEHYEKLEG	119	1.4000	16.67
11	MQGLLALPL	151	1.2000	14.29
12	LFAKSSMKK	200	1.2000	14.29
13	LLALPLLAG	154	1.0000	11.90
14	LAIMVRGNL	139	0.8000	9.52
15	FTDFLRRQA	24	0.7000	8.33
16	VRGIFPTAV	243	0.7000	8.33
17	VMAGDRRST	69	0.6000	7.14

18	LTFAGKINR	130	0.6000	7.14
19	FAGKINRLA	132	0.6000	7.14
20	IHASDPQSA	165	0.3000	3.57
21	LRVAVEALY	220	0.3000	3.57
22	VEFARLYAV	109	0.2000	2.38
23	LLPASISGG	35	0.1000	1.19
24	VALKYPGGV	60	0.1000	1.19
25	IAELARAII	266	-0.1000	0
26	INSLSGTPA	10	-0.2000	0
27	MKKLYSQVT	206	-0.2000	0
28	LPLLAGYDI	157	-0.3000	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	INRLAIMVR	136	4.1000	47.13
2	LLALPLLAG	154	3.2000	36.78
3	MQGLLALPL	151	2.9600	34.02
4	VRGNLAAAM	143	2.5000	28.74
5	LTFAGKINR	130	2.4000	27.59
6	IVSFDAAGG	176	2.1000	24.14
7	LAIMVRGNL	139	2.0600	23.68
8	WPLPDRLSI	2	1.9000	21.84
9	LEHYEKLEG	119	1.8000	20.69
10	VRGIFPTAV	243	1.8000	20.69
11	FARLYAVEL	111	1.1600	13.33
12	IVALKYPGG	59	1.1500	13.22
13	YQAVGSGSL	192	1.0600	12.18
14	FPTAVIIDA	247	1.0000	11.49
15	FLRRQAPEL	27	0.9100	10.46
16	YPGGVVMAG	64	0.9000	10.34
17	IFPTAVIID	246	0.9000	10.34
18	VVMAGDRRS	68	0.8000	9.20

19	IMVRGNLAA	141	0.8000	9.20
20	LRRQAPELL	28	0.6600	7.59
21	LRVAVEALY	220	0.6000	6.90
22	IAELARAII	266	0.5000	5.75
23	VRKVYITDD	87	0.4000	4.60
24	MVRGNLAAA	142	0.3000	3.45
25	LFAKSSMKK	200	0.3000	3.45
26	LLPASISGG	35	0.1000	1.15
27	LPLLAGYDI	157	0.1000	1.15
28	LAGYDIHAS	160	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	VRGNLAAAM	143	3.6000	40.91
2	IVSFDAAGG	176	3.5000	39.77
3	VVMAGDRRS	68	3.4000	38.64
4	INRLAIMVR	136	3.1000	35.23
5	LRRQAPELL	28	2.9600	33.64
6	ISGRDVRKV	82	2.8000	31.82
7	LEHYEKLEG	119	2.8000	31.82
8	LAGYDIHAS	160	2.7000	30.68
9	LLALPLLAG	154	2.4000	27.27
10	MQGLLALPL	151	2.1600	24.55
11	LTFAGKINR	130	2.1000	23.86
12	LAIMVRGNL	139	1.7600	20.00
13	VRGIFPTAV	243	1.7000	19.32
14	IMVRGNLAA	141	1.6000	18.18
15	LRVAVEALY	220	1.6000	18.18
16	LLPASISGG	35	1.5000	17.05
17	MVRGNLAAA	142	1.5000	17.05
18	VMAGDRRST	69	1.3000	14.77
19	LFAKSSMKK	200	1.3000	14.77

20	VEFARLYAV	109	1.2000	13.64
21	VALKYPGGV	60	1.1000	12.50
22	IVALKYPGG	59	1.0000	11.36
23	VAVEFARLY	107	0.9000	10.23
24	LARAIIESR	269	0.9000	10.23
25	IAELARAII	266	0.8000	9.09
26	FTDFLRRQA	24	0.7000	7.95
27	LKYPGGVVM	62	0.7000	7.95
28	FAGKINRLA	132	0.6000	6.82
29	LPLLAGYDI	157	0.6000	6.82

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	VRGNLAAAM	143	2.6000	29.55
2	IVSFDAAGG	176	2.5000	28.41
3	VVMAGDRRS	68	2.4000	27.27
4	INRLAIMVR	136	2.1000	23.86
5	LRRQAPELL	28	1.9600	22.27
6	ISGRDVRKV	82	1.8000	20.45
7	LEHYEKLEG	119	1.8000	20.45
8	FTDFLRRQA	24	1.7000	19.32
9	LAGYDIHAS	160	1.7000	19.32
10	FAGKINRLA	132	1.6000	18.18
11	LLALPLLAG	154	1.4000	15.91
12	FLRRQAPEL	27	1.3600	15.45
13	MQGLLALPL	151	1.1600	13.18
14	LTFAGKINR	130	1.1000	12.50
15	WPLPDRLSI	2	1.0000	11.36
16	FARLYAVEL	111	0.9600	10.91
17	LAIMVRGNL	139	0.7600	8.64
18	VRGIFPTAV	243	0.7000	7.95
19	IMVRGNLAA	141	0.6000	6.82

20	LRVAVEALY	220	0.6000	6.82
21	LLPASISGG	35	0.5000	5.68
22	MVRGNLAAA	142	0.5000	5.68
23	VMAGDRRST	69	0.3000	3.41
24	LFAKSSMKK	200	0.3000	3.41
25	VEFARLYAV	109	0.2000	2.27
26	VALKYPGGV	60	0.1000	1.14
27	VAVEFARLY	107	-0.1000	0

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	IVSFDAAGG	176	3.4000	37.78
2	VRGNLAAAM	143	3.2000	35.56
3	LRRQAPELL	28	3.0000	33.33
4	VVMAGDRRS	68	3.0000	33.33
5	LEHYEKLEG	119	2.7000	30.00
6	LLALPLLAG	154	2.3000	25.56
7	LAGYDIHAS	160	2.3000	25.56
8	MQGLLALPL	151	2.2000	24.44
9	ISGRDVRKV	82	2.1000	23.33
10	VRKVYITDD	87	2.1000	23.33
11	LYSQVTDGD	209	2.0000	22.22
12	LAIMVRGNL	139	1.8000	20.00
13	IFPTAVIID	246	1.7000	18.89
14	INRLAIMVR	136	1.6000	17.78
15	IMVRGNLAA	141	1.6000	17.78
16	VMAGDRRST	69	1.5000	16.67
17	MVRGNLAAA	142	1.5000	16.67
18	LLPASISGG	35	1.4000	15.56
19	LRVAVEALY	220	1.4000	15.56
20	VRGIFPTAV	243	1.0000	11.11
21	IVALKYPGG	59	0.9000	10.00

22	FTDFLRRQA	24	0.7000	7.78
23	VAVEFARLY	107	0.7000	7.78
24	MKKLYSQVT	206	0.7000	7.78
25	LTFAGKINR	130	0.6000	6.67
26	FAGKINRLA	132	0.6000	6.67
27	VEFARLYAV	109	0.5000	5.56
28	LFAKSSMKK	200	0.5000	5.56
29	FLRRQAPEL	27	0.4000	4.44

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	INRLAIMVR	136	4.1000	47.13
2	LLALPLLAG	154	3.2000	36.78
3	MQGLLALPL	151	2.9600	34.02
4	VRGNLAAAM	143	2.5000	28.74
5	LTFAGKINR	130	2.4000	27.59
6	IVSFDAAGG	176	2.1000	24.14
7	LAIMVRGNL	139	2.0600	23.68
8	WPLPDRLSI	2	1.9000	21.84
9	LEHYEKLEG	119	1.8000	20.69
10	VRGIFPTAV	243	1.8000	20.69
11	FARLYAVEL	111	1.1600	13.33
12	IVALKYPGG	59	1.1500	13.22
13	YQAVGSGSL	192	1.0600	12.18
14	FPTAVIIDA	247	1.0000	11.49
15	FLRRQAPEL	27	0.9100	10.46
16	YPGGVVMAG	64	0.9000	10.34
17	IFPTAVIID	246	0.9000	10.34
18	VVMAGDRRS	68	0.8000	9.20
19	IMVRGNLAA	141	0.8000	9.20
20	LRRQAPELL	28	0.6600	7.59
21	LRVAVEALY	220	0.6000	6.90

22	IAELARAII	266	0.5000	5.75
23	VRKVYITDD	87	0.4000	4.60
24	MVRGNLAAA	142	0.3000	3.45
25	LFAKSSMKK	200	0.3000	3.45
26	LLPASISGG	35	0.1000	1.15
27	LPLLAGYDI	157	0.1000	1.15
28	LAGYDIHAS	160	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	INRLAIMVR	136	1.0000	14.71
2	LAIMVRGNL	139	1.0000	14.71
3	VRGNLAAAM	143	1.0000	14.71
4	IVSFDAAGG	176	0.7000	10.29
5	MVRGNLAAA	142	0.3000	4.41
6	VVMAGDRRS	68	0.2000	2.94
7	MQGLLALPL	151	0.2000	2.94
8	FARLYAVEL	111	-0.3000	0
9	VRGIFPTAV	243	-0.3000	0
10	IAELARAII	266	-0.4000	0
11	FTDFLRRQA	24	-0.5000	0
12	FPTAVIIDA	247	-0.6000	0
13	LTFAGKINR	130	-0.7000	0
14	LRVAVEALY	220	-0.7000	0
15	WPLPDRLSI	2	-0.8000	0
16	WNIEEEGYQ	185	-0.8000	0
17	IMVRGNLAA	141	-1.0000	0
18	LAGYDIHAS	160	-1.0000	0
19	YTATGIAGT	96	-1.1000	0
20	FLRRQAPEL	27	-1.2000	0
21	VALKYPGGV	60	-1.2000	0
22	LLPASISGG	35	-1.3000	0

23	MKKLYSQVT	206	-1.3000	0
24	LRRQAPELL	28	-1.4000	0
25	IVALKYPGG	59	-1.4000	0
26	LEHYEKLEG	119	-1.4000	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	INRLAIMVR	136	3.6000	43.37
2	MQGLLALPL	151	3.0000	36.14
3	LLALPLLAG	154	2.8000	33.73
4	LAIMVRGNL	139	2.1000	25.30
5	VRGNLAAAM	143	2.0000	24.10
6	LTFAGKINR	130	1.9000	22.89
7	IMVRGNLAA	141	1.8000	21.69
8	VRGIFPTAV	243	1.8000	21.69
9	IVSFDAAGG	176	1.7000	20.48
10	VVMAGDRRS	68	1.4000	16.87
11	LEHYEKLEG	119	1.4000	16.87
12	MVRGNLAAA	142	1.3000	15.66
13	LFAKSSMKK	200	1.2000	14.46
14	IFPTAVIID	246	0.8000	9.64
15	IVALKYPGG	59	0.7500	9.04
16	LRRQAPELL	28	0.7000	8.43
17	LAGYDIHAS	160	0.7000	8.43
18	IAELARAII	266	0.6000	7.23
19	VRKVYITDD	87	0.3000	3.61
20	LRVAVEALY	220	0.3000	3.61
21	LPLLAGYDI	157	0.2000	2.41
22	INSLSGTPA	10	0.1000	1.20
23	VALKYPGGV	60	-0.1000	0
24	MKKLYSQVT	206	-0.2000	0
25	LLPASISGG	35	-0.3000	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	LLALPLLAG	154	3.1000	34.83
2	MQGLLALPL	151	3.0000	33.71
3	INRLAIMVR	136	2.6000	29.21
4	IFPTAVIID	246	2.5000	28.09
5	LAIMVRGNL	139	2.1000	23.60
6	VRGNLAAAM	143	2.1000	23.60
7	VRKVYITDD	87	2.0000	22.47
8	IVSFDAAGG	176	2.0000	22.47
9	LEHYEKLEG	119	1.7000	19.10
10	WPLPDRLSI	2	1.2000	13.48
11	FARLYAVEL	111	1.2000	13.48
12	YQAVGSGSL	192	1.1000	12.36
13	VRGIFPTAV	243	1.1000	12.36
14	IVALKYPGG	59	1.0500	11.80
15	FPTAVIIDA	247	1.0000	11.24
16	FLRRQAPEL	27	0.9500	10.67
17	LTFAGKINR	130	0.9000	10.11
18	YPGGVVMAG	64	0.8000	8.99
19	IMVRGNLAA	141	0.8000	8.99
20	LRRQAPELL	28	0.7000	7.87
21	VVMAGDRRS	68	0.4000	4.49
22	LRVAVEALY	220	0.4000	4.49
23	MVRGNLAAA	142	0.3000	3.37
24	WNIEEEGYQ	185	0.1000	1.12
25	YEKLEGVPL	122	-0.1000	0
26	YTATGIAGT	96	-0.2000	0
27	IAELARAII	266	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVMAGDRRS	68	3.0000	35.71
2	LAGYDIHAS	160	2.3000	27.38
3	VRGNLAAAM	143	2.1000	25.00
4	IVSFDAAGG	176	2.1000	25.00
5	LRRQAPELL	28	2.0000	23.81
6	ISGRDVRKV	82	1.8000	21.43
7	INRLAIMVR	136	1.6000	19.05
8	IMVRGNLAA	141	1.6000	19.05
9	MVRGNLAAA	142	1.5000	17.86
10	LEHYEKLEG	119	1.4000	16.67
11	MQGLLALPL	151	1.2000	14.29
12	LFAKSSMKK	200	1.2000	14.29
13	LLALPLLAG	154	1.0000	11.90
14	LAIMVRGNL	139	0.8000	9.52
15	FTDFLRRQA	24	0.7000	8.33
16	VRGIFPTAV	243	0.7000	8.33
17	VMAGDRRST	69	0.6000	7.14
18	LTFAGKINR	130	0.6000	7.14
19	FAGKINRLA	132	0.6000	7.14
20	IHASDPQSA	165	0.3000	3.57
21	LRVAVEALY	220	0.3000	3.57
22	VEFARLYAV	109	0.2000	2.38
23	LLPASISGG	35	0.1000	1.19
24	VALKYPGGV	60	0.1000	1.19
25	IAELARAII	266	-0.1000	0
26	INSLSGTPA	10	-0.2000	0
27	MKKLYSQVT	206	-0.2000	0
28	LPLLAGYDI	157	-0.3000	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	VVMAGDRRS	68	2.0000	23.81
2	FTDFLRRQA	24	1.7000	20.24
3	FAGKINRLA	132	1.6000	19.05
4	LAGYDIHAS	160	1.3000	15.48
5	VRGNLAAAM	143	1.1000	13.10
6	IVSFDAAGG	176	1.1000	13.10
7	LRRQAPELL	28	1.0000	11.90
8	ISGRDVRKV	82	0.8000	9.52
9	INRLAIMVR	136	0.6000	7.14
10	IMVRGNLAA	141	0.6000	7.14
11	YDIHASDPQ	163	0.6000	7.14
12	MVRGNLAAA	142	0.5000	5.95
13	FLRRQAPEL	27	0.4000	4.76
14	LEHYEKLEG	119	0.4000	4.76
15	MQGLLALPL	151	0.2000	2.38
16	LFAKSSMKK	200	0.2000	2.38
17	WPLPDRLSI	2	0.1000	1.19
18	LAIMVRGNL	139	-0.2000	0
19	VRGIFPTAV	243	-0.3000	0
20	FPTAVIIDA	247	-0.3000	0
21	VMAGDRRST	69	-0.4000	0
22	LTFAGKINR	130	-0.4000	0
23	IHASDPQSA	165	-0.7000	0
24	LRVAVEALY	220	-0.7000	0
25	VEFARLYAV	109	-0.8000	0
26	LLPASISGG	35	-0.9000	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	VRGNLAAAM	143	3.6000	40.91
2	IVSFDAAGG	176	3.5000	39.77
3	VVMAGDRRS	68	3.4000	38.64
4	INRLAIMVR	136	3.1000	35.23
5	LRRQAPELL	28	2.9600	33.64
6	ISGRDVRKV	82	2.8000	31.82
7	LEHYEKLEG	119	2.8000	31.82
8	LAGYDIHAS	160	2.7000	30.68
9	LLALPLLAG	154	2.4000	27.27
10	MQGLLALPL	151	2.1600	24.55
11	LTFAGKINR	130	2.1000	23.86
12	LAIMVRGNL	139	1.7600	20.00
13	VRGIFPTAV	243	1.7000	19.32
14	IMVRGNLAA	141	1.6000	18.18
15	LRVAVEALY	220	1.6000	18.18
16	LLPASISGG	35	1.5000	17.05
17	MVRGNLAAA	142	1.5000	17.05
18	VMAGDRRST	69	1.3000	14.77
19	LFAKSSMKK	200	1.3000	14.77
20	VEFARLYAV	109	1.2000	13.64
21	VALKYPGGV	60	1.1000	12.50
22	IVALKYPGG	59	1.0000	11.36
23	VAVEFARLY	107	0.9000	10.23
24	LARAIIESR	269	0.9000	10.23
25	IAELARAII	266	0.8000	9.09
26	FTDFLRRQA	24	0.7000	7.95
27	LKYPGGVVM	62	0.7000	7.95
28	FAGKINRLA	132	0.6000	6.82
29	LPLLAGYDI	157	0.6000	6.82

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	VRGNLAAAM	143	3.6000	40.91
2	IVSFDAAGG	176	3.5000	39.77
3	VVMAGDRRS	68	3.4000	38.64
4	INRLAIMVR	136	3.1000	35.23
5	LRRQAPELL	28	2.9600	33.64
6	ISGRDVRKV	82	2.8000	31.82
7	LEHYEKLEG	119	2.8000	31.82
8	LAGYDIHAS	160	2.7000	30.68
9	LLALPLLAG	154	2.4000	27.27
10	MQGLLALPL	151	2.1600	24.55
11	LTFAGKINR	130	2.1000	23.86
12	LAIMVRGNL	139	1.7600	20.00
13	VRGIFPTAV	243	1.7000	19.32
14	IMVRGNLAA	141	1.6000	18.18
15	LRVAVEALY	220	1.6000	18.18
16	LLPASISGG	35	1.5000	17.05
17	MVRGNLAAA	142	1.5000	17.05
18	VMAGDRRST	69	1.3000	14.77
19	LFAKSSMKK	200	1.3000	14.77
20	VEFARLYAV	109	1.2000	13.64
21	VALKYPGGV	60	1.1000	12.50
22	IVALKYPGG	59	1.0000	11.36
23	VAVEFARLY	107	0.9000	10.23
24	LARAIIESR	269	0.9000	10.23
25	IAELARAII	266	0.8000	9.09
26	FTDFLRRQA	24	0.7000	7.95
27	LKYPGGVVM	62	0.7000	7.95
28	FAGKINRLA	132	0.6000	6.82
29	LPLLAGYDI	157	0.6000	6.82

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	IMVRGNLAA	141	4.4000	44.90
2	MQGLLALPL	151	4.3000	43.88
3	LAIMVRGNL	139	4.0000	40.82
4	IVSFDAAGG	176	3.9000	39.80
5	LEHYEKLEG	119	3.6000	36.73
6	VRGIFPTAV	243	3.3000	33.67
7	LAGYDIHAS	160	3.0500	31.12
8	MVRGNLAAA	142	3.0000	30.61
9	LPLLAGYDI	157	2.9000	29.59
10	WPLPDRLSI	2	2.8000	28.57
11	LLALPLLAG	154	2.8000	28.57
12	LVRGIFPTA	242	2.8000	28.57
13	INRLAIMVR	136	2.7500	28.06
14	IVALKYPGG	59	2.5000	25.51
15	LKYPGGVVM	62	2.4800	25.31
16	VYITDDYTA	90	2.4000	24.49
17	LSSFTDFLR	21	2.3000	23.47
18	VVMAGDRRS	68	2.3000	23.47
19	VRGNLAAAM	143	2.2800	23.27
20	INSLSGTPA	10	2.2000	22.45
21	VEFARLYAV	109	2.1000	21.43
22	LLAGYDIHA	159	2.1000	21.43
23	VIIDADGAV	251	2.1000	21.43
24	FLRRQAPEL	27	1.7000	17.35
25	LRRQAPELL	28	1.7000	17.35
26	MKKLYSQVT	206	1.7000	17.35
27	YQAVGSGSL	192	1.5000	15.31
28	VMAGDRRST	69	1.4000	14.29
29	LSINSLSGT	8	1.3000	13.27

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	WPLPDRLSI	2	3.8000	38.78
2	IMVRGNLAA	141	3.4000	34.69
3	MQGLLALPL	151	3.3000	33.67
4	LAIMVRGNL	139	3.0000	30.61
5	IVSFDAAGG	176	2.9000	29.59
6	FLRRQAPEL	27	2.7000	27.55
7	LEHYEKLEG	119	2.6000	26.53
8	YQAVGSGSL	192	2.5000	25.51
9	VRGIFPTAV	243	2.3000	23.47
10	LAGYDIHAS	160	2.0500	20.92
11	FARLYAVEL	111	2.0000	20.41
12	MVRGNLAAA	142	2.0000	20.41
13	YEKLEGVPL	122	1.9000	19.39
14	LPLLAGYDI	157	1.9000	19.39
15	LLALPLLAG	154	1.8000	18.37
16	LVRGIFPTA	242	1.8000	18.37
17	INRLAIMVR	136	1.7500	17.86
18	FTDFLRRQA	24	1.6000	16.33
19	IVALKYPGG	59	1.5000	15.31
20	LKYPGGVVM	62	1.4800	15.10
21	VYITDDYTA	90	1.4000	14.29
22	LSSFTDFLR	21	1.3000	13.27
23	VVMAGDRRS	68	1.3000	13.27
24	VRGNLAAAM	143	1.2800	13.06
25	INSLSGTPA	10	1.2000	12.24
26	YITDDYTAT	91	1.1000	11.22
27	VEFARLYAV	109	1.1000	11.22
28	LLAGYDIHA	159	1.1000	11.22
29	VIIDADGAV	251	1.1000	11.22

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	IMVRGNLAA	141	4.4000	44.90
2	MQGLLALPL	151	4.3000	43.88
3	LAIMVRGNL	139	4.0000	40.82
4	IVSFDAAGG	176	3.9000	39.80
5	LEHYEKLEG	119	3.6000	36.73
6	VRGIFPTAV	243	3.3000	33.67
7	LAGYDIHAS	160	3.0500	31.12
8	MVRGNLAAA	142	3.0000	30.61
9	LPLLAGYDI	157	2.9000	29.59
10	WPLPDRLSI	2	2.8000	28.57
11	LLALPLLAG	154	2.8000	28.57
12	LVRGIFPTA	242	2.8000	28.57
13	INRLAIMVR	136	2.7500	28.06
14	IVALKYPGG	59	2.5000	25.51
15	LKYPGGVVM	62	2.4800	25.31
16	VYITDDYTA	90	2.4000	24.49
17	LSSFTDFLR	21	2.3000	23.47
18	VVMAGDRRS	68	2.3000	23.47
19	VRGNLAAAM	143	2.2800	23.27
20	INSLSGTPA	10	2.2000	22.45
21	VEFARLYAV	109	2.1000	21.43
22	LLAGYDIHA	159	2.1000	21.43
23	VIIDADGAV	251	2.1000	21.43
24	FLRRQAPEL	27	1.7000	17.35
25	LRRQAPELL	28	1.7000	17.35
26	MKKLYSQVT	206	1.7000	17.35
27	YQAVGSGSL	192	1.5000	15.31
28	VMAGDRRST	69	1.4000	14.29
29	LSINSLSGT	8	1.3000	13.27

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	YQAVGSGSL	192	3.7000	37.76
2	VRGIFPTAV	243	3.0000	30.61
3	MQGLLALPL	151	2.9000	29.59
4	LAIMVRGNL	139	2.8000	28.57
5	INRLAIMVR	136	2.6000	26.53
6	VVMAGDRRS	68	2.5000	25.51
7	FARLYAVEL	111	2.3000	23.47
8	LPLLAGYDI	157	2.2000	22.45
9	LTFAGKINR	130	2.0000	20.41
10	LRRQAPELL	28	1.8000	18.37
11	VPLTFAGKI	128	1.6000	16.33
12	YEKLEGVPL	122	1.4000	14.29
13	VGSGSLFAK	195	1.3000	13.27
14	IVSFDAAGG	176	1.1000	11.22
15	LRVAVEALY	220	1.0000	10.20
16	VYITDDYTA	90	0.9000	9.18
17	VAVEFARLY	107	0.8000	8.16
18	FLRRQAPEL	27	0.7000	7.14
19	LFAKSSMKK	200	0.7000	7.14
20	MKKLYSQVT	206	0.7000	7.14
21	INSLSGTPA	10	0.6000	6.12
22	LLALPLLAG	154	0.6000	6.12
23	IVALKYPGG	59	0.5000	5.10
24	LYAVELEHY	114	0.4000	4.08
25	LSSFTDFLR	21	0.3000	3.06
26	WNIEEEGYQ	185	0.3000	3.06
27	LSGTPAVDL	13	0.2000	2.04
28	VRGNLAAAM	143	0.2000	2.04
29	IHASDPQSA	165	0.2000	2.04

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YQAVGSGSL	192	3.7000	37.76
2	VRGIFPTAV	243	3.0000	30.61
3	MQGLLALPL	151	2.9000	29.59
4	LAIMVRGNL	139	2.8000	28.57
5	INRLAIMVR	136	2.6000	26.53
6	VVMAGDRRS	68	2.5000	25.51
7	FARLYAVEL	111	2.3000	23.47
8	LPLLAGYDI	157	2.2000	22.45
9	LTFAGKINR	130	2.0000	20.41
10	LRRQAPELL	28	1.8000	18.37
11	VPLTFAGKI	128	1.6000	16.33
12	YEKLEGVPL	122	1.4000	14.29
13	VGSGSLFAK	195	1.3000	13.27
14	IVSFDAAGG	176	1.1000	11.22
15	LRVAVEALY	220	1.0000	10.20
16	VYITDDYTA	90	0.9000	9.18
17	VAVEFARLY	107	0.8000	8.16
18	FLRRQAPEL	27	0.7000	7.14
19	LFAKSSMKK	200	0.7000	7.14
20	MKKLYSQVT	206	0.7000	7.14
21	INSLSGTPA	10	0.6000	6.12
22	LLALPLLAG	154	0.6000	6.12
23	IVALKYPGG	59	0.5000	5.10
24	LYAVELEHY	114	0.4000	4.08
25	LSSFTDFLR	21	0.3000	3.06
26	WNIEEEGYQ	185	0.3000	3.06
27	LSGTPAVDL	13	0.2000	2.04
28	VRGNLAAAM	143	0.2000	2.04
29	IHASDPQSA	165	0.2000	2.04