MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sat Jan 30 23:54:55 2010
Length of input sequence	304 amino acids
Number of nanomers from input sequence	296
Number of nanomers with obligatory P1 anchor residue	74
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	30

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	IVLMTALAT	271	3.0000	50.00
2	YLVLGGMGV	223	2.4900	41.50
3	FVWMITVAF	213	2.0000	33.33
4	IRRIDPWST	192	1.9200	32.00
5	FVYNLITDL	283	1.6300	27.17
6	VSLLLSVAL	203	1.2000	20.00
7	LIGLVNIVL	265	1.2000	20.00
8	FLIGLVNIV	264	1.1000	18.33
9	WMITVAFLY	215	1.0000	16.67

10	WQRAATRQS	45	0.4900	8.17
11	FISGASAPV	84	0.3000	5.00
12	LLLSVALFF	205	0.2000	3.33
13	VWMITVAFL	214	0.2000	3.33
14	LVNIVLMTA	268	0.1900	3.17
15	VNIVLMTAL	269	0.0400	0.67
16	VLGGMGVWA	225	-0.1000	0
17	WSTLKVSLL	198	-0.2000	0
18	LNNASGSSA	243	-0.2000	0
19	FGGAFLIGL	260	-0.2000	0
20	FLYLVLGGM	221	-0.3200	0
21	LFFVWMITV	211	-0.3500	0
22	VALFFVWMI	209	-0.4000	0
23	WAKLNSNVG	232	-0.4000	0
24	LMTALATIG	273	-0.6100	0
25	IGLVNIVLM	266	-0.6700	0
26	MTALATIGA	274	-0.7000	0
27	LVSSGTIFG	253	-0.8000	0
28	IGGIEVTLA	292	-0.8100	0
29	VLMTALATI	272	-0.9000	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6

Rank	Sequence	At Position	Score	% of Highest Score
1	IVLMTALAT	271	4.0000	66.67
2	IRRIDPWST	192	2.9200	48.67
3	VSLLLSVAL	203	2.2000	36.67
4	LIGLVNIVL	265	2.2000	36.67
5	FVWMITVAF	213	2.0000	33.33
6	FVYNLITDL	283	1.6300	27.17
7	YLVLGGMGV	223	1.4900	24.83
8	LLLSVALFF	205	1.2000	20.00
9	VWMITVAFL	214	1.2000	20.00

10	LVNIVLMTA	268	1.1900	19.83
11	FLIGLVNIV	264	1.1000	18.33
12	VNIVLMTAL	269	1.0400	17.33
13	VLGGMGVWA	225	0.9000	15.00
14	LNNASGSSA	243	0.8000	13.33
15	LFFVWMITV	211	0.6500	10.83
16	VALFFVWMI	209	0.6000	10.00
17	LMTALATIG	273	0.3900	6.50
18	IGLVNIVLM	266	0.3300	5.50
19	FISGASAPV	84	0.3000	5.00
20	MTALATIGA	274	0.3000	5.00
21	LVSSGTIFG	253	0.2000	3.33
22	IGGIEVTLA	292	0.1900	3.17
23	VLMTALATI	272	0.1000	1.67
24	LATIGAFVY	277	-0.1000	0
25	FGGAFLIGL	260	-0.2000	0
26	VYNLITDLI	284	-0.2000	0
27	ISGASAPVT	85	-0.2300	0
28	LLSVALFFV	206	-0.2500	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	LITDLIGGI	287	4.8000	50.53
2	LVSSGTIFG	253	4.6000	48.42
3	LVNIVLMTA	268	4.4000	46.32
4	LLLSVALFF	205	3.8000	40.00
5	VQLSARRSR	175	3.5000	36.84
6	VRASMQIRR	186	3.5000	36.84
7	IGLVNIVLM	266	3.5000	36.84
8	FLIGLVNIV	264	3.4100	35.89
9	LKVSLLLSV	201	3.0000	31.58
10	FVWMITVAF	213	3.0000	31.58

11	VWMITVAFL	214	2.9600	31.16
12	IRRIDPWST	192	2.8000	29.47
13	LLNNASGSS	242	2.8000	29.47
14	IVLMTALAT	271	2.8000	29.47
15	FVYNLITDL	283	2.6600	28.00
16	MGVWAKLNS	229	2.6000	27.37
17	IGGIEVTLA	292	2.3000	24.21
18	LLSVALFFV	206	2.2000	23.16
19	FLYLVLGGM	221	2.2000	23.16
20	VLMTALATI	272	2.2000	23.16
21	VYNLITDLI	284	2.2000	23.16
22	VSSGTIFGG	254	2.0000	21.05
23	WQRAATRQS	45	1.9000	20.00
24	LVLGGMGVW	224	1.8000	18.95
25	LYLVLGGMG	222	1.7000	17.89
26	LNRFISGAS	81	1.6000	16.84
27	VAFLYLVLG	219	1.6000	16.84
28	LFFVWMITV	211	1.4000	14.74
29	WMITVAFLY	215	1.4000	14.74
30	LMTALATIG	273	1.4000	14.74

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	FLIGLVNIV	264	3.4100	37.47
2	LVNIVLMTA	268	3.4000	37.36
3	LITDLIGGI	287	2.9000	31.87
4	FVYNLITDL	283	2.7000	29.67
5	WQRAATRQS	45	2.5000	27.47
6	LVSSGTIFG	253	2.2000	24.18
7	FVWMITVAF	213	2.1000	23.08
8	FLYLVLGGM	221	1.7000	18.68
9	LLNNASGSS	242	1.4000	15.38

10	IGGIEVTLA	292	1.3000	14.29
11	YLVLGGMGV	223	1.2000	13.19
12	MGVWAKLNS	229	1.2000	13.19
13	IRRIDPWST	192	1.1000	12.09
14	WMITVAFLY	215	1.1000	12.09
15	IVLMTALAT	271	1.1000	12.09
16	FISGASAPV	84	1.0000	10.99
17	VQLSARRSR	175	1.0000	10.99
18	VRASMQIRR	186	1.0000	10.99
19	LKVSLLLSV	201	1.0000	10.99
20	VWMITVAFL	214	1.0000	10.99
21	IGLVNIVLM	266	1.0000	10.99
22	LLLSVALFF	205	0.9000	9.89
23	FFVWMITVA	212	0.9000	9.89
24	LVLGGMGVW	224	0.8000	8.79
25	FGGAFLIGL	260	0.3000	3.30
26	VLMTALATI	272	0.3000	3.30
27	VYNLITDLI	284	0.3000	3.30
28	LNRFISGAS	81	0.2000	2.20
29	LLSVALFFV	206	0.2000	2.20
30	VLGGMGVWA	225	0.2000	2.20

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	LVNIVLMTA	268	4.1000	46.59
2	FLIGLVNIV	264	3.1000	35.23
3	LVSSGTIFG	253	2.8800	32.73
4	MGVWAKLNS	229	2.7000	30.68
5	IVLMTALAT	271	2.6000	29.55
6	LKVSLLLSV	201	2.5000	28.41
7	LITDLIGGI	287	2.5000	28.41
8	LLLSVALFF	205	2.4000	27.27

9	IGGIEVTLA	292	2.3000	26.14
10	VWMITVAFL	214	2.0000	22.73
11	IGLVNIVLM	266	1.8800	21.36
12	VQLSARRSR	175	1.7000	19.32
13	FVYNLITDL	283	1.7000	19.32
14	VRASMQIRR	186	1.6800	19.09
15	VYNLITDLI	284	1.6000	18.18
16	IRRIDPWST	192	1.3000	14.77
17	VLMTALATI	272	1.3000	14.77
18	WQRAATRQS	45	1.2000	13.64
19	MQIRRIDPW	190	1.1000	12.50
20	VLGGMGVWA	225	1.0800	12.27
21	LLNNASGSS	242	1.0000	11.36
22	FVWMITVAF	213	0.9800	11.14
23	MTALATIGA	274	0.8800	10.00
24	LVLGGMGVW	224	0.4000	4.55
25	LNNASGSSA	243	0.4000	4.55
26	VNIVLMTAL	269	0.3000	3.41
27	LGGMGVWAK	226	0.2000	2.27
28	LGCGDGSPA	110	0.1000	1.14
29	LFFVWMITV	211	0.0800	0.91
30	VAFLYLVLG	219	0.0800	0.91

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	LVNIVLMTA	268	4.1000	46.59
2	FLIGLVNIV	264	3.1000	35.23
3	LVSSGTIFG	253	2.8800	32.73
4	MGVWAKLNS	229	2.7000	30.68
5	IVLMTALAT	271	2.6000	29.55
6	LKVSLLLSV	201	2.5000	28.41
7	LITDLIGGI	287	2.5000	28.41

8	LLLSVALFF	205	2.4000	27.27
9	IGGIEVTLA	292	2.3000	26.14
10	VWMITVAFL	214	2.0000	22.73
11	IGLVNIVLM	266	1.8800	21.36
12	VQLSARRSR	175	1.7000	19.32
13	FVYNLITDL	283	1.7000	19.32
14	VRASMQIRR	186	1.6800	19.09
15	VYNLITDLI	284	1.6000	18.18
16	IRRIDPWST	192	1.3000	14.77
17	VLMTALATI	272	1.3000	14.77
18	WQRAATRQS	45	1.2000	13.64
19	MQIRRIDPW	190	1.1000	12.50
20	VLGGMGVWA	225	1.0800	12.27
21	LLNNASGSS	242	1.0000	11.36
22	FVWMITVAF	213	0.9800	11.14
23	MTALATIGA	274	0.8800	10.00
24	LVLGGMGVW	224	0.4000	4.55
25	LNNASGSSA	243	0.4000	4.55
26	VNIVLMTAL	269	0.3000	3.41
27	LGGMGVWAK	226	0.2000	2.27
28	LGCGDGSPA	110	0.1000	1.14
29	LFFVWMITV	211	0.0800	0.91
30	VAFLYLVLG	219	0.0800	0.91

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	LVNIVLMTA	268	4.1000	46.59
2	FLIGLVNIV	264	3.1000	35.23
3	LVSSGTIFG	253	2.8800	32.73
4	MGVWAKLNS	229	2.7000	30.68
5	IVLMTALAT	271	2.6000	29.55
6	LKVSLLLSV	201	2.5000	28.41

7	LITDLIGGI	287	2.5000	28.41
8	LLLSVALFF	205	2.4000	27.27
9	IGGIEVTLA	292	2.3000	26.14
10	VWMITVAFL	214	2.0000	22.73
11	IGLVNIVLM	266	1.8800	21.36
12	VQLSARRSR	175	1.7000	19.32
13	FVYNLITDL	283	1.7000	19.32
14	VRASMQIRR	186	1.6800	19.09
15	VYNLITDLI	284	1.6000	18.18
16	IRRIDPWST	192	1.3000	14.77
17	VLMTALATI	272	1.3000	14.77
18	WQRAATRQS	45	1.2000	13.64
19	MQIRRIDPW	190	1.1000	12.50
20	VLGGMGVWA	225	1.0800	12.27
21	LLNNASGSS	242	1.0000	11.36
22	FVWMITVAF	213	0.9800	11.14
23	MTALATIGA	274	0.8800	10.00
24	LVLGGMGVW	224	0.4000	4.55
25	LNNASGSSA	243	0.4000	4.55
26	VNIVLMTAL	269	0.3000	3.41
27	LGGMGVWAK	226	0.2000	2.27
28	LGCGDGSPA	110	0.1000	1.14
29	LFFVWMITV	211	0.0800	0.91
30	VAFLYLVLG	219	0.0800	0.91

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	FLIGLVNIV	264	4.4100	46.42
2	FVWMITVAF	213	4.0000	42.11
3	LITDLIGGI	287	3.8000	40.00
4	FVYNLITDL	283	3.6600	38.53
5	LVSSGTIFG	253	3.6000	37.89

6	LVNIVLMTA	268	3.4000	35.79
7	FLYLVLGGM	221	3.2000	33.68
8	WQRAATRQS	45	2.9000	30.53
9	LLLSVALFF	205	2.8000	29.47
10	VQLSARRSR	175	2.5000	26.32
11	VRASMQIRR	186	2.5000	26.32
12	IGLVNIVLM	266	2.5000	26.32
13	WMITVAFLY	215	2.4000	25.26
14	YLVLGGMGV	223	2.2000	23.16
15	FISGASAPV	84	2.0000	21.05
16	LKVSLLLSV	201	2.0000	21.05
17	VWMITVAFL	214	1.9600	20.63
18	IRRIDPWST	192	1.8000	18.95
19	LLNNASGSS	242	1.8000	18.95
20	IVLMTALAT	271	1.8000	18.95
21	MGVWAKLNS	229	1.6000	16.84
22	IGGIEVTLA	292	1.3000	13.68
23	FGGAFLIGL	260	1.2600	13.26
24	LLSVALFFV	206	1.2000	12.63
25	VLMTALATI	272	1.2000	12.63
26	VYNLITDLI	284	1.2000	12.63
27	VSSGTIFGG	254	1.0000	10.53
28	WSTLKVSLL	198	0.9300	9.79
29	FFVWMITVA	212	0.9000	9.47
30	LVLGGMGVW	224	0.8000	8.42

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVNIVLMTA	268	4.1000	46.59
2	FLIGLVNIV	264	3.1000	35.23
3	LVSSGTIFG	253	2.8800	32.73
4	MGVWAKLNS	229	2.7000	30.68

5	IVLMTALAT	271	2.6000	29.55
6	LKVSLLLSV	201	2.5000	28.41
7	LITDLIGGI	287	2.5000	28.41
8	LLLSVALFF	205	2.4000	27.27
9	IGGIEVTLA	292	2.3000	26.14
10	VWMITVAFL	214	2.0000	22.73
11	IGLVNIVLM	266	1.8800	21.36
12	VQLSARRSR	175	1.7000	19.32
13	FVYNLITDL	283	1.7000	19.32
14	VRASMQIRR	186	1.6800	19.09
15	VYNLITDLI	284	1.6000	18.18
16	IRRIDPWST	192	1.3000	14.77
17	VLMTALATI	272	1.3000	14.77
18	WQRAATRQS	45	1.2000	13.64
19	MQIRRIDPW	190	1.1000	12.50
20	VLGGMGVWA	225	1.0800	12.27
21	LLNNASGSS	242	1.0000	11.36
22	FVWMITVAF	213	0.9800	11.14
23	MTALATIGA	274	0.8800	10.00
24	LVLGGMGVW	224	0.4000	4.55
25	LNNASGSSA	243	0.4000	4.55
26	VNIVLMTAL	269	0.3000	3.41
27	LGGMGVWAK	226	0.2000	2.27
28	LGCGDGSPA	110	0.1000	1.14
29	LFFVWMITV	211	0.0800	0.91
30	VAFLYLVLG	219	0.0800	0.91

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	FVWMITVAF	213	3.9800	46.28
2	WQRAATRQS	45	3.3000	38.37
3	LVSSGTIFG	253	3.0800	35.81

4	FVYNLITDL	283	2.6000	30.23
5	IVLMTALAT	271	2.5000	29.07
6	VYNLITDLI	284	2.5000	29.07
7	YASELPDLS	121	2.1000	24.42
8	LVNIVLMTA	268	2.1000	24.42
9	LLNNASGSS	242	1.8000	20.93
10	MTALATIGA	274	1.7800	20.70
11	FLIGLVNIV	264	1.7000	19.77
12	VGDLLNNAS	239	1.6000	18.60
13	LLLSVALFF	205	1.5000	17.44
14	LIGLVNIVL	265	1.4800	17.21
15	WAKLNSNVG	232	1.4000	16.28
16	WMITVAFLY	215	1.3000	15.12
17	IGGIEVTLA	292	1.3000	15.12
18	YNLITDLIG	285	1.2000	13.95
19	VWMITVAFL	214	1.0000	11.63
20	YLVLGGMGV	223	0.9000	10.47
21	VLMTALATI	272	0.7000	8.14
22	VSLLLSVAL	203	0.5800	6.74
23	LKVSLLLSV	201	0.3000	3.49
24	WSTLKVSLL	198	0.2000	2.33
25	IRRIDPWST	192	0.1000	1.16
26	FFVWMITVA	212	-0.1000	0
27	FLYLVLGGM	221	-0.2000	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	WQRAATRQS	45	5.2000	54.17
2	IVLMTALAT	271	3.5000	36.46
3	VALFFVWMI	209	3.3000	34.38
4	LGGMGVWAK	226	3.3000	34.38
5	IRRIDPWST	192	3.1800	33.13

6	IDPWSTLKV	195	2.8000	29.17
7	FVWMITVAF	213	2.8000	29.17
8	LVSSGTIFG	253	2.7000	28.13
9	LVNIVLMTA	268	2.3800	24.79
10	LSARRSRGP	177	2.1000	21.88
11	FFVWMITVA	212	1.9000	19.79
12	MGVWAKLNS	229	1.9000	19.79
13	MTALATIGA	274	1.8000	18.75
14	IGGIEVTLA	292	1.7800	18.54
15	FLIGLVNIV	264	1.6000	16.67
16	LIGLVNIVL	265	1.5000	15.62
17	LNRFISGAS	81	1.4000	14.58
18	VWMITVAFL	214	1.2800	13.33
19	VGDLLNNAS	239	1.2000	12.50
20	LLLSVALFF	205	1.0000	10.42
21	LLNNASGSS	242	0.7000	7.29
22	WMITVAFLY	215	0.6000	6.25
23	MQIRRIDPW	190	0.5000	5.21
24	IGLVNIVLM	266	0.5000	5.21
25	VLMTALATI	272	0.5000	5.21
26	FVYNLITDL	283	0.5000	5.21
27	VSLLLSVAL	203	0.3000	3.12
28	VYNLITDLI	284	0.3000	3.12
29	VWAKLNSNV	231	0.2000	2.08
30	LMTALATIG	273	0.2000	2.08

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	IVLMTALAT	271	4.0000	45.45
2	FVWMITVAF	213	3.7000	42.05
3	LVNIVLMTA	268	3.3000	37.50
4	IGGIEVTLA	292	3.1000	35.23

5	LNRFISGAS	81	3.0000	34.09
6	MTALATIGA	274	2.9800	33.86
7	VGDLLNNAS	239	2.9000	32.95
8	VYNLITDLI	284	2.8000	31.82
9	LIGLVNIVL	265	2.6800	30.45
10	WQRAATRQS	45	2.6000	29.55
11	LVSSGTIFG	253	2.5800	29.32
12	LGGMGVWAK	226	2.4000	27.27
13	VWMITVAFL	214	2.3000	26.14
14	IRRIDPWST	192	2.1000	23.86
15	VALFFVWMI	209	1.9000	21.59
16	VSLLLSVAL	203	1.6000	18.18
17	IGLVNIVLM	266	1.4000	15.91
18	LLNNASGSS	242	1.3000	14.77
19	VNIVLMTAL	269	1.1000	12.50
20	WAKLNSNVG	232	0.7000	7.95
21	LLLSVALFF	205	0.6000	6.82
22	FFVWMITVA	212	0.5500	6.25
23	LMTALATIG	273	0.5000	5.68
24	FVYNLITDL	283	0.5000	5.68
25	IDPWSTLKV	195	0.4500	5.11
26	IGAFVYNLI	280	0.4000	4.55
27	LFFVWMITV	211	0.3800	4.32
28	LNNASGSSA	243	0.3000	3.41
29	WSTLKVSLL	198	0.1000	1.14
30	VLMTALATI	272	0.1000	1.14

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	FVWMITVAF	213	5.6000	59.57
2	IVLMTALAT	271	3.9000	41.49
3	WQRAATRQS	45	3.6000	38.30

4	WAKLNSNVG	232	3.0000	31.91
5	LVSSGTIFG	253	2.8800	30.64
6	LIGLVNIVL	265	2.6800	28.51
7	FVYNLITDL	283	2.5000	26.60
8	YNLITDLIG	285	2.4000	25.53
9	VWMITVAFL	214	2.3000	24.47
10	LVNIVLMTA	268	2.3000	24.47
11	WSTLKVSLL	198	2.1000	22.34
12	IGGIEVTLA	292	2.1000	22.34
13	LNRFISGAS	81	2.0000	21.28
14	IRRIDPWST	192	2.0000	21.28
15	VYNLITDLI	284	2.0000	21.28
16	MTALATIGA	274	1.9800	21.06
17	VGDLLNNAS	239	1.9000	20.21
18	WMITVAFLY	215	1.7500	18.62
19	VSLLLSVAL	203	1.6000	17.02
20	FFVWMITVA	212	1.5500	16.49
21	IGLVNIVLM	266	1.5000	15.96
22	YLVLGGMGV	223	1.3000	13.83
23	FLIGLVNIV	264	1.3000	13.83
24	FLYLVLGGM	221	1.2000	12.77
25	VALFFVWMI	209	1.1000	11.70
26	VNIVLMTAL	269	1.1000	11.70
27	LMTALATIG	273	0.8000	8.51
28	LGGMGVWAK	226	0.7000	7.45
29	LLLSVALFF	205	0.5000	5.32
30	LLNNASGSS	242	0.3000	3.19

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	FVWMITVAF	213	4.7000	53.41
2	WQRAATRQS	45	3.6000	40.91

3	IVLMTALAT	271	3.0000	34.09
4	LVNIVLMTA	268	2.3000	26.14
5	IGGIEVTLA	292	2.1000	23.86
6	LNRFISGAS	81	2.0000	22.73
7	MTALATIGA	274	1.9800	22.50
8	VGDLLNNAS	239	1.9000	21.59
9	VYNLITDLI	284	1.8000	20.45
10	WAKLNSNVG	232	1.7000	19.32
11	LIGLVNIVL	265	1.6800	19.09
12	LVSSGTIFG	253	1.5800	17.95
13	FFVWMITVA	212	1.5500	17.61
14	FVYNLITDL	283	1.5000	17.05
15	LGGMGVWAK	226	1.4000	15.91
16	VWMITVAFL	214	1.3000	14.77
17	IRRIDPWST	192	1.1000	12.50
18	WSTLKVSLL	198	1.1000	12.50
19	YNLITDLIG	285	1.1000	12.50
20	YLVLGGMGV	223	1.0000	11.36
21	FLIGLVNIV	264	1.0000	11.36
22	VALFFVWMI	209	0.9000	10.23
23	WMITVAFLY	215	0.6500	7.39
24	VSLLLSVAL	203	0.6000	6.82
25	IGLVNIVLM	266	0.4000	4.55
26	LLNNASGSS	242	0.3000	3.41
27	FLYLVLGGM	221	0.1000	1.14
28	VNIVLMTAL	269	0.1000	1.14
29	LLLSVALFF	205	-0.4000	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	IVLMTALAT	271	4.9000	52.13
2	FVWMITVAF	213	4.6000	48.94

3	LVSSGTIFG	253	3.8800	41.28
4	LIGLVNIVL	265	3.6800	39.15
5	VWMITVAFL	214	3.3000	35.11
6	LVNIVLMTA	268	3.3000	35.11
7	IGGIEVTLA	292	3.1000	32.98
8	LNRFISGAS	81	3.0000	31.91
9	IRRIDPWST	192	3.0000	31.91
10	VYNLITDLI	284	3.0000	31.91
11	MTALATIGA	274	2.9800	31.70
12	VGDLLNNAS	239	2.9000	30.85
13	WQRAATRQS	45	2.6000	27.66
14	VSLLLSVAL	203	2.6000	27.66
15	IGLVNIVLM	266	2.5000	26.60
16	VALFFVWMI	209	2.1000	22.34
17	VNIVLMTAL	269	2.1000	22.34
18	WAKLNSNVG	232	2.0000	21.28
19	LMTALATIG	273	1.8000	19.15
20	LGGMGVWAK	226	1.7000	18.09
21	LLLSVALFF	205	1.5000	15.96
22	FVYNLITDL	283	1.5000	15.96
23	YNLITDLIG	285	1.4000	14.89
24	LLNNASGSS	242	1.3000	13.83
25	LATIGAFVY	277	1.1500	12.23
26	WSTLKVSLL	198	1.1000	11.70
27	VAFLYLVLG	219	0.9000	9.57
28	MITVAFLYL	216	0.8000	8.51
29	IDPWSTLKV	195	0.7500	7.98
30	WMITVAFLY	215	0.7500	7.98

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	FVWMITVAF	213	5.8800	65.33

2	LVSSGTIFG	253	4.4800	49.78
3	WQRAATRQS	45	3.7000	41.11
4	FVYNLITDL	283	3.5600	39.56
5	LLLSVALFF	205	3.4000	37.78
6	VYNLITDLI	284	3.4000	37.78
7	IVLMTALAT	271	3.2000	35.56
8	WAKLNSNVG	232	2.8000	31.11
9	FLIGLVNIV	264	2.7000	30.00
10	WMITVAFLY	215	2.6000	28.89
11	YNLITDLIG	285	2.6000	28.89
12	YASELPDLS	121	2.5000	27.78
13	LIGLVNIVL	265	2.4400	27.11
14	LLNNASGSS	242	2.2000	24.44
15	LVNIVLMTA	268	2.1000	23.33
16	VGDLLNNAS	239	2.0000	22.22
17	VWMITVAFL	214	1.9600	21.78
18	YLVLGGMGV	223	1.9000	21.11
19	MTALATIGA	274	1.7800	19.78
20	VLMTALATI	272	1.6000	17.78
21	VSLLLSVAL	203	1.5400	17.11
22	LKVSLLLSV	201	1.3000	14.44
23	FLYLVLGGM	221	1.3000	14.44
24	IGGIEVTLA	292	1.3000	14.44
25	WSTLKVSLL	198	1.1600	12.89
26	VRASMQIRR	186	1.0800	12.00
27	FISGASAPV	84	1.0000	11.11
28	IRRIDPWST	192	0.8000	8.89
29	LITDLIGGI	287	0.7000	7.78
30	IGLVNIVLM	266	0.6800	7.56

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	IVLMTALAT	271	4.0000	45.45
2	FVWMITVAF	213	3.7000	42.05
3	LVNIVLMTA	268	3.3000	37.50
4	IGGIEVTLA	292	3.1000	35.23
5	LNRFISGAS	81	3.0000	34.09
6	MTALATIGA	274	2.9800	33.86
7	VGDLLNNAS	239	2.9000	32.95
8	VYNLITDLI	284	2.8000	31.82
9	LIGLVNIVL	265	2.6800	30.45
10	WQRAATRQS	45	2.6000	29.55
11	LVSSGTIFG	253	2.5800	29.32
12	LGGMGVWAK	226	2.4000	27.27
13	VWMITVAFL	214	2.3000	26.14
14	IRRIDPWST	192	2.1000	23.86
15	VALFFVWMI	209	1.9000	21.59
16	VSLLLSVAL	203	1.6000	18.18
17	IGLVNIVLM	266	1.4000	15.91
18	LLNNASGSS	242	1.3000	14.77
19	VNIVLMTAL	269	1.1000	12.50
20	WAKLNSNVG	232	0.7000	7.95
21	LLLSVALFF	205	0.6000	6.82
22	FFVWMITVA	212	0.5500	6.25
23	LMTALATIG	273	0.5000	5.68
24	FVYNLITDL	283	0.5000	5.68
25	IDPWSTLKV	195	0.4500	5.11
26	IGAFVYNLI	280	0.4000	4.55
27	LFFVWMITV	211	0.3800	4.32
28	LNNASGSSA	243	0.3000	3.41
29	WSTLKVSLL	198	0.1000	1.14
30	VLMTALATI	272	0.1000	1.14

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	FVWMITVAF	213	3.9800	46.28
2	WQRAATRQS	45	3.3000	38.37
3	LVSSGTIFG	253	3.0800	35.81
4	FVYNLITDL	283	2.6000	30.23
5	IVLMTALAT	271	2.5000	29.07
6	VYNLITDLI	284	2.5000	29.07
7	YASELPDLS	121	2.1000	24.42
8	LVNIVLMTA	268	2.1000	24.42
9	LLNNASGSS	242	1.8000	20.93
10	MTALATIGA	274	1.7800	20.70
11	FLIGLVNIV	264	1.7000	19.77
12	VGDLLNNAS	239	1.6000	18.60
13	LLLSVALFF	205	1.5000	17.44
14	LIGLVNIVL	265	1.4800	17.21
15	WAKLNSNVG	232	1.4000	16.28
16	WMITVAFLY	215	1.3000	15.12
17	IGGIEVTLA	292	1.3000	15.12
18	YNLITDLIG	285	1.2000	13.95
19	VWMITVAFL	214	1.0000	11.63
20	YLVLGGMGV	223	0.9000	10.47
21	VLMTALATI	272	0.7000	8.14
22	VSLLLSVAL	203	0.5800	6.74
23	LKVSLLLSV	201	0.3000	3.49
24	WSTLKVSLL	198	0.2000	2.33
25	IRRIDPWST	192	0.1000	1.16
26	FFVWMITVA	212	-0.1000	0
27	FLYLVLGGM	221	-0.2000	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	WMITVAFLY	215	7.2000	62.07

2	LLLSVALFF	205	6.8000	58.62
3	MITVAFLYL	216	5.8000	50.00
4	VNIVLMTAL	269	5.7000	49.14
5	FGGAFLIGL	260	5.6000	48.28
6	FVYNLITDL	283	5.6000	48.28
7	LKVSLLLSV	201	5.4000	46.55
8	FVWMITVAF	213	5.3200	45.86
9	VLMTALATI	272	5.3000	45.69
10	VALFFVWMI	209	5.1000	43.97
11	LFFVWMITV	211	5.1000	43.97
12	VWMITVAFL	214	4.9000	42.24
13	FLIGLVNIV	264	4.9000	42.24
14	LIGLVNIVL	265	4.7000	40.52
15	LVSSGTIFG	253	4.5200	38.97
16	VSLLLSVAL	203	4.5000	38.79
17	IGLVNIVLM	266	4.5000	38.79
18	IRRIDPWST	192	4.3000	37.07
19	LLSVALFFV	206	4.3000	37.07
20	IVLMTALAT	271	4.3000	37.07
21	YLVLGGMGV	223	3.9000	33.62
22	LVNIVLMTA	268	3.6000	31.03
23	IGAFVYNLI	280	3.5000	30.17
24	LATIGAFVY	277	3.3000	28.45
25	VRASMQIRR	186	3.2000	27.59
26	FISGASAPV	84	2.8000	24.14
27	WSTLKVSLL	198	2.8000	24.14
28	ITVAFLYLV	217	2.3000	19.83
29	WQRAATRQS	45	2.2200	19.14
30	FLYLVLGGM	221	2.1000	18.10

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	WMITVAFLY	215	7.2000	62.07
2	LLLSVALFF	205	6.8000	58.62
3	MITVAFLYL	216	5.8000	50.00
4	VNIVLMTAL	269	5.7000	49.14
5	FGGAFLIGL	260	5.6000	48.28
6	FVYNLITDL	283	5.6000	48.28
7	LKVSLLLSV	201	5.4000	46.55
8	FVWMITVAF	213	5.3200	45.86
9	VLMTALATI	272	5.3000	45.69
10	VALFFVWMI	209	5.1000	43.97
11	LFFVWMITV	211	5.1000	43.97
12	VWMITVAFL	214	4.9000	42.24
13	FLIGLVNIV	264	4.9000	42.24
14	LIGLVNIVL	265	4.7000	40.52
15	LVSSGTIFG	253	4.5200	38.97
16	VSLLLSVAL	203	4.5000	38.79
17	IGLVNIVLM	266	4.5000	38.79
18	IRRIDPWST	192	4.3000	37.07
19	LLSVALFFV	206	4.3000	37.07
20	IVLMTALAT	271	4.3000	37.07
21	YLVLGGMGV	223	3.9000	33.62
22	LVNIVLMTA	268	3.6000	31.03
23	IGAFVYNLI	280	3.5000	30.17
24	LATIGAFVY	277	3.3000	28.45
25	VRASMQIRR	186	3.2000	27.59
26	FISGASAPV	84	2.8000	24.14
27	WSTLKVSLL	198	2.8000	24.14
28	ITVAFLYLV	217	2.3000	19.83
29	WQRAATRQS	45	2.2200	19.14
30	FLYLVLGGM	221	2.1000	18.10

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	FVWMITVAF	213	3.1000	36.05
2	FLYLVLGGM	221	2.9000	33.72
3	IVLMTALAT	271	2.9000	33.72
4	WQRAATRQS	45	2.8000	32.56
5	MQIRRIDPW	190	2.2000	25.58
6	VWMITVAFL	214	1.8000	20.93
7	LVNIVLMTA	268	1.8000	20.93
8	MGVWAKLNS	229	1.7000	19.77
9	IRRIDPWST	192	1.2000	13.95
10	FVYNLITDL	283	1.2000	13.95
11	LNRFISGAS	81	1.1000	12.79
12	IGLVNIVLM	266	1.1000	12.79
13	FLIGLVNIV	264	1.0000	11.63
14	WMITVAFLY	215	0.8000	9.30
15	YLVLGGMGV	223	0.8000	9.30
16	LLNNASGSS	242	0.6000	6.98
17	LVSSGTIFG	253	0.6000	6.98
18	VLMTALATI	272	0.5000	5.81
19	LVDRGGAHR	20	0.4000	4.65
20	VALFFVWMI	209	0.4000	4.65
21	WSTLKVSLL	198	0.3000	3.49
22	LYLVLGGMG	222	0.3000	3.49
23	LGGMGVWAK	226	0.1000	1.16
24	FGGAFLIGL	260	0.1000	1.16
25	VAFLYLVLG	219	-0.1000	0
26	FISGASAPV	84	-0.2000	0
27	MTALATIGA	274	-0.3000	0
28	YNLITDLIG	285	-0.3000	0
29	VQLSARRSR	175	-0.4000	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	WQRAATRQS	45	2.8000	35.00
2	FVWMITVAF	213	2.2000	27.50
3	IVLMTALAT	271	2.0000	25.00
4	FLYLVLGGM	221	1.8000	22.50
5	LVNIVLMTA	268	1.8000	22.50
6	MGVWAKLNS	229	1.7000	21.25
7	MQIRRIDPW	190	1.3000	16.25
8	LNRFISGAS	81	1.1000	13.75
9	VWMITVAFL	214	0.8000	10.00
10	LGGMGVWAK	226	0.8000	10.00
11	FLIGLVNIV	264	0.7000	8.75
12	LLNNASGSS	242	0.6000	7.50
13	YLVLGGMGV	223	0.5000	6.25
14	LVDRGGAHR	20	0.4000	5.00
15	IRRIDPWST	192	0.3000	3.75
16	VLMTALATI	272	0.3000	3.75
17	VALFFVWMI	209	0.2000	2.50
18	FVYNLITDL	283	0.2000	2.50
19	WMITVAFLY	215	-0.3000	0
20	MTALATIGA	274	-0.3000	0
21	VQLSARRSR	175	-0.4000	0
22	FFVWMITVA	212	-0.4000	0
23	FISGASAPV	84	-0.5000	0
24	WSTLKVSLL	198	-0.7000	0
25	LVSSGTIFG	253	-0.7000	0
26	VYNLITDLI	284	-0.8000	0
27	LLSVALFFV	206	-0.9000	0
28	FGGAFLIGL	260	-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	IVLMTALAT	271	3.0000	37.50
2	LVNIVLMTA	268	2.8000	35.00
3	MGVWAKLNS	229	2.7000	33.75
4	MQIRRIDPW	190	2.3000	28.75
5	LNRFISGAS	81	2.1000	26.25
6	WQRAATRQS	45	1.8000	22.50
7	VWMITVAFL	214	1.8000	22.50
8	LGGMGVWAK	226	1.8000	22.50
9	LLNNASGSS	242	1.6000	20.00
10	LVDRGGAHR	20	1.4000	17.50
11	IRRIDPWST	192	1.3000	16.25
12	VLMTALATI	272	1.3000	16.25
13	VALFFVWMI	209	1.2000	15.00
14	FVWMITVAF	213	1.2000	15.00
15	IGLVNIVLM	266	1.0000	12.50
16	FLYLVLGGM	221	0.8000	10.00
17	MTALATIGA	274	0.7000	8.75
18	VQLSARRSR	175	0.6000	7.50
19	LVSSGTIFG	253	0.3000	3.75
20	VYNLITDLI	284	0.2000	2.50
21	LLSVALFFV	206	0.1000	1.25
22	LKVSLLLSV	201	-0.2000	0
23	IGGIEVTLA	292	-0.2000	0
24	LLLSVALFF	205	-0.3000	0
25	LVLGGMGVW	224	-0.3000	0
26	FLIGLVNIV	264	-0.3000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IVLMTALAT	271	3.9000	45.35
2	MQIRRIDPW	190	3.2000	37.21
3	VWMITVAFL	214	2.8000	32.56

4	LVNIVLMTA	268	2.8000	32.56
5	MGVWAKLNS	229	2.7000	31.40
6	IRRIDPWST	192	2.2000	25.58
7	LNRFISGAS	81	2.1000	24.42
8	FVWMITVAF	213	2.1000	24.42
9	IGLVNIVLM	266	2.1000	24.42
10	FLYLVLGGM	221	1.9000	22.09
11	WQRAATRQS	45	1.8000	20.93
12	LLNNASGSS	242	1.6000	18.60
13	LVSSGTIFG	253	1.6000	18.60
14	VLMTALATI	272	1.5000	17.44
15	LVDRGGAHR	20	1.4000	16.28
16	VALFFVWMI	209	1.4000	16.28
17	LYLVLGGMG	222	1.3000	15.12
18	LGGMGVWAK	226	1.1000	12.79
19	VAFLYLVLG	219	0.9000	10.47
20	MTALATIGA	274	0.7000	8.14
21	VQLSARRSR	175	0.6000	6.98
22	LLLSVALFF	205	0.6000	6.98
23	LVLGGMGVW	224	0.6000	6.98
24	LIGLVNIVL	265	0.6000	6.98
25	LSARRSRGP	177	0.4000	4.65
26	LLSVALFFV	206	0.4000	4.65
27	VYNLITDLI	284	0.4000	4.65
28	VRTPQPDPD	99	0.3000	3.49
29	VSLLLSVAL	203	0.2000	2.33
30	FVYNLITDL	283	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	FVWMITVAF	213	3.2000	36.78
2	FVYNLITDL	283	3.0000	34.48

3	LVNIVLMTA	268	2.8000	32.18
4	FLIGLVNIV	264	2.7000	31.03
5	IVLMTALAT	271	2.6000	29.89
6	WQRAATRQS	45	2.5000	28.74
7	MQIRRIDPW	190	2.5000	28.74
8	FFVWMITVA	212	2.4000	27.59
9	MGVWAKLNS	229	2.3000	26.44
10	IGGIEVTLA	292	1.6000	18.39
11	YLVLGGMGV	223	1.5000	17.24
12	LGGMGVWAK	226	1.3000	14.94
13	WSTLKVSLL	198	1.1000	12.64
14	FLYLVLGGM	221	1.1000	12.64
15	IGLVNIVLM	266	1.0000	11.49
16	IRRIDPWST	192	0.8000	9.20
17	VWMITVAFL	214	0.8000	9.20
18	VALFFVWMI	209	0.7000	8.05
19	MTALATIGA	274	0.5800	6.67
20	WMITVAFLY	215	0.5500	6.32
21	LVDRGGAHR	20	0.4000	4.60
22	LNRFISGAS	81	0.4000	4.60
23	VWAKLNSNV	231	0.4000	4.60
24	VYNLITDLI	284	0.4000	4.60
25	WAKLNSNVG	232	0.3000	3.45
26	VLMTALATI	272	0.3000	3.45
27	LVSSGTIFG	253	0.1800	2.07
28	LNNASGSSA	243	0.1000	1.15
29	VNIVLMTAL	269	0.1000	1.15

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	IVLMTALAT	271	4.7000	46.53
2	FVWMITVAF	213	3.6000	35.64

3	MGVWAKLNS	229	3.5000	34.65
4	LVNIVLMTA	268	3.4000	33.66
5	WQRAATRQS	45	3.0000	29.70
6	FLYLVLGGM	221	3.0000	29.70
7	YLVLGGMGV	223	2.4000	23.76
8	FVYNLITDL	283	2.3000	22.77
9	LVSSGTIFG	253	2.2000	21.78
10	IRRIDPWST	192	2.0000	19.80
11	MQIRRIDPW	190	1.9000	18.81
12	VWMITVAFL	214	1.8000	17.82
13	FGGAFLIGL	260	1.7000	16.83
14	IGLVNIVLM	266	1.6000	15.84
15	YNLITDLIG	285	1.5000	14.85
16	LLLSVALFF	205	1.4000	13.86
17	WMITVAFLY	215	1.3000	12.87
18	FLIGLVNIV	264	1.3000	12.87
19	MTALATIGA	274	1.3000	12.87
20	LNRFISGAS	81	1.2000	11.88
21	VALFFVWMI	209	1.2000	11.88
22	LIGLVNIVL	265	1.2000	11.88
23	LKVSLLLSV	201	0.9000	8.91
24	LGGMGVWAK	226	0.9000	8.91
25	FFVWMITVA	212	0.7000	6.93
26	LLNNASGSS	242	0.7000	6.93
27	MITVAFLYL	216	0.5000	4.95
28	VLMTALATI	272	0.5000	4.95
29	LVDRGGAHR	20	0.4000	3.96
30	LFFVWMITV	211	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	LVNIVLMTA	268	4.0000	48.19

2	MGVWAKLNS	229	3.4000	40.96
3	IVLMTALAT	271	3.4000	40.96
4	WQRAATRQS	45	3.0000	36.14
5	YLVLGGMGV	223	2.5000	30.12
6	FVWMITVAF	213	2.3000	27.71
7	FLYLVLGGM	221	2.3000	27.71
8	IRRIDPWST	192	1.7000	20.48
9	MTALATIGA	274	1.7000	20.48
10	VWMITVAFL	214	1.4000	16.87
11	FVYNLITDL	283	1.3000	15.66
12	LGGMGVWAK	226	1.2000	14.46
13	LVSSGTIFG	253	1.2000	14.46
14	LNRFISGAS	81	1.1000	13.25
15	LKVSLLLSV	201	0.9000	10.84
16	VALFFVWMI	209	0.9000	10.84
17	LLLSVALFF	205	0.8000	9.64
18	YNLITDLIG	285	0.8000	9.64
19	LLNNASGSS	242	0.7000	8.43
20	FGGAFLIGL	260	0.7000	8.43
21	VLMTALATI	272	0.7000	8.43
22	FFVWMITVA	212	0.6000	7.23
23	WMITVAFLY	215	0.6000	7.23
24	LIGLVNIVL	265	0.6000	7.23
25	IGLVNIVLM	266	0.6000	7.23
26	IGGIEVTLA	292	0.5000	6.02
27	FLIGLVNIV	264	0.3000	3.61
28	LFFVWMITV	211	0.2000	2.41
29	VQLSARRSR	175	0.1000	1.20

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	MGVWAKLNS	229	4.1000	48.81

2	WQRAATRQS	45	3.6000	42.86
3	VALFFVWMI	209	3.1000	36.90
4	IVLMTALAT	271	3.1000	36.90
5	VQLSARRSR	175	2.8000	33.33
6	LGGMGVWAK	226	2.8000	33.33
7	LVNIVLMTA	268	2.2000	26.19
8	IRRIDPWST	192	2.0000	23.81
9	FVWMITVAF	213	1.6000	19.05
10	LNRFISGAS	81	1.4000	16.67
11	VLMTALATI	272	1.2000	14.29
12	MQIRRIDPW	190	1.1000	13.10
13	LVSSGTIFG	253	1.0000	11.90
14	LKVSLLLSV	201	0.9000	10.71
15	VWMITVAFL	214	0.9000	10.71
16	LLLSVALFF	205	0.8000	9.52
17	FFVWMITVA	212	0.8000	9.52
18	IGLVNIVLM	266	0.8000	9.52
19	FVYNLITDL	283	0.8000	9.52
20	VYNLITDLI	284	0.8000	9.52
21	LLNNASGSS	242	0.7000	8.33
22	MTALATIGA	274	0.7000	8.33
23	FLIGLVNIV	264	0.6000	7.14
24	LLSVALFFV	206	0.4000	4.76
25	IGGIEVTLA	292	0.4000	4.76
26	VAFLYLVLG	219	0.3000	3.57
27	IDPWSTLKV	195	0.2000	2.38
28	WMITVAFLY	215	0.1000	1.19
29	VSLLLSVAL	203	-0.1000	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	LVNIVLMTA	268	5.0000	60.24

2	MGVWAKLNS	229	4.4000	53.01
3	IVLMTALAT	271	4.4000	53.01
4	IRRIDPWST	192	2.7000	32.53
5	MTALATIGA	274	2.7000	32.53
6	VWMITVAFL	214	2.4000	28.92
7	LGGMGVWAK	226	2.2000	26.51
8	LVSSGTIFG	253	2.2000	26.51
9	LNRFISGAS	81	2.1000	25.30
10	WQRAATRQS	45	2.0000	24.10
11	LKVSLLLSV	201	1.9000	22.89
12	VALFFVWMI	209	1.9000	22.89
13	LLLSVALFF	205	1.8000	21.69
14	LLNNASGSS	242	1.7000	20.48
15	VLMTALATI	272	1.7000	20.48
16	LIGLVNIVL	265	1.6000	19.28
17	IGLVNIVLM	266	1.6000	19.28
18	YLVLGGMGV	223	1.5000	18.07
19	IGGIEVTLA	292	1.5000	18.07
20	FVWMITVAF	213	1.3000	15.66
21	FLYLVLGGM	221	1.3000	15.66
22	LFFVWMITV	211	1.2000	14.46
23	VQLSARRSR	175	1.1000	13.25
24	VRASMQIRR	186	1.0000	12.05
25	LLSVALFFV	206	0.7000	8.43
26	MITVAFLYL	216	0.6000	7.23
27	IDPWSTLKV	195	0.5000	6.02
28	VAFLYLVLG	219	0.5000	6.02
29	FVYNLITDL	283	0.3000	3.61
30	VYNLITDLI	284	0.3000	3.61

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	LVNIVLMTA	268	5.0000	60.24
2	MGVWAKLNS	229	4.4000	53.01
3	IVLMTALAT	271	4.4000	53.01
4	IRRIDPWST	192	2.7000	32.53
5	MTALATIGA	274	2.7000	32.53
6	VWMITVAFL	214	2.4000	28.92
7	LGGMGVWAK	226	2.2000	26.51
8	LVSSGTIFG	253	2.2000	26.51
9	LNRFISGAS	81	2.1000	25.30
10	WQRAATRQS	45	2.0000	24.10
11	LKVSLLLSV	201	1.9000	22.89
12	VALFFVWMI	209	1.9000	22.89
13	LLLSVALFF	205	1.8000	21.69
14	LLNNASGSS	242	1.7000	20.48
15	VLMTALATI	272	1.7000	20.48
16	LIGLVNIVL	265	1.6000	19.28
17	IGLVNIVLM	266	1.6000	19.28
18	YLVLGGMGV	223	1.5000	18.07
19	IGGIEVTLA	292	1.5000	18.07
20	FVWMITVAF	213	1.3000	15.66
21	FLYLVLGGM	221	1.3000	15.66
22	LFFVWMITV	211	1.2000	14.46
23	VQLSARRSR	175	1.1000	13.25
24	VRASMQIRR	186	1.0000	12.05
25	LLSVALFFV	206	0.7000	8.43
26	MITVAFLYL	216	0.6000	7.23
27	IDPWSTLKV	195	0.5000	6.02
28	VAFLYLVLG	219	0.5000	6.02
29	FVYNLITDL	283	0.3000	3.61
30	VYNLITDLI	284	0.3000	3.61

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	LVNIVLMTA	268	4.4000	48.35
2	LITDLIGGI	287	3.9000	42.86
3	LVSSGTIFG	253	3.2000	35.16
4	FLIGLVNIV	264	2.4100	26.48
5	LLNNASGSS	242	2.4000	26.37
6	IGGIEVTLA	292	2.3000	25.27
7	MGVWAKLNS	229	2.2000	24.18
8	IRRIDPWST	192	2.1000	23.08
9	IVLMTALAT	271	2.1000	23.08
10	VQLSARRSR	175	2.0000	21.98
11	VRASMQIRR	186	2.0000	21.98
12	LKVSLLLSV	201	2.0000	21.98
13	VWMITVAFL	214	2.0000	21.98
14	IGLVNIVLM	266	2.0000	21.98
15	LLLSVALFF	205	1.9000	20.88
16	LVLGGMGVW	224	1.8000	19.78
17	FVYNLITDL	283	1.7000	18.68
18	WQRAATRQS	45	1.5000	16.48
19	VLMTALATI	272	1.3000	14.29
20	VYNLITDLI	284	1.3000	14.29
21	LNRFISGAS	81	1.2000	13.19
22	LLSVALFFV	206	1.2000	13.19
23	VLGGMGVWA	225	1.2000	13.19
24	MTALATIGA	274	1.2000	13.19
25	FVWMITVAF	213	1.1000	12.09
26	LGGMGVWAK	226	1.0000	10.99
27	MQIRRIDPW	190	0.8000	8.79
28	FLYLVLGGM	221	0.7000	7.69
29	LNNASGSSA	243	0.6700	7.36
30	VSSGTIFGG	254	0.6000	6.59

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

	1.3	

Rank	Sequence	At Position	Score	% of Highest Score
1	WQRAATRQS	45	4.6000	54.76
2	MGVWAKLNS	229	3.1000	36.90
3	FVWMITVAF	213	2.6000	30.95
4	VALFFVWMI	209	2.1000	25.00
5	IVLMTALAT	271	2.1000	25.00
6	VQLSARRSR	175	1.8000	21.43
7	FFVWMITVA	212	1.8000	21.43
8	LGGMGVWAK	226	1.8000	21.43
9	FVYNLITDL	283	1.8000	21.43
10	FLIGLVNIV	264	1.6000	19.05
11	LVNIVLMTA	268	1.2000	14.29
12	WMITVAFLY	215	1.1000	13.10
13	IRRIDPWST	192	1.0000	11.90
14	FLYLVLGGM	221	0.5000	5.95
15	YLVLGGMGV	223	0.5000	5.95
16	LNRFISGAS	81	0.4000	4.76
17	VLMTALATI	272	0.2000	2.38
18	MQIRRIDPW	190	0.1000	1.19
19	LKVSLLLSV	201	-0.1000	0
20	VWMITVAFL	214	-0.1000	0
21	LLLSVALFF	205	-0.2000	0
22	IGLVNIVLM	266	-0.2000	0
23	VYNLITDLI	284	-0.2000	0
24	LLNNASGSS	242	-0.3000	0
25	MTALATIGA	274	-0.3000	0
26	WSTLKVSLL	198	-0.6000	0
27	LLSVALFFV	206	-0.6000	0
28	WAKLNSNVG	232	-0.6000	0

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

	2.1	

Rank	Sequence	At Position	Score	% of Highest Score
1	WQRAATRQS	45	5.0000	56.82
2	FVWMITVAF	213	4.5000	51.14
3	MGVWAKLNS	229	3.5000	39.77
4	VQLSARRSR	175	3.3000	37.50
5	VALFFVWMI	209	3.0000	34.09
6	IVLMTALAT	271	2.8000	31.82
7	FVYNLITDL	283	2.7600	31.36
8	FLIGLVNIV	264	2.6000	29.55
9	WMITVAFLY	215	2.4000	27.27
10	FLYLVLGGM	221	2.0000	22.73
11	LGGMGVWAK	226	1.9000	21.59
12	FFVWMITVA	212	1.8000	20.45
13	IRRIDPWST	192	1.7000	19.32
14	LLLSVALFF	205	1.7000	19.32
15	YLVLGGMGV	223	1.5000	17.05
16	LVSSGTIFG	253	1.4000	15.91
17	IGLVNIVLM	266	1.3000	14.77
18	LVNIVLMTA	268	1.2000	13.64
19	VLMTALATI	272	1.1000	12.50
20	LKVSLLLSV	201	0.9000	10.23
21	VWMITVAFL	214	0.8600	9.77
22	LNRFISGAS	81	0.8000	9.09
23	WAKLNSNVG	232	0.8000	9.09
24	VAFLYLVLG	219	0.7000	7.95
25	VYNLITDLI	284	0.7000	7.95
26	LLSVALFFV	206	0.4000	4.55
27	WSTLKVSLL	198	0.3600	4.09
28	FGGAFLIGL	260	0.3600	4.09
29	VRASMQIRR	186	0.3000	3.41
30	IDPWSTLKV	195	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MGVWAKLNS	229	4.1000	48.81
2	WQRAATRQS	45	3.6000	42.86
3	VALFFVWMI	209	3.1000	36.90
4	IVLMTALAT	271	3.1000	36.90
5	VQLSARRSR	175	2.8000	33.33
6	LGGMGVWAK	226	2.8000	33.33
7	LVNIVLMTA	268	2.2000	26.19
8	IRRIDPWST	192	2.0000	23.81
9	FVWMITVAF	213	1.6000	19.05
10	LNRFISGAS	81	1.4000	16.67
11	VLMTALATI	272	1.2000	14.29
12	MQIRRIDPW	190	1.1000	13.10
13	LVSSGTIFG	253	1.0000	11.90
14	LKVSLLLSV	201	0.9000	10.71
15	VWMITVAFL	214	0.9000	10.71
16	LLLSVALFF	205	0.8000	9.52
17	FFVWMITVA	212	0.8000	9.52
18	IGLVNIVLM	266	0.8000	9.52
19	FVYNLITDL	283	0.8000	9.52
20	VYNLITDLI	284	0.8000	9.52
21	LLNNASGSS	242	0.7000	8.33
22	MTALATIGA	274	0.7000	8.33
23	FLIGLVNIV	264	0.6000	7.14
24	LLSVALFFV	206	0.4000	4.76
25	IGGIEVTLA	292	0.4000	4.76
26	VAFLYLVLG	219	0.3000	3.57
27	IDPWSTLKV	195	0.2000	2.38
28	WMITVAFLY	215	0.1000	1.19
29	VSLLLSVAL	203	-0.1000	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	FVWMITVAF	213	4.2000	48.28
2	IVLMTALAT	271	4.1000	47.13
3	LVNIVLMTA	268	4.0000	45.98
4	FLYLVLGGM	221	3.8000	43.68
5	MGVWAKLNS	229	3.8000	43.68
6	YLVLGGMGV	223	3.5000	40.23
7	WQRAATRQS	45	3.4000	39.08
8	LLLSVALFF	205	2.7000	31.03
9	LVSSGTIFG	253	2.6000	29.89
10	IRRIDPWST	192	2.4000	27.59
11	VWMITVAFL	214	2.3600	27.13
12	FVYNLITDL	283	2.2600	25.98
13	YNLITDLIG	285	2.2000	25.29
14	IGLVNIVLM	266	2.1000	24.14
15	LKVSLLLSV	201	1.9000	21.84
16	WMITVAFLY	215	1.9000	21.84
17	VALFFVWMI	209	1.8000	20.69
18	MTALATIGA	274	1.7000	19.54
19	FGGAFLIGL	260	1.6600	19.08
20	VQLSARRSR	175	1.6000	18.39
21	VLMTALATI	272	1.6000	18.39
22	LIGLVNIVL	265	1.5600	17.93
23	LNRFISGAS	81	1.5000	17.24
24	VRASMQIRR	186	1.5000	17.24
25	LGGMGVWAK	226	1.3000	14.94
26	FLIGLVNIV	264	1.3000	14.94
27	LFFVWMITV	211	1.2000	13.79
28	LLNNASGSS	242	1.1000	12.64
29	VAFLYLVLG	219	0.9000	10.34
30	LLSVALFFV	206	0.7000	8.05

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	MGVWAKLNS	229	4.5000	51.14
2	VQLSARRSR	175	4.3000	48.86
3	WQRAATRQS	45	4.0000	45.45
4	VALFFVWMI	209	4.0000	45.45
5	IVLMTALAT	271	3.8000	43.18
6	FVWMITVAF	213	3.5000	39.77
7	LGGMGVWAK	226	2.9000	32.95
8	IRRIDPWST	192	2.7000	30.68
9	LLLSVALFF	205	2.7000	30.68
10	LVSSGTIFG	253	2.4000	27.27
11	IGLVNIVLM	266	2.3000	26.14
12	LVNIVLMTA	268	2.2000	25.00
13	VLMTALATI	272	2.1000	23.86
14	LKVSLLLSV	201	1.9000	21.59
15	VWMITVAFL	214	1.8600	21.14
16	LNRFISGAS	81	1.8000	20.45
17	FVYNLITDL	283	1.7600	20.00
18	VAFLYLVLG	219	1.7000	19.32
19	VYNLITDLI	284	1.7000	19.32
20	FLIGLVNIV	264	1.6000	18.18
21	LLSVALFFV	206	1.4000	15.91
22	WMITVAFLY	215	1.4000	15.91
23	VRASMQIRR	186	1.3000	14.77
24	IDPWSTLKV	195	1.2000	13.64
25	MQIRRIDPW	190	1.1000	12.50
26	LLNNASGSS	242	1.1000	12.50
27	FLYLVLGGM	221	1.0000	11.36
28	VSLLLSVAL	203	0.8600	9.77
29	LVDRGGAHR	20	0.8000	9.09
30	FFVWMITVA	212	0.8000	9.09

ALLELE: DRB1_1302	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	WQRAATRQS	45	5.0000	56.82
2	FVWMITVAF	213	4.5000	51.14
3	MGVWAKLNS	229	3.5000	39.77
4	VQLSARRSR	175	3.3000	37.50
5	VALFFVWMI	209	3.0000	34.09
6	IVLMTALAT	271	2.8000	31.82
7	FVYNLITDL	283	2.7600	31.36
8	FLIGLVNIV	264	2.6000	29.55
9	WMITVAFLY	215	2.4000	27.27
10	FLYLVLGGM	221	2.0000	22.73
11	LGGMGVWAK	226	1.9000	21.59
12	FFVWMITVA	212	1.8000	20.45
13	IRRIDPWST	192	1.7000	19.32
14	LLLSVALFF	205	1.7000	19.32
15	YLVLGGMGV	223	1.5000	17.05
16	LVSSGTIFG	253	1.4000	15.91
17	IGLVNIVLM	266	1.3000	14.77
18	LVNIVLMTA	268	1.2000	13.64
19	VLMTALATI	272	1.1000	12.50
20	LKVSLLLSV	201	0.9000	10.23
21	VWMITVAFL	214	0.8600	9.77
22	LNRFISGAS	81	0.8000	9.09
23	WAKLNSNVG	232	0.8000	9.09
24	VAFLYLVLG	219	0.7000	7.95
25	VYNLITDLI	284	0.7000	7.95
26	LLSVALFFV	206	0.4000	4.55
27	WSTLKVSLL	198	0.3600	4.09
28	FGGAFLIGL	260	0.3600	4.09
29	VRASMQIRR	186	0.3000	3.41
30	IDPWSTLKV	195	0.2000	2.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MGVWAKLNS	229	4.1000	45.56
2	IVLMTALAT	271	4.0000	44.44
3	WQRAATRQS	45	3.6000	40.00
4	VALFFVWMI	209	3.3000	36.67
5	IRRIDPWST	192	2.9000	32.22
6	VQLSARRSR	175	2.8000	31.11
7	FVWMITVAF	213	2.5000	27.78
8	LVSSGTIFG	253	2.3000	25.56
9	LVNIVLMTA	268	2.2000	24.44
10	LGGMGVWAK	226	2.1000	23.33
11	MQIRRIDPW	190	2.0000	22.22
12	VWMITVAFL	214	1.9000	21.11
13	IGLVNIVLM	266	1.9000	21.11
14	FVYNLITDL	283	1.8000	20.00
15	LLLSVALFF	205	1.7000	18.89
16	VAFLYLVLG	219	1.6000	17.78
17	LNRFISGAS	81	1.4000	15.56
18	VLMTALATI	272	1.4000	15.56
19	LKVSLLLSV	201	1.2000	13.33
20	WMITVAFLY	215	1.2000	13.33
21	VYNLITDLI	284	1.0000	11.11
22	VSLLLSVAL	203	0.9000	10.00
23	FLIGLVNIV	264	0.9000	10.00
24	FFVWMITVA	212	0.8000	8.89
25	VRTPQPDPD	99	0.7000	7.78
26	LLSVALFFV	206	0.7000	7.78
27	LLNNASGSS	242	0.7000	7.78
28	MTALATIGA	274	0.7000	7.78
29	FLYLVLGGM	221	0.6000	6.67

30	LIGLVNIVL	265	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	FVWMITVAF	213	4.2000	48.28
2	IVLMTALAT	271	4.1000	47.13
3	LVNIVLMTA	268	4.0000	45.98
4	FLYLVLGGM	221	3.8000	43.68
5	MGVWAKLNS	229	3.8000	43.68
6	YLVLGGMGV	223	3.5000	40.23
7	WQRAATRQS	45	3.4000	39.08
8	LLLSVALFF	205	2.7000	31.03
9	LVSSGTIFG	253	2.6000	29.89
10	IRRIDPWST	192	2.4000	27.59
11	VWMITVAFL	214	2.3600	27.13
12	FVYNLITDL	283	2.2600	25.98
13	YNLITDLIG	285	2.2000	25.29
14	IGLVNIVLM	266	2.1000	24.14
15	LKVSLLLSV	201	1.9000	21.84
16	WMITVAFLY	215	1.9000	21.84
17	VALFFVWMI	209	1.8000	20.69
18	MTALATIGA	274	1.7000	19.54
19	FGGAFLIGL	260	1.6600	19.08
20	VQLSARRSR	175	1.6000	18.39
21	VLMTALATI	272	1.6000	18.39
22	LIGLVNIVL	265	1.5600	17.93
23	LNRFISGAS	81	1.5000	17.24
24	VRASMQIRR	186	1.5000	17.24
25	LGGMGVWAK	226	1.3000	14.94
26	FLIGLVNIV	264	1.3000	14.94
27	LFFVWMITV	211	1.2000	13.79
28	LLNNASGSS	242	1.1000	12.64

29	VAFLYLVLG	219	0.9000	10.34
30	LLSVALFFV	206	0.7000	8.05

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	WQRAATRQS	45	2.8000	41.18
2	LVNIVLMTA	268	2.4000	35.29
3	FLYLVLGGM	221	2.2000	32.35
4	FVWMITVAF	213	1.8000	26.47
5	MGVWAKLNS	229	1.6000	23.53
6	IVLMTALAT	271	1.6000	23.53
7	VWMITVAFL	214	1.4000	20.59
8	LNRFISGAS	81	1.0000	14.71
9	IRRIDPWST	192	0.9000	13.24
10	YLVLGGMGV	223	0.9000	13.24
11	VLMTALATI	272	0.7000	10.29
12	LLNNASGSS	242	0.6000	8.82
13	LGGMGVWAK	226	0.4000	5.88
14	FVYNLITDL	283	0.2000	2.94
15	VALFFVWMI	209	0.1000	1.47
16	WMITVAFLY	215	0.1000	1.47
17	IGLVNIVLM	266	0.1000	1.47
18	MTALATIGA	274	0.1000	1.47
19	VQLSARRSR	175	-0.1000	0
20	WSTLKVSLL	198	-0.3000	0
21	LVSSGTIFG	253	-0.4000	0
22	VYNLITDLI	284	-0.4000	0
23	FFVWMITVA	212	-0.5000	0
24	IGGIEVTLA	292	-0.6000	0
25	LLSVALFFV	206	-0.8000	0
26	LKVSLLLSV	201	-0.9000	0
27	LYLVLGGMG	222	-0.9000	0

28	FGGAFLIGL	260	-0.9000	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	LVNIVLMTA	268	5.0000	60.24
2	MGVWAKLNS	229	4.4000	53.01
3	IVLMTALAT	271	4.4000	53.01
4	IRRIDPWST	192	2.7000	32.53
5	MTALATIGA	274	2.7000	32.53
6	VWMITVAFL	214	2.4000	28.92
7	LGGMGVWAK	226	2.2000	26.51
8	LVSSGTIFG	253	2.2000	26.51
9	LNRFISGAS	81	2.1000	25.30
10	WQRAATRQS	45	2.0000	24.10
11	LKVSLLLSV	201	1.9000	22.89
12	VALFFVWMI	209	1.9000	22.89
13	LLLSVALFF	205	1.8000	21.69
14	LLNNASGSS	242	1.7000	20.48
15	VLMTALATI	272	1.7000	20.48
16	LIGLVNIVL	265	1.6000	19.28
17	IGLVNIVLM	266	1.6000	19.28
18	YLVLGGMGV	223	1.5000	18.07
19	IGGIEVTLA	292	1.5000	18.07
20	FVWMITVAF	213	1.3000	15.66
21	FLYLVLGGM	221	1.3000	15.66
22	LFFVWMITV	211	1.2000	14.46
23	VQLSARRSR	175	1.1000	13.25
24	VRASMQIRR	186	1.0000	12.05
25	LLSVALFFV	206	0.7000	8.43
26	MITVAFLYL	216	0.6000	7.23
27	IDPWSTLKV	195	0.5000	6.02
28	VAFLYLVLG	219	0.5000	6.02

29	FVYNLITDL	283	0.3000	3.61
30	VYNLITDLI	284	0.3000	3.61

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	IVLMTALAT	271	4.3000	48.31
2	LVNIVLMTA	268	4.0000	44.94
3	FLYLVLGGM	221	3.4000	38.20
4	MGVWAKLNS	229	3.4000	38.20
5	FVWMITVAF	213	3.2000	35.96
6	WQRAATRQS	45	3.0000	33.71
7	YLVLGGMGV	223	2.8000	31.46
8	IRRIDPWST	192	2.6000	29.21
9	LVSSGTIFG	253	2.5000	28.09
10	VWMITVAFL	214	2.4000	26.97
11	FVYNLITDL	283	2.3000	25.84
12	YNLITDLIG	285	2.1000	23.60
13	LLLSVALFF	205	1.7000	19.10
14	WMITVAFLY	215	1.7000	19.10
15	FGGAFLIGL	260	1.7000	19.10
16	IGLVNIVLM	266	1.7000	19.10
17	MTALATIGA	274	1.7000	19.10
18	LIGLVNIVL	265	1.6000	17.98
19	LKVSLLLSV	201	1.2000	13.48
20	LNRFISGAS	81	1.1000	12.36
21	VALFFVWMI	209	1.1000	12.36
22	VLMTALATI	272	0.9000	10.11
23	VAFLYLVLG	219	0.8000	8.99
24	WSTLKVSLL	198	0.7000	7.87
25	LLNNASGSS	242	0.7000	7.87
26	FFVWMITVA	212	0.6000	6.74
27	MITVAFLYL	216	0.6000	6.74

28	FLIGLVNIV	264	0.6000	6.74
29	LFFVWMITV	211	0.5000	5.62
30	LYLVLGGMG	222	0.5000	5.62

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	MGVWAKLNS	229	4.1000	48.81
2	WQRAATRQS	45	3.6000	42.86
3	VALFFVWMI	209	3.1000	36.90
4	IVLMTALAT	271	3.1000	36.90
5	VQLSARRSR	175	2.8000	33.33
6	LGGMGVWAK	226	2.8000	33.33
7	LVNIVLMTA	268	2.2000	26.19
8	IRRIDPWST	192	2.0000	23.81
9	FVWMITVAF	213	1.6000	19.05
10	LNRFISGAS	81	1.4000	16.67
11	VLMTALATI	272	1.2000	14.29
12	MQIRRIDPW	190	1.1000	13.10
13	LVSSGTIFG	253	1.0000	11.90
14	LKVSLLLSV	201	0.9000	10.71
15	VWMITVAFL	214	0.9000	10.71
16	LLLSVALFF	205	0.8000	9.52
17	FFVWMITVA	212	0.8000	9.52
18	IGLVNIVLM	266	0.8000	9.52
19	FVYNLITDL	283	0.8000	9.52
20	VYNLITDLI	284	0.8000	9.52
21	LLNNASGSS	242	0.7000	8.33
22	MTALATIGA	274	0.7000	8.33
23	FLIGLVNIV	264	0.6000	7.14
24	LLSVALFFV	206	0.4000	4.76
25	IGGIEVTLA	292	0.4000	4.76
26	VAFLYLVLG	219	0.3000	3.57

27	IDPWSTLKV	195	0.2000	2.38
28	WMITVAFLY	215	0.1000	1.19
29	VSLLLSVAL	203	-0.1000	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	WQRAATRQS	45	4.6000	54.76
2	MGVWAKLNS	229	3.1000	36.90
3	FVWMITVAF	213	2.6000	30.95
4	VALFFVWMI	209	2.1000	25.00
5	IVLMTALAT	271	2.1000	25.00
6	VQLSARRSR	175	1.8000	21.43
7	FFVWMITVA	212	1.8000	21.43
8	LGGMGVWAK	226	1.8000	21.43
9	FVYNLITDL	283	1.8000	21.43
10	FLIGLVNIV	264	1.6000	19.05
11	LVNIVLMTA	268	1.2000	14.29
12	WMITVAFLY	215	1.1000	13.10
13	IRRIDPWST	192	1.0000	11.90
14	FLYLVLGGM	221	0.5000	5.95
15	YLVLGGMGV	223	0.5000	5.95
16	LNRFISGAS	81	0.4000	4.76
17	VLMTALATI	272	0.2000	2.38
18	MQIRRIDPW	190	0.1000	1.19
19	LKVSLLLSV	201	-0.1000	0
20	VWMITVAFL	214	-0.1000	0
21	LLLSVALFF	205	-0.2000	0
22	IGLVNIVLM	266	-0.2000	0
23	VYNLITDLI	284	-0.2000	0
24	LLNNASGSS	242	-0.3000	0
25	MTALATIGA	274	-0.3000	0
26	WSTLKVSLL	198	-0.6000	0

27	LLSVALFFV	206	-0.6000	0
28	WAKLNSNVG	232	-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	MGVWAKLNS	229	4.5000	51.14
2	VQLSARRSR	175	4.3000	48.86
3	WQRAATRQS	45	4.0000	45.45
4	VALFFVWMI	209	4.0000	45.45
5	IVLMTALAT	271	3.8000	43.18
6	FVWMITVAF	213	3.5000	39.77
7	LGGMGVWAK	226	2.9000	32.95
8	IRRIDPWST	192	2.7000	30.68
9	LLLSVALFF	205	2.7000	30.68
10	LVSSGTIFG	253	2.4000	27.27
11	IGLVNIVLM	266	2.3000	26.14
12	LVNIVLMTA	268	2.2000	25.00
13	VLMTALATI	272	2.1000	23.86
14	LKVSLLLSV	201	1.9000	21.59
15	VWMITVAFL	214	1.8600	21.14
16	LNRFISGAS	81	1.8000	20.45
17	FVYNLITDL	283	1.7600	20.00
18	VAFLYLVLG	219	1.7000	19.32
19	VYNLITDLI	284	1.7000	19.32
20	FLIGLVNIV	264	1.6000	18.18
21	LLSVALFFV	206	1.4000	15.91
22	WMITVAFLY	215	1.4000	15.91
23	VRASMQIRR	186	1.3000	14.77
24	IDPWSTLKV	195	1.2000	13.64
25	MQIRRIDPW	190	1.1000	12.50
26	LLNNASGSS	242	1.1000	12.50
27	FLYLVLGGM	221	1.0000	11.36

28	VSLLLSVAL	203	0.8600	9.77
29	LVDRGGAHR	20	0.8000	9.09
30	FFVWMITVA	212	0.8000	9.09

ALLELE: DRB1_1328	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	MGVWAKLNS	229	4.5000	51.14
2	VQLSARRSR	175	4.3000	48.86
3	WQRAATRQS	45	4.0000	45.45
4	VALFFVWMI	209	4.0000	45.45
5	IVLMTALAT	271	3.8000	43.18
6	FVWMITVAF	213	3.5000	39.77
7	LGGMGVWAK	226	2.9000	32.95
8	IRRIDPWST	192	2.7000	30.68
9	LLLSVALFF	205	2.7000	30.68
10	LVSSGTIFG	253	2.4000	27.27
11	IGLVNIVLM	266	2.3000	26.14
12	LVNIVLMTA	268	2.2000	25.00
13	VLMTALATI	272	2.1000	23.86
14	LKVSLLLSV	201	1.9000	21.59
15	VWMITVAFL	214	1.8600	21.14
16	LNRFISGAS	81	1.8000	20.45
17	FVYNLITDL	283	1.7600	20.00
18	VAFLYLVLG	219	1.7000	19.32
19	VYNLITDLI	284	1.7000	19.32
20	FLIGLVNIV	264	1.6000	18.18
21	LLSVALFFV	206	1.4000	15.91
22	WMITVAFLY	215	1.4000	15.91
23	VRASMQIRR	186	1.3000	14.77
24	IDPWSTLKV	195	1.2000	13.64
25	MQIRRIDPW	190	1.1000	12.50
26	LLNNASGSS	242	1.1000	12.50

27	FLYLVLGGM	221	1.0000	11.36
28	VSLLLSVAL	203	0.8600	9.77
29	LVDRGGAHR	20	0.8000	9.09
30	FFVWMITVA	212	0.8000	9.09

ALLELE: DRB1_1501	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	IVLMTALAT	271	5.8000	59.18
2	LVNIVLMTA	268	5.1000	52.04
3	IGAFVYNLI	280	4.7000	47.96
4	LIGLVNIVL	265	4.5000	45.92
5	VALFFVWMI	209	4.4000	44.90
6	LNRFISGAS	81	4.2000	42.86
7	IRRIDPWST	192	3.7000	37.76
8	LKVSLLLSV	201	3.7000	37.76
9	LFFVWMITV	211	3.7000	37.76
10	YLVLGGMGV	223	3.5000	35.71
11	MITVAFLYL	216	3.4000	34.69
12	LLSVALFFV	206	3.3000	33.67
13	VNIVLMTAL	269	3.3000	33.67
14	LLLSVALFF	205	3.2000	32.65
15	VLMTALATI	272	3.0000	30.61
16	MGVWAKLNS	229	2.7000	27.55
17	LVSSGTIFG	253	2.6600	27.14
18	VSLLLSVAL	203	2.6000	26.53
19	FVYNLITDL	283	2.4500	25.00
20	FLIGLVNIV	264	2.2000	22.45
21	IGLVNIVLM	266	2.1300	21.73
22	VWMITVAFL	214	2.1000	21.43
23	LNNASGSSA	243	2.1000	21.43
24	YNLITDLIG	285	2.1000	21.43
25	VLGGMGVWA	225	2.0000	20.41

26	FVWMITVAF	213	1.9600	20.00
27	MTALATIGA	274	1.9600	20.00
28	FGGAFLIGL	260	1.9000	19.39
29	VYNLITDLI	284	1.8600	18.98
30	WMITVAFLY	215	1.8000	18.37

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	IVLMTALAT	271	4.8000	48.98
2	YLVLGGMGV	223	4.5000	45.92
3	LVNIVLMTA	268	4.1000	41.84
4	IGAFVYNLI	280	3.7000	37.76
5	LIGLVNIVL	265	3.5000	35.71
6	FVYNLITDL	283	3.4500	35.20
7	VALFFVWMI	209	3.4000	34.69
8	LNRFISGAS	81	3.2000	32.65
9	FLIGLVNIV	264	3.2000	32.65
10	YNLITDLIG	285	3.1000	31.63
11	FVWMITVAF	213	2.9600	30.20
12	FGGAFLIGL	260	2.9000	29.59
13	WMITVAFLY	215	2.8000	28.57
14	IRRIDPWST	192	2.7000	27.55
15	LKVSLLLSV	201	2.7000	27.55
16	LFFVWMITV	211	2.7000	27.55
17	FLYLVLGGM	221	2.5800	26.33
18	MITVAFLYL	216	2.4000	24.49
19	LLSVALFFV	206	2.3000	23.47
20	VNIVLMTAL	269	2.3000	23.47
21	FISGASAPV	84	2.2000	22.45
22	LLLSVALFF	205	2.2000	22.45
23	VLMTALATI	272	2.0000	20.41
24	FFVWMITVA	212	1.9500	19.90

25	MGVWAKLNS	229	1.7000	17.35
26	LVSSGTIFG	253	1.6600	16.94
27	VSLLLSVAL	203	1.6000	16.33
28	IGLVNIVLM	266	1.1300	11.53
29	VWMITVAFL	214	1.1000	11.22
30	LNNASGSSA	243	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	IVLMTALAT	271	5.8000	59.18
2	LVNIVLMTA	268	5.1000	52.04
3	IGAFVYNLI	280	4.7000	47.96
4	LIGLVNIVL	265	4.5000	45.92
5	VALFFVWMI	209	4.4000	44.90
6	LNRFISGAS	81	4.2000	42.86
7	IRRIDPWST	192	3.7000	37.76
8	LKVSLLLSV	201	3.7000	37.76
9	LFFVWMITV	211	3.7000	37.76
10	YLVLGGMGV	223	3.5000	35.71
11	MITVAFLYL	216	3.4000	34.69
12	LLSVALFFV	206	3.3000	33.67
13	VNIVLMTAL	269	3.3000	33.67
14	LLLSVALFF	205	3.2000	32.65
15	VLMTALATI	272	3.0000	30.61
16	MGVWAKLNS	229	2.7000	27.55
17	LVSSGTIFG	253	2.6600	27.14
18	VSLLLSVAL	203	2.6000	26.53
19	FVYNLITDL	283	2.4500	25.00
20	FLIGLVNIV	264	2.2000	22.45
21	IGLVNIVLM	266	2.1300	21.73
22	VWMITVAFL	214	2.1000	21.43
23	LNNASGSSA	243	2.1000	21.43

24	YNLITDLIG	285	2.1000	21.43
25	VLGGMGVWA	225	2.0000	20.41
26	FVWMITVAF	213	1.9600	20.00
27	MTALATIGA	274	1.9600	20.00
28	FGGAFLIGL	260	1.9000	19.39
29	VYNLITDLI	284	1.8600	18.98
30	WMITVAFLY	215	1.8000	18.37

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	WMITVAFLY	215	5.7000	58.16
2	IVLMTALAT	271	4.2000	42.86
3	FVWMITVAF	213	3.9000	39.80
4	IRRIDPWST	192	3.6000	36.73
5	VQLSARRSR	175	3.2000	32.65
6	LGGMGVWAK	226	3.2000	32.65
7	WQRAATRQS	45	3.1000	31.63
8	LATIGAFVY	277	3.1000	31.63
9	VRASMQIRR	186	3.0000	30.61
10	LYLVLGGMG	222	2.7000	27.55
11	FLYLVLGGM	221	2.5000	25.51
12	VNIVLMTAL	269	2.5000	25.51
13	LLLSVALFF	205	2.3000	23.47
14	LVNIVLMTA	268	2.3000	23.47
15	FGGAFLIGL	260	2.2000	22.45
16	LIGLVNIVL	265	2.1000	21.43
17	YNLITDLIG	285	2.1000	21.43
18	YLVLGGMGV	223	2.0000	20.41
19	VLMTALATI	272	1.9000	19.39
20	LLSVALFFV	206	1.6000	16.33
21	VWMITVAFL	214	1.6000	16.33
22	LVSSGTIFG	253	1.6000	16.33

23	MITVAFLYL	216	1.4000	14.29
24	FVYNLITDL	283	1.4000	14.29
25	LFFVWMITV	211	1.2000	12.24
26	WAKLNSNVG	232	1.0000	10.20
27	VSLLLSVAL	203	0.8000	8.16
28	LMTALATIG	273	0.8000	8.16
29	LNRFISGAS	81	0.7000	7.14
30	IGLVNIVLM	266	0.4000	4.08

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	WMITVAFLY	215	5.7000	58.16
2	IVLMTALAT	271	4.2000	42.86
3	FVWMITVAF	213	3.9000	39.80
4	IRRIDPWST	192	3.6000	36.73
5	VQLSARRSR	175	3.2000	32.65
6	LGGMGVWAK	226	3.2000	32.65
7	WQRAATRQS	45	3.1000	31.63
8	LATIGAFVY	277	3.1000	31.63
9	VRASMQIRR	186	3.0000	30.61
10	LYLVLGGMG	222	2.7000	27.55
11	FLYLVLGGM	221	2.5000	25.51
12	VNIVLMTAL	269	2.5000	25.51
13	LLLSVALFF	205	2.3000	23.47
14	LVNIVLMTA	268	2.3000	23.47
15	FGGAFLIGL	260	2.2000	22.45
16	LIGLVNIVL	265	2.1000	21.43
17	YNLITDLIG	285	2.1000	21.43
18	YLVLGGMGV	223	2.0000	20.41
19	VLMTALATI	272	1.9000	19.39
20	LLSVALFFV	206	1.6000	16.33
21	VWMITVAFL	214	1.6000	16.33

22	LVSSGTIFG	253	1.6000	16.33
23	MITVAFLYL	216	1.4000	14.29
24	FVYNLITDL	283	1.4000	14.29
25	LFFVWMITV	211	1.2000	12.24
26	WAKLNSNVG	232	1.0000	10.20
27	VSLLLSVAL	203	0.8000	8.16
28	LMTALATIG	273	0.8000	8.16
29	LNRFISGAS	81	0.7000	7.14
30	IGLVNIVLM	266	0.4000	4.08