MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

```
INPUT & PARAMETER INFORMATION
```

Antigen Name	test
Scanned on	Wed Mar 10 00:03:00 2010
Length of input sequence	284 amino acids
Number of nanomers from input sequence	276
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	28

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	FFFLRPKDI	44	2.8000	46.67
2	MRIATAYPN	109	2.0000	33.33
3	FRYAAPAGR	91	1.8000	30.00
4	WVAIRALVP	246	1.8000	30.00
5	IRLDGAVEI	133	1.2000	20.00
6	LRVAVPNKG	1	0.8000	13.33
7	IRALVPRRD	249	0.0900	1.50
8	VVFGQQYLM	205	-0.0200	0

9	VARVQGVVF	199	-0.3500	0
10	LKKATAITP	223	-0.4000	0
11	VIRLDGAVE	132	-0.5000	0
12	YPNLVRKDL	115	-0.6000	0
13	LTVIDPVNN	33	-0.7000	0
14	IATAYPNLV	111	-0.8000	0
15	VQLGVADAI	143	-0.8000	0
16	YVGSGELDF	55	-0.9000	0
17	VNNVEFFFL	39	-1.0500	0
18	VFGQQYLML	206	-1.1000	0
19	LVAFGEPLC	166	-1.1500	0
20	ILAEAGYRR	18	-1.2000	0
21	LVCDSGAQV	70	-1.3000	0
22	VEISVQLGV	139	-1.3000	0
23	LGVADAIAD	145	-1.3000	0
24	VVGSGRTLS	154	-1.4100	0
25	LALGFGSSS	82	-1.5000	0
26	FLRPKDIAI	46	-1.6000	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	MRIATAYPN	109	3.0000	50.00
2	FFFLRPKDI	44	2.8000	46.67
3	IRLDGAVEI	133	2.2000	36.67
4	LRVAVPNKG	1	1.8000	30.00
5	FRYAAPAGR	91	1.8000	30.00
6	IRALVPRRD	249	1.0900	18.17
7	LAAIGAKAI	265	1.0000	16.67
8	VVFGQQYLM	205	0.9800	16.33
9	WVAIRALVP	246	0.8000	13.33
10	VARVQGVVF	199	0.6500	10.83
11	LKKATAITP	223	0.6000	10.00

12	VIRLDGAVE	132	0.5000	8.33
13	LTVIDPVNN	33	0.3000	5.00
14	IATAYPNLV	111	0.2000	3.33
15	VQLGVADAI	143	0.2000	3.33
16	VNNVEFFFL	39	-0.0500	0
17	VFGQQYLML	206	-0.1000	0
18	LVAFGEPLC	166	-0.1500	0
19	ILAEAGYRR	18	-0.2000	0
20	LVCDSGAQV	70	-0.3000	0
21	VEISVQLGV	139	-0.3000	0
22	LGVADAIAD	145	-0.3000	0
23	VVGSGRTLS	154	-0.4100	0
24	LALGFGSSS	82	-0.5000	0
25	LCDSEAVLI	173	-0.6000	0
26	LAGMRIATA	106	-0.9000	0
27	VLIERAGTD	179	-0.9000	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	IRLDGAVEI	133	6.3000	66.32
2	VVGSGRTLS	154	5.0000	52.63
3	VRKDLATKG	119	4.8000	50.53
4	LASDIRFCR	274	4.5000	47.37
5	VVFGQQYLM	205	4.1500	43.68
6	LVCDSGAQV	70	4.0000	42.11
7	LRVAVPNKG	1	3.5100	36.95
8	MLRVAVPNK	0	3.4000	35.79
9	MRIATAYPN	109	3.0500	32.11
10	FRYAAPAGR	91	3.0000	31.58
11	VQLGVADAI	143	2.7000	28.42
12	LRPKDIAIY	47	2.5000	26.32
13	VEISVQLGV	139	2.5000	26.32

14	LMLDYDCPR	212	2.5000	26.32
15	LGFGSSSFR	84	2.2700	23.89
16	VGSGRTLSQ	155	2.0000	21.05
17	LALGFGSSS	82	1.9700	20.74
18	LVRKDLATK	118	1.8000	18.95
19	YVGSGELDF	55	1.7000	17.89
20	WVAIRALVP	246	1.5000	15.79
21	IGAKAILAS	268	1.5000	15.79
22	ILASDIRFC	273	1.5000	15.79
23	VAFGEPLCD	167	1.4000	14.74
24	LDYDCPRSA	214	1.4000	14.74
25	VAIRALVPR	247	1.4000	14.74
26	VGSGELDFG	56	1.2000	12.63
27	LVARVQGVV	198	1.2000	12.63
28	LKKATAITP	223	1.2000	12.63

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	IRLDGAVEI	133	4.4000	48.35
2	VVGSGRTLS	154	3.6000	39.56
3	FRYAAPAGR	91	2.5000	27.47
4	VRKDLATKG	119	2.4000	26.37
5	MLRVAVPNK	0	2.3000	25.27
6	LVCDSGAQV	70	2.0000	21.98
7	LASDIRFCR	274	2.0000	21.98
8	VGSGRTLSQ	155	1.7000	18.68
9	VVFGQQYLM	205	1.6500	18.13
10	FFLRPKDIA	45	1.5000	16.48
11	WVAIRALVP	246	1.5000	16.48
12	MRIATAYPN	109	1.2500	13.74
13	LRVAVPNKG	1	1.1100	12.20
14	FFFLRPKDI	44	0.9000	9.89

15	YVGSGELDF	55	0.8000	8.79
16	VQLGVADAI	143	0.8000	8.79
17	FGITGRDLV	63	0.7000	7.69
18	LVRKDLATK	118	0.7000	7.69
19	LALGFGSSS	82	0.5700	6.26
20	VEISVQLGV	139	0.5000	5.49
21	IERAGTDGQ	181	0.5000	5.49
22	ILASDIRFC	273	0.5000	5.49
23	LDYDCPRSA	214	0.4000	4.40
24	LRPKDIAIY	47	0.2000	2.20
25	FGQQYLMLD	207	0.1000	1.10
26	IGAKAILAS	268	0.1000	1.10

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRLDGAVEI	133	5.2800	60.00
2	VVGSGRTLS	154	4.6000	52.27
3	VRKDLATKG	119	3.4000	38.64
4	VGSGRTLSQ	155	3.2000	36.36
5	LVCDSGAQV	70	3.0000	34.09
6	LRVAVPNKG	1	2.8000	31.82
7	VQLGVADAI	143	2.1000	23.86
8	VEISVQLGV	139	2.0000	22.73
9	MLRVAVPNK	0	1.9000	21.59
10	IERAGTDGQ	181	1.8000	20.45
11	LVRKDLATK	118	1.7000	19.32
12	IGAKAILAS	268	1.6000	18.18
13	FRYAAPAGR	91	1.5000	17.05
14	VVFGQQYLM	205	1.5000	17.05
15	LASDIRFCR	274	1.5000	17.05
16	LALGFGSSS	82	1.3000	14.77
17	LRPKDIAIY	47	1.2000	13.64

18	ILASDIRFC	273	1.2000	13.64
19	MRIATAYPN	109	1.1000	12.50
20	LDYDCPRSA	214	1.1000	12.50
21	LMLDYDCPR	212	1.0000	11.36
22	WVAIRALVP	246	1.0000	11.36
23	LAGMRIATA	106	0.9000	10.23
24	FFLRPKDIA	45	0.8000	9.09
25	VAFGEPLCD	167	0.8000	9.09
26	VPRRDVNGI	253	0.7000	7.95
27	FFFLRPKDI	44	0.5000	5.68
28	LGFGSSSFR	84	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRLDGAVEI	133	5.2800	60.00
2	VVGSGRTLS	154	4.6000	52.27
3	VRKDLATKG	119	3.4000	38.64
4	VGSGRTLSQ	155	3.2000	36.36
5	LVCDSGAQV	70	3.0000	34.09
6	LRVAVPNKG	1	2.8000	31.82
7	VQLGVADAI	143	2.1000	23.86
8	VEISVQLGV	139	2.0000	22.73
9	MLRVAVPNK	0	1.9000	21.59
10	IERAGTDGQ	181	1.8000	20.45
11	LVRKDLATK	118	1.7000	19.32
12	IGAKAILAS	268	1.6000	18.18
13	FRYAAPAGR	91	1.5000	17.05
14	VVFGQQYLM	205	1.5000	17.05
15	LASDIRFCR	274	1.5000	17.05
16	LALGFGSSS	82	1.3000	14.77
17	LRPKDIAIY	47	1.2000	13.64
18	ILASDIRFC	273	1.2000	13.64

19	MRIATAYPN	109	1.1000	12.50
20	LDYDCPRSA	214	1.1000	12.50
21	LMLDYDCPR	212	1.0000	11.36
22	WVAIRALVP	246	1.0000	11.36
23	LAGMRIATA	106	0.9000	10.23
24	FFLRPKDIA	45	0.8000	9.09
25	VAFGEPLCD	167	0.8000	9.09
26	VPRRDVNGI	253	0.7000	7.95
27	FFFLRPKDI	44	0.5000	5.68
28	LGFGSSSFR	84	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRLDGAVEI	133	5.2800	60.00
2	VVGSGRTLS	154	4.6000	52.27
3	VRKDLATKG	119	3.4000	38.64
4	VGSGRTLSQ	155	3.2000	36.36
5	LVCDSGAQV	70	3.0000	34.09
6	LRVAVPNKG	1	2.8000	31.82
7	VQLGVADAI	143	2.1000	23.86
8	VEISVQLGV	139	2.0000	22.73
9	MLRVAVPNK	0	1.9000	21.59
10	IERAGTDGQ	181	1.8000	20.45
11	LVRKDLATK	118	1.7000	19.32
12	IGAKAILAS	268	1.6000	18.18
13	FRYAAPAGR	91	1.5000	17.05
14	VVFGQQYLM	205	1.5000	17.05
15	LASDIRFCR	274	1.5000	17.05
16	LALGFGSSS	82	1.3000	14.77
17	LRPKDIAIY	47	1.2000	13.64
18	ILASDIRFC	273	1.2000	13.64
19	MRIATAYPN	109	1.1000	12.50

20	LDYDCPRSA	214	1.1000	12.50
21	LMLDYDCPR	212	1.0000	11.36
22	WVAIRALVP	246	1.0000	11.36
23	LAGMRIATA	106	0.9000	10.23
24	FFLRPKDIA	45	0.8000	9.09
25	VAFGEPLCD	167	0.8000	9.09
26	VPRRDVNGI	253	0.7000	7.95
27	FFFLRPKDI	44	0.5000	5.68
28	LGFGSSSFR	84	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRLDGAVEI	133	5.3000	55.79
2	FRYAAPAGR	91	4.0000	42.11
3	VVGSGRTLS	154	4.0000	42.11
4	VRKDLATKG	119	3.8000	40.00
5	LASDIRFCR	274	3.5000	36.84
6	VVFGQQYLM	205	3.1500	33.16
7	LVCDSGAQV	70	3.0000	31.58
8	YVGSGELDF	55	2.7000	28.42
9	LRVAVPNKG	1	2.5100	26.42
10	WVAIRALVP	246	2.5000	26.32
11	MLRVAVPNK	0	2.4000	25.26
12	MRIATAYPN	109	2.0500	21.58
13	FFFLRPKDI	44	1.8000	18.95
14	FGITGRDLV	63	1.7000	17.89
15	VQLGVADAI	143	1.7000	17.89
16	FFLRPKDIA	45	1.5000	15.79
17	LRPKDIAIY	47	1.5000	15.79
18	VEISVQLGV	139	1.5000	15.79
19	LMLDYDCPR	212	1.5000	15.79
20	WTTADLAGM	101	1.3000	13.68

21	LGFGSSSFR	84	1.2700	13.37
22	FGQQYLMLD	207	1.2000	12.63
23	VGSGRTLSQ	155	1.0000	10.53
24	LALGFGSSS	82	0.9700	10.21
25	LVRKDLATK	118	0.8000	8.42
26	IGAKAILAS	268	0.5000	5.26
27	ILASDIRFC	273	0.5000	5.26
28	VAFGEPLCD	167	0.4000	4.21

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	IRLDGAVEI	133	5.2800	60.00
2	VVGSGRTLS	154	4.6000	52.27
3	VRKDLATKG	119	3.4000	38.64
4	VGSGRTLSQ	155	3.2000	36.36
5	LVCDSGAQV	70	3.0000	34.09
6	LRVAVPNKG	1	2.8000	31.82
7	VQLGVADAI	143	2.1000	23.86
8	VEISVQLGV	139	2.0000	22.73
9	MLRVAVPNK	0	1.9000	21.59
10	IERAGTDGQ	181	1.8000	20.45
11	LVRKDLATK	118	1.7000	19.32
12	IGAKAILAS	268	1.6000	18.18
13	FRYAAPAGR	91	1.5000	17.05
14	VVFGQQYLM	205	1.5000	17.05
15	LASDIRFCR	274	1.5000	17.05
16	LALGFGSSS	82	1.3000	14.77
17	LRPKDIAIY	47	1.2000	13.64
18	ILASDIRFC	273	1.2000	13.64
19	MRIATAYPN	109	1.1000	12.50
20	LDYDCPRSA	214	1.1000	12.50
21	LMLDYDCPR	212	1.0000	11.36

22	WVAIRALVP	246	1.0000	11.36
23	LAGMRIATA	106	0.9000	10.23
24	FFLRPKDIA	45	0.8000	9.09
25	VAFGEPLCD	167	0.8000	9.09
26	VPRRDVNGI	253	0.7000	7.95
27	FFFLRPKDI	44	0.5000	5.68
28	LGFGSSSFR	84	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRLDGAVEI	133	3.3800	39.30
2	WVAIRALVP	246	2.3000	26.74
3	FRYAAPAGR	91	2.0000	23.26
4	IERAGTDGQ	181	1.9000	22.09
5	FFFLRPKDI	44	1.8000	20.93
6	VRKDLATKG	119	1.5000	17.44
7	LRVAVPNKG	1	1.3000	15.12
8	VGSGRTLSQ	155	1.2000	13.95
9	YVGSGELDF	55	0.4000	4.65
10	LMLDYDCPR	212	0.4000	4.65
11	LVCDSGAQV	70	0.3000	3.49
12	VVGSGRTLS	154	0.3000	3.49
13	MRIATAYPN	109	0.1000	1.16
14	YLMLDYDCP	211	0.1000	1.16
15	VEISVQLGV	139	-0.1000	0
16	VNGIMDELA	258	-0.1000	0
17	MLRVAVPNK	0	-0.3000	0
18	ILASDIRFC	273	-0.5000	0
19	FGITGRDLV	63	-0.7000	0
20	FGQQYLMLD	207	-0.7000	0
21	IMDELAAIG	261	-0.7000	0
22	FGSSSFRYA	86	-0.8000	0

23	LAAIGAKAI	265	-0.8000	0
24	IRALVPRRD	249	-0.9000	0
25	IGAKAILAS	268	-0.9000	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	VGSGRTLSQ	155	3.4000	35.42
2	MRIATAYPN	109	3.2000	33.33
3	VPRRDVNGI	253	2.4000	25.00
4	LRVAVPNKG	1	2.3000	23.96
5	IGAKAILAS	268	2.2000	22.92
6	VRERLALGF	78	2.0000	20.83
7	IRALVPRRD	249	1.6000	16.67
8	ILASDIRFC	273	1.6000	16.67
9	VEFFFLRPK	42	1.5000	15.62
10	LRPKDIAIY	47	1.5000	15.62
11	LVRKDLATK	118	1.5000	15.62
12	LVPRRDVNG	252	1.5000	15.62
13	VVFGQQYLM	205	1.2000	12.50
14	IERAGTDGQ	181	1.1000	11.46
15	FRYAAPAGR	91	1.0000	10.42
16	WVAIRALVP	246	0.8800	9.17
17	IRLDGAVEI	133	0.8000	8.33
18	LAGMRIATA	106	0.7000	7.29
19	MLRVAVPNK	0	0.6000	6.25
20	VAIRALVPR	247	0.6000	6.25
21	LKKATAITP	223	0.3000	3.12
22	LGFGSSSFR	84	0.2000	2.08
23	IATAYPNLV	111	-0.1000	0
24	LGVADAIAD	145	-0.2000	0
25	LAAIGAKAI	265	-0.2200	0
26	YRRRTDSKD	24	-0.3000	0

27	FFFLRPKDI	44	-0.3000	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	LRVAVPNKG	1	2.4000	27.27
2	MRIATAYPN	109	2.1000	23.86
3	IERAGTDGQ	181	2.0000	22.73
4	LAGMRIATA	106	1.9000	21.59
5	MLRVAVPNK	0	1.8000	20.45
6	IRLDGAVEI	133	1.7000	19.32
7	WVAIRALVP	246	1.2000	13.64
8	FRYAAPAGR	91	1.0000	11.36
9	VGSGRTLSQ	155	1.0000	11.36
10	IRALVPRRD	249	0.6000	6.82
11	VRKDLATKG	119	0.5000	5.68
12	VVGSGRTLS	154	0.3000	3.41
13	VNGIMDELA	258	0.3000	3.41
14	LTVIDPVNN	33	0.1000	1.14
15	VQGVVFGQQ	202	0.1000	1.14
16	LRPKDIAIY	47	-0.1000	0
17	LVRKDLATK	118	-0.1000	0
18	IGAKAILAS	268	-0.1000	0
19	LKKATAITP	223	-0.1200	0
20	IDPVNNVEF	36	-0.3000	0
21	LVAFGEPLC	166	-0.3000	0
22	VNNVEFFFL	39	-0.3500	0
23	VEFFFLRPK	42	-0.4000	0
24	VIRLDGAVE	132	-0.4000	0
25	LAAIGAKAI	265	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MRIATAYPN	109	3.1000	32.98
2	LRVAVPNKG	1	2.7000	28.72
3	WVAIRALVP	246	2.6000	27.66
4	IRALVPRRD	249	2.3000	24.47
5	FRYAAPAGR	91	2.0000	21.28
6	IERAGTDGQ	181	1.8000	19.15
7	VIRLDGAVE	132	1.6000	17.02
8	FFFLRPKDI	44	1.2000	12.77
9	LTVIDPVNN	33	1.1000	11.70
10	FGQQYLMLD	207	1.1000	11.70
11	LGVADAIAD	145	1.0800	11.49
12	YRRRTDSKD	24	0.9000	9.57
13	LAGMRIATA	106	0.9000	9.57
14	IRLDGAVEI	133	0.9000	9.57
15	VIDPVNNVE	35	0.8000	8.51
16	VRKDLATKG	119	0.8000	8.51
17	VGSGRTLSQ	155	0.8000	8.51
18	IAIYVGSGE	52	0.4000	4.26
19	VLIERAGTD	179	0.2000	2.13
20	MLRVAVPNK	0	0.1000	1.06
21	VQGVVFGQQ	202	-0.1000	0
22	YLMLDYDCP	211	-0.2000	0
23	VNNVEFFFL	39	-0.3500	0
24	IDPVNNVEF	36	-0.4000	0
25	WTTADLAGM	101	-0.4000	0
26	YVGSGELDF	55	-0.6000	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	WVAIRALVP	246	2.2000	25.00
2	FRYAAPAGR	91	2.0000	22.73
3	LRVAVPNKG	1	1.4000	15.91
4	MRIATAYPN	109	1.1000	12.50
5	FFFLRPKDI	44	1.0000	11.36
6	IERAGTDGQ	181	1.0000	11.36
7	LAGMRIATA	106	0.9000	10.23
8	MLRVAVPNK	0	0.8000	9.09
9	IRLDGAVEI	133	0.7000	7.95
10	IRALVPRRD	249	-0.4000	0
11	VRKDLATKG	119	-0.5000	0
12	YLMLDYDCP	211	-0.6000	0
13	VVGSGRTLS	154	-0.7000	0
14	VNGIMDELA	258	-0.7000	0
15	LTVIDPVNN	33	-0.9000	0
16	VQGVVFGQQ	202	-0.9000	0
17	FLRPKDIAI	46	-0.9200	0
18	IATAYPNLV	111	-1.0000	0
19	LRPKDIAIY	47	-1.1000	0
20	LVRKDLATK	118	-1.1000	0
21	IGAKAILAS	268	-1.1000	0
22	LKKATAITP	223	-1.1200	0
23	IDPVNNVEF	36	-1.3000	0
24	LVAFGEPLC	166	-1.3000	0
25	VNNVEFFFL	39	-1.3500	0
26	VEFFFLRPK	42	-1.4000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MRIATAYPN	109	4.1000	43.62
2	LRVAVPNKG	1	3.7000	39.36

3	IRALVPRRD	249	3.3000	35.11
4	IERAGTDGQ	181	2.8000	29.79
5	VIRLDGAVE	132	2.6000	27.66
6	LTVIDPVNN	33	2.1000	22.34
7	LGVADAIAD	145	2.0800	22.13
8	LAGMRIATA	106	1.9000	20.21
9	IRLDGAVEI	133	1.9000	20.21
10	VIDPVNNVE	35	1.8000	19.15
11	VRKDLATKG	119	1.8000	19.15
12	VGSGRTLSQ	155	1.8000	19.15
13	WVAIRALVP	246	1.6000	17.02
14	IAIYVGSGE	52	1.4000	14.89
15	VLIERAGTD	179	1.2000	12.77
16	MLRVAVPNK	0	1.1000	11.70
17	LRPKDIAIY	47	1.0000	10.64
18	FRYAAPAGR	91	1.0000	10.64
19	VQGVVFGQQ	202	0.9000	9.57
20	VNNVEFFFL	39	0.6500	6.91
21	IDPVNNVEF	36	0.6000	6.38
22	IATAYPNLV	111	0.3000	3.19
23	VVGSGRTLS	154	0.3000	3.19
24	VNGIMDELA	258	0.3000	3.19
25	LKKATAITP	223	0.2800	2.98
26	FFFLRPKDI	44	0.2000	2.13
27	VPNKGALSE	5	0.1000	1.06
28	FGQQYLMLD	207	0.1000	1.06

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	IRLDGAVEI	133	4.2800	47.56
2	FRYAAPAGR	91	3.5000	38.89
3	WVAIRALVP	246	3.3000	36.67

4	VRKDLATKG	119	2.9000	32.22
5	LRVAVPNKG	1	2.7000	30.00
6	FFFLRPKDI	44	2.7000	30.00
7	YVGSGELDF	55	2.3000	25.56
8	LMLDYDCPR	212	1.9000	21.11
9	LVCDSGAQV	70	1.3000	14.44
10	IERAGTDGQ	181	1.2000	13.33
11	VLIERAGTD	179	1.1000	12.22
12	YLMLDYDCP	211	1.1000	12.22
13	MRIATAYPN	109	0.9000	10.00
14	VEISVQLGV	139	0.9000	10.00
15	VVGSGRTLS	154	0.7000	7.78
16	IMDELAAIG	261	0.7000	7.78
17	VGSGRTLSQ	155	0.5000	5.56
18	FGQQYLMLD	207	0.4000	4.44
19	FGITGRDLV	63	0.3000	3.33
20	IRALVPRRD	249	0.2000	2.22
21	LAAIGAKAI	265	0.1000	1.11
22	VFGQQYLML	206	-0.0400	0
23	IATAYPNLV	111	-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	LRVAVPNKG	1	2.4000	27.27
2	MRIATAYPN	109	2.1000	23.86
3	IERAGTDGQ	181	2.0000	22.73
4	LAGMRIATA	106	1.9000	21.59
5	MLRVAVPNK	0	1.8000	20.45
6	IRLDGAVEI	133	1.7000	19.32
7	WVAIRALVP	246	1.2000	13.64
8	FRYAAPAGR	91	1.0000	11.36
9	VGSGRTLSQ	155	1.0000	11.36

10	IRALVPRRD	249	0.6000	6.82
11	VRKDLATKG	119	0.5000	5.68
12	VVGSGRTLS	154	0.3000	3.41
13	VNGIMDELA	258	0.3000	3.41
14	LTVIDPVNN	33	0.1000	1.14
15	VQGVVFGQQ	202	0.1000	1.14
16	LRPKDIAIY	47	-0.1000	0
17	LVRKDLATK	118	-0.1000	0
18	IGAKAILAS	268	-0.1000	0
19	LKKATAITP	223	-0.1200	0
20	IDPVNNVEF	36	-0.3000	0
21	LVAFGEPLC	166	-0.3000	0
22	VNNVEFFFL	39	-0.3500	0
23	VEFFFLRPK	42	-0.4000	0
24	VIRLDGAVE	132	-0.4000	0
25	LAAIGAKAI	265	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRLDGAVEI	133	3.3800	39.30
2	WVAIRALVP	246	2.3000	26.74
3	FRYAAPAGR	91	2.0000	23.26
4	IERAGTDGQ	181	1.9000	22.09
5	FFFLRPKDI	44	1.8000	20.93
6	VRKDLATKG	119	1.5000	17.44
7	LRVAVPNKG	1	1.3000	15.12
8	VGSGRTLSQ	155	1.2000	13.95
9	YVGSGELDF	55	0.4000	4.65
10	LMLDYDCPR	212	0.4000	4.65
11	LVCDSGAQV	70	0.3000	3.49
12	VVGSGRTLS	154	0.3000	3.49
13	MRIATAYPN	109	0.1000	1.16

14	YLMLDYDCP	211	0.1000	1.16
15	VEISVQLGV	139	-0.1000	0
16	VNGIMDELA	258	-0.1000	0
17	MLRVAVPNK	0	-0.3000	0
18	ILASDIRFC	273	-0.5000	0
19	FGITGRDLV	63	-0.7000	0
20	FGQQYLMLD	207	-0.7000	0
21	IMDELAAIG	261	-0.7000	0
22	FGSSSFRYA	86	-0.8000	0
23	LAAIGAKAI	265	-0.8000	0
24	IRALVPRRD	249	-0.9000	0
25	IGAKAILAS	268	-0.9000	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	VNNVEFFFL	39	5.9000	50.86
2	YVGSGELDF	55	5.6000	48.28
3	IRLDGAVEI	133	5.6000	48.28
4	VEISVQLGV	139	5.2000	44.83
5	WVAIRALVP	246	4.8000	41.38
6	FFFLRPKDI	44	4.2000	36.21
7	LCDSEAVLI	173	4.2000	36.21
8	LAAIGAKAI	265	4.0000	34.48
9	MRIATAYPN	109	3.9000	33.62
10	FLRPKDIAI	46	3.8000	32.76
11	VARVQGVVF	199	3.7000	31.90
12	VVFGQQYLM	205	3.4000	29.31
13	VRERLALGF	78	3.2000	27.59
14	VFGQQYLML	206	3.1000	26.72
15	FGITGRDLV	63	3.0000	25.86
16	VPRRDVNGI	253	3.0000	25.86
17	VVGSGRTLS	154	2.3000	19.83

18	VQLGVADAI	143	2.2000	18.97
19	FGSSSFRYA	86	2.1000	18.10
20	LRVAVPNKG	1	2.0000	17.24
21	IDPVNNVEF	36	2.0000	17.24
22	YPNLVRKDL	115	2.0000	17.24
23	IATAYPNLV	111	1.9000	16.38
24	LKKATAITP	223	1.9000	16.38
25	FRYAAPAGR	91	1.7000	14.66
26	ILASDIRFC	273	1.7000	14.66
27	LSQHDLVAF	161	1.6000	13.79
28	LTVIDPVNN	33	1.2000	10.34

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	VNNVEFFFL	39	5.9000	50.86
2	YVGSGELDF	55	5.6000	48.28
3	IRLDGAVEI	133	5.6000	48.28
4	VEISVQLGV	139	5.2000	44.83
5	WVAIRALVP	246	4.8000	41.38
6	FFFLRPKDI	44	4.2000	36.21
7	LCDSEAVLI	173	4.2000	36.21
8	LAAIGAKAI	265	4.0000	34.48
9	MRIATAYPN	109	3.9000	33.62
10	FLRPKDIAI	46	3.8000	32.76
11	VARVQGVVF	199	3.7000	31.90
12	VVFGQQYLM	205	3.4000	29.31
13	VRERLALGF	78	3.2000	27.59
14	VFGQQYLML	206	3.1000	26.72
15	FGITGRDLV	63	3.0000	25.86
16	VPRRDVNGI	253	3.0000	25.86
17	VVGSGRTLS	154	2.3000	19.83
18	VQLGVADAI	143	2.2000	18.97

19	FGSSSFRYA	86	2.1000	18.10
20	LRVAVPNKG	1	2.0000	17.24
21	IDPVNNVEF	36	2.0000	17.24
22	YPNLVRKDL	115	2.0000	17.24
23	IATAYPNLV	111	1.9000	16.38
24	LKKATAITP	223	1.9000	16.38
25	FRYAAPAGR	91	1.7000	14.66
26	ILASDIRFC	273	1.7000	14.66
27	LSQHDLVAF	161	1.6000	13.79
28	LTVIDPVNN	33	1.2000	10.34

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	LRPKDIAIY	47	4.6000	53.49
2	LVRKDLATK	118	3.3000	38.37
3	FFLRPKDIA	45	3.0000	34.88
4	IGAKAILAS	268	2.9000	33.72
5	IRALVPRRD	249	2.8000	32.56
6	YRRRTDSKD	24	2.5000	29.07
7	FRYAAPAGR	91	2.5000	29.07
8	VPNKGALSE	5	2.3000	26.74
9	MRIATAYPN	109	2.2000	25.58
10	LVARVQGVV	198	2.2000	25.58
11	VIRLDGAVE	132	2.1000	24.42
12	IAIYVGSGE	52	2.0000	23.26
13	FFFLRPKDI	44	1.9000	22.09
14	VRERLALGF	78	1.9000	22.09
15	ITGRDLVCD	65	1.6000	18.60
16	LAGMRIATA	106	1.3000	15.12
17	VPRRDVNGI	253	1.3000	15.12
18	LRVAVPNKG	1	1.2000	13.95
19	WVAIRALVP	246	1.2000	13.95

20	VLIERAGTD	179	1.0000	11.63
21	WTTADLAGM	101	0.9000	10.47
22	YPNLVRKDL	115	0.9000	10.47
23	VAIRALVPR	247	0.9000	10.47
24	VGSGRTLSQ	155	0.5000	5.81
25	LVPRRDVNG	252	0.5000	5.81
26	FGQQYLMLD	207	0.4000	4.65
27	MLDYDCPRS	213	0.4000	4.65
28	LGVADAIAD	145	0.2000	2.33

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	LVRKDLATK	118	4.0000	50.00
2	LRPKDIAIY	47	3.5000	43.75
3	FFLRPKDIA	45	3.0000	37.50
4	IGAKAILAS	268	2.9000	36.25
5	FRYAAPAGR	91	2.5000	31.25
6	LVARVQGVV	198	1.9000	23.75
7	FFFLRPKDI	44	1.7000	21.25
8	LAGMRIATA	106	1.3000	16.25
9	VPRRDVNGI	253	1.1000	13.75
10	VRERLALGF	78	1.0000	12.50
11	VAIRALVPR	247	0.9000	11.25
12	WVAIRALVP	246	0.8000	10.00
13	MLRVAVPNK	0	0.7000	8.75
14	MLDYDCPRS	213	0.4000	5.00
15	MRIATAYPN	109	0.2000	2.50
16	IRALVPRRD	249	0.1000	1.25
17	LRVAVPNKG	1	-0.1000	0
18	YPNLVRKDL	115	-0.1000	0
19	YRRRTDSKD	24	-0.2000	0
20	WTTADLAGM	101	-0.2000	0

21	IRLDGAVEI	133	-0.2000	0
22	VEFFFLRPK	42	-0.3000	0
23	VGSGRTLSQ	155	-0.3000	0
24	VVGSGRTLS	154	-0.4000	0
25	VPNKGALSE	5	-0.7000	0
26	VQGVVFGQQ	202	-0.7000	0
27	LVPRRDVNG	252	-0.8000	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	LVRKDLATK	118	5.0000	62.50
2	LRPKDIAIY	47	4.5000	56.25
3	IGAKAILAS	268	3.9000	48.75
4	LVARVQGVV	198	2.9000	36.25
5	LAGMRIATA	106	2.3000	28.75
6	VPRRDVNGI	253	2.1000	26.25
7	FFLRPKDIA	45	2.0000	25.00
8	VRERLALGF	78	2.0000	25.00
9	VAIRALVPR	247	1.9000	23.75
10	MLRVAVPNK	0	1.7000	21.25
11	FRYAAPAGR	91	1.5000	18.75
12	MLDYDCPRS	213	1.4000	17.50
13	MRIATAYPN	109	1.2000	15.00
14	IRALVPRRD	249	1.1000	13.75
15	LRVAVPNKG	1	0.9000	11.25
16	IRLDGAVEI	133	0.8000	10.00
17	VEFFFLRPK	42	0.7000	8.75
18	FFFLRPKDI	44	0.7000	8.75
19	VGSGRTLSQ	155	0.7000	8.75
20	VVGSGRTLS	154	0.6000	7.50
21	VPNKGALSE	5	0.3000	3.75
22	VQGVVFGQQ	202	0.3000	3.75

23	LVPRRDVNG	252	0.2000	2.50
24	VIRLDGAVE	132	0.1000	1.25
25	VVFGQQYLM	205	0.1000	1.25
26	ILASDIRFC	273	0.1000	1.25

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRPKDIAIY	47	5.6000	65.12
2	LVRKDLATK	118	4.3000	50.00
3	IGAKAILAS	268	3.9000	45.35
4	IRALVPRRD	249	3.8000	44.19
5	VPNKGALSE	5	3.3000	38.37
6	MRIATAYPN	109	3.2000	37.21
7	LVARVQGVV	198	3.2000	37.21
8	VIRLDGAVE	132	3.1000	36.05
9	IAIYVGSGE	52	3.0000	34.88
10	VRERLALGF	78	2.9000	33.72
11	ITGRDLVCD	65	2.6000	30.23
12	LAGMRIATA	106	2.3000	26.74
13	VPRRDVNGI	253	2.3000	26.74
14	LRVAVPNKG	1	2.2000	25.58
15	FFLRPKDIA	45	2.0000	23.26
16	VLIERAGTD	179	2.0000	23.26
17	VAIRALVPR	247	1.9000	22.09
18	YRRRTDSKD	24	1.5000	17.44
19	FRYAAPAGR	91	1.5000	17.44
20	VGSGRTLSQ	155	1.5000	17.44
21	LVPRRDVNG	252	1.5000	17.44
22	MLDYDCPRS	213	1.4000	16.28
23	LGVADAIAD	145	1.2000	13.95
24	VVFGQQYLM	205	1.2000	13.95
25	VQGVVFGQQ	202	1.1000	12.79

26	MLRVAVPNK	0	1.0000	11.63
27	IRLDGAVEI	133	1.0000	11.63
28	VAFGEPLCD	167	1.0000	11.63

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	FFLRPKDIA	45	4.2000	48.28
2	LVRKDLATK	118	4.0000	45.98
3	LRPKDIAIY	47	3.5000	40.23
4	IGAKAILAS	268	3.5000	40.23
5	VPRRDVNGI	253	3.1000	35.63
6	FRYAAPAGR	91	2.5000	28.74
7	VVGSGRTLS	154	2.4000	27.59
8	LRVAVPNKG	1	1.9000	21.84
9	VAIRALVPR	247	1.9000	21.84
10	YRRRTDSKD	24	1.6000	18.39
11	VRERLALGF	78	1.6000	18.39
12	WVAIRALVP	246	1.4000	16.09
13	LAGMRIATA	106	1.3000	14.94
14	FFFLRPKDI	44	1.2000	13.79
15	LVARVQGVV	198	1.2000	13.79
16	MRIATAYPN	109	1.1000	12.64
17	MLRVAVPNK	0	0.9000	10.34
18	IAIYVGSGE	52	0.8000	9.20
19	IRLDGAVEI	133	0.8000	9.20
20	MLDYDCPRS	213	0.6000	6.90
21	VGSGRTLSQ	155	0.3000	3.45
22	LVPRRDVNG	252	0.2000	2.30
23	FGITGRDLV	63	0.1000	1.15
24	LATKGIEAT	123	0.1000	1.15
25	VPNKGALSE	5	-0.1000	0
26	ITGRDLVCD	65	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IGAKAILAS	268	4.7000	46.53
2	LRPKDIAIY	47	4.6000	45.54
3	VPNKGALSE	5	4.1000	40.59
4	VRERLALGF	78	3.7000	36.63
5	LVRKDLATK	118	3.3000	32.67
6	WVAIRALVP	246	3.0000	29.70
7	IRALVPRRD	249	3.0000	29.70
8	MRIATAYPN	109	2.9000	28.71
9	FFLRPKDIA	45	2.7000	26.73
10	YRRRTDSKD	24	2.5000	24.75
11	FFFLRPKDI	44	2.5000	24.75
12	FRYAAPAGR	91	2.5000	24.75
13	VGSGRTLSQ	155	2.3000	22.77
14	LVARVQGVV	198	2.3000	22.77
15	ITGRDLVCD	65	2.1000	20.79
16	VIRLDGAVE	132	2.1000	20.79
17	IAIYVGSGE	52	2.0000	19.80
18	FGQQYLMLD	207	2.0000	19.80
19	LGVADAIAD	145	1.8000	17.82
20	VAFGEPLCD	167	1.8000	17.82
21	VPRRDVNGI	253	1.6000	15.84
22	MLDYDCPRS	213	1.5500	15.35
23	LRVAVPNKG	1	1.5000	14.85
24	YPNLVRKDL	115	1.5000	14.85
25	VAIRALVPR	247	1.4000	13.86
26	YVGSGELDF	55	1.3000	12.87
27	LAGMRIATA	106	1.3000	12.87
28	MLRVAVPNK	0	1.1500	11.39

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	WVAIRALVP	246	3.2000	38.55
2	FFFLRPKDI	44	2.7000	32.53
3	FRYAAPAGR	91	2.5000	30.12
4	MLRVAVPNK	0	1.9500	23.49
5	IGAKAILAS	268	1.9000	22.89
6	LVRKDLATK	118	1.2000	14.46
7	VVGSGRTLS	154	1.0000	12.05
8	LAGMRIATA	106	0.9000	10.84
9	MRIATAYPN	109	0.9000	10.84
10	YPNLVRKDL	115	0.9000	10.84
11	VGSGRTLSQ	155	0.8000	9.64
12	LRPKDIAIY	47	0.7000	8.43
13	YVGSGELDF	55	0.7000	8.43
14	IRALVPRRD	249	0.7000	8.43
15	VEISVQLGV	139	0.4000	4.82
16	LRVAVPNKG	1	0.2000	2.41
17	LVAFGEPLC	166	0.0500	0.60
18	FGQQYLMLD	207	-0.1000	0
19	VEFFFLRPK	42	-0.2000	0
20	VRERLALGF	78	-0.2000	0
21	WTTADLAGM	101	-0.2000	0
22	FFLRPKDIA	45	-0.3000	0
23	IRLDGAVEI	133	-0.4000	0
24	LKKATAITP	223	-0.4000	0
25	ILASDIRFC	273	-0.4000	0
26	VIRLDGAVE	132	-0.5000	0
27	VQGVVFGQQ	202	-0.5000	0

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

	1.8	

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRKDLATK	118	3.5000	41.67
2	IGAKAILAS	268	3.1000	36.90
3	LRPKDIAIY	47	3.0000	35.71
4	VEFFFLRPK	42	2.8000	33.33
5	IRALVPRRD	249	2.6000	30.95
6	VVGSGRTLS	154	2.5000	29.76
7	LRVAVPNKG	1	2.3000	27.38
8	ILASDIRFC	273	2.3000	27.38
9	MRIATAYPN	109	2.1000	25.00
10	LAGMRIATA	106	1.7000	20.24
11	FRYAAPAGR	91	1.5000	17.86
12	IRLDGAVEI	133	1.4000	16.67
13	VPRRDVNGI	253	1.4000	16.67
14	MLRVAVPNK	0	1.2000	14.29
15	FFFLRPKDI	44	1.2000	14.29
16	LVAFGEPLC	166	1.0000	11.90
17	VGSGRTLSQ	155	0.9000	10.71
18	FFLRPKDIA	45	0.8000	9.52
19	VAIRALVPR	247	0.8000	9.52
20	VRERLALGF	78	0.6000	7.14
21	IERAGTDGQ	181	0.6000	7.14
22	VVFGQQYLM	205	0.5000	5.95
23	VEISVQLGV	139	0.4000	4.76
24	LSQHDLVAF	161	0.3000	3.57
25	MLDYDCPRS	213	0.3000	3.57
26	IATAYPNLV	111	-0.1000	0
27	VIRLDGAVE	132	-0.2000	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	MLRVAVPNK	0	2.9500	35.54
2	IGAKAILAS	268	2.9000	34.94
3	LVRKDLATK	118	2.2000	26.51
4	WVAIRALVP	246	2.2000	26.51
5	VVGSGRTLS	154	2.0000	24.10
6	LAGMRIATA	106	1.9000	22.89
7	MRIATAYPN	109	1.9000	22.89
8	VGSGRTLSQ	155	1.8000	21.69
9	FFFLRPKDI	44	1.7000	20.48
10	LRPKDIAIY	47	1.7000	20.48
11	IRALVPRRD	249	1.7000	20.48
12	FRYAAPAGR	91	1.5000	18.07
13	VEISVQLGV	139	1.4000	16.87
14	LRVAVPNKG	1	1.2000	14.46
15	LVAFGEPLC	166	1.0500	12.65
16	VEFFFLRPK	42	0.8000	9.64
17	VRERLALGF	78	0.8000	9.64
18	IRLDGAVEI	133	0.6000	7.23
19	LKKATAITP	223	0.6000	7.23
20	ILASDIRFC	273	0.6000	7.23
21	VIRLDGAVE	132	0.5000	6.02
22	VQGVVFGQQ	202	0.5000	6.02
23	LAAIGAKAI	265	0.4000	4.82
24	LGVADAIAD	145	0.1000	1.20
25	VVFGQQYLM	205	0.1000	1.20
26	LTVIDPVNN	33	-0.1000	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	MLRVAVPNK	0	2.9500	35.54
2	IGAKAILAS	268	2.9000	34.94

3	LVRKDLATK	118	2.2000	26.51
4	WVAIRALVP	246	2.2000	26.51
5	VVGSGRTLS	154	2.0000	24.10
6	LAGMRIATA	106	1.9000	22.89
7	MRIATAYPN	109	1.9000	22.89
8	VGSGRTLSQ	155	1.8000	21.69
9	FFFLRPKDI	44	1.7000	20.48
10	LRPKDIAIY	47	1.7000	20.48
11	IRALVPRRD	249	1.7000	20.48
12	FRYAAPAGR	91	1.5000	18.07
13	VEISVQLGV	139	1.4000	16.87
14	LRVAVPNKG	1	1.2000	14.46
15	LVAFGEPLC	166	1.0500	12.65
16	VEFFFLRPK	42	0.8000	9.64
17	VRERLALGF	78	0.8000	9.64
18	IRLDGAVEI	133	0.6000	7.23
19	LKKATAITP	223	0.6000	7.23
20	ILASDIRFC	273	0.6000	7.23
21	VIRLDGAVE	132	0.5000	6.02
22	VQGVVFGQQ	202	0.5000	6.02
23	LAAIGAKAI	265	0.4000	4.82
24	LGVADAIAD	145	0.1000	1.20
25	VVFGQQYLM	205	0.1000	1.20
26	LTVIDPVNN	33	-0.1000	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	IRLDGAVEI	133	5.4000	59.34
2	VVGSGRTLS	154	4.6000	50.55
3	VRKDLATKG	119	3.4000	37.36
4	MLRVAVPNK	0	3.3000	36.26
5	LVCDSGAQV	70	3.0000	32.97

6	LASDIRFCR	274	3.0000	32.97
7	VGSGRTLSQ	155	2.7000	29.67
8	VVFGQQYLM	205	2.6500	29.12
9	MRIATAYPN	109	2.2500	24.73
10	LRVAVPNKG	1	2.1100	23.19
11	VQLGVADAI	143	1.8000	19.78
12	LVRKDLATK	118	1.7000	18.68
13	LALGFGSSS	82	1.5700	17.25
14	FRYAAPAGR	91	1.5000	16.48
15	VEISVQLGV	139	1.5000	16.48
16	IERAGTDGQ	181	1.5000	16.48
17	ILASDIRFC	273	1.5000	16.48
18	LDYDCPRSA	214	1.4000	15.38
19	LRPKDIAIY	47	1.2000	13.19
20	IGAKAILAS	268	1.1000	12.09
21	LMLDYDCPR	212	1.0000	10.99
22	LAGMRIATA	106	0.9000	9.89
23	LGFGSSSFR	84	0.7700	8.46
24	VQGVVFGQQ	202	0.6000	6.59
25	FFLRPKDIA	45	0.5000	5.49
26	WVAIRALVP	246	0.5000	5.49
27	LVAFGEPLC	166	0.4000	4.40
28	LTVIDPVNN	33	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	FRYAAPAGR	91	2.5000	29.76
2	LVRKDLATK	118	2.5000	29.76
3	FFFLRPKDI	44	2.2000	26.19
4	IGAKAILAS	268	2.1000	25.00
5	LRPKDIAIY	47	2.0000	23.81
6	VEFFFLRPK	42	1.8000	21.43

7	FFLRPKDIA	45	1.8000	21.43
8	IRALVPRRD	249	1.6000	19.05
9	VVGSGRTLS	154	1.5000	17.86
10	LRVAVPNKG	1	1.3000	15.48
11	ILASDIRFC	273	1.3000	15.48
12	MRIATAYPN	109	1.1000	13.10
13	LAGMRIATA	106	0.7000	8.33
14	WVAIRALVP	246	0.6000	7.14
15	YPNLVRKDL	115	0.4000	4.76
16	IRLDGAVEI	133	0.4000	4.76
17	VPRRDVNGI	253	0.4000	4.76
18	MLRVAVPNK	0	0.2000	2.38
19	FGSSSFRYA	86	-0.1000	0
20	VGSGRTLSQ	155	-0.1000	0
21	WTTADLAGM	101	-0.2000	0
22	VAIRALVPR	247	-0.2000	0
23	YVGSGELDF	55	-0.3000	0
24	FGITGRDLV	63	-0.3000	0
25	VRERLALGF	78	-0.4000	0
26	IERAGTDGQ	181	-0.4000	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	FRYAAPAGR	91	4.0000	45.45
2	LRPKDIAIY	47	3.3000	37.50
3	FFFLRPKDI	44	3.1000	35.23
4	LRVAVPNKG	1	2.7000	30.68
5	IRALVPRRD	249	2.7000	30.68
6	LVRKDLATK	118	2.6000	29.55
7	IGAKAILAS	268	2.5000	28.41
8	VEFFFLRPK	42	1.9000	21.59
9	MRIATAYPN	109	1.9000	21.59

10	VVGSGRTLS	154	1.9000	21.59
11	FFLRPKDIA	45	1.8000	20.45
12	YVGSGELDF	55	1.6000	18.18
13	WVAIRALVP	246	1.6000	18.18
14	VRERLALGF	78	1.5000	17.05
15	YPNLVRKDL	115	1.3600	15.45
16	WTTADLAGM	101	1.3000	14.77
17	IRLDGAVEI	133	1.3000	14.77
18	VAIRALVPR	247	1.3000	14.77
19	VPRRDVNGI	253	1.3000	14.77
20	ILASDIRFC	273	1.3000	14.77
21	LSQHDLVAF	161	1.2000	13.64
22	VVFGQQYLM	205	1.0000	11.36
23	FGITGRDLV	63	0.7000	7.95
24	LAGMRIATA	106	0.7000	7.95
25	FGQQYLMLD	207	0.7000	7.95
26	VEISVQLGV	139	0.4000	4.55
27	MLRVAVPNK	0	0.3000	3.41
28	VIRLDGAVE	132	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	LVRKDLATK	118	3.5000	41.67
2	IGAKAILAS	268	3.1000	36.90
3	LRPKDIAIY	47	3.0000	35.71
4	VEFFFLRPK	42	2.8000	33.33
5	IRALVPRRD	249	2.6000	30.95
6	VVGSGRTLS	154	2.5000	29.76
7	LRVAVPNKG	1	2.3000	27.38
8	ILASDIRFC	273	2.3000	27.38
9	MRIATAYPN	109	2.1000	25.00
10	LAGMRIATA	106	1.7000	20.24

11	FRYAAPAGR	91	1.5000	17.86
12	IRLDGAVEI	133	1.4000	16.67
13	VPRRDVNGI	253	1.4000	16.67
14	MLRVAVPNK	0	1.2000	14.29
15	FFFLRPKDI	44	1.2000	14.29
16	LVAFGEPLC	166	1.0000	11.90
17	VGSGRTLSQ	155	0.9000	10.71
18	FFLRPKDIA	45	0.8000	9.52
19	VAIRALVPR	247	0.8000	9.52
20	VRERLALGF	78	0.6000	7.14
21	IERAGTDGQ	181	0.6000	7.14
22	VVFGQQYLM	205	0.5000	5.95
23	VEISVQLGV	139	0.4000	4.76
24	LSQHDLVAF	161	0.3000	3.57
25	MLDYDCPRS	213	0.3000	3.57
26	IATAYPNLV	111	-0.1000	0
27	VIRLDGAVE	132	-0.2000	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	WVAIRALVP	246	4.2000	48.28
2	FRYAAPAGR	91	4.0000	45.98
3	FFFLRPKDI	44	3.6000	41.38
4	YVGSGELDF	55	2.6000	29.89
5	IGAKAILAS	268	2.3000	26.44
6	MLRVAVPNK	0	2.0500	23.56
7	LRPKDIAIY	47	2.0000	22.99
8	YPNLVRKDL	115	1.8600	21.38
9	IRALVPRRD	249	1.8000	20.69
10	VRERLALGF	78	1.7000	19.54
11	MRIATAYPN	109	1.7000	19.54
12	LRVAVPNKG	1	1.6000	18.39

13	VEISVQLGV	139	1.4000	16.09
14	VVGSGRTLS	154	1.4000	16.09
15	WTTADLAGM	101	1.3000	14.94
16	LVRKDLATK	118	1.3000	14.94
17	FGQQYLMLD	207	1.0000	11.49
18	LAGMRIATA	106	0.9000	10.34
19	VIRLDGAVE	132	0.9000	10.34
20	VVFGQQYLM	205	0.6000	6.90
21	LKKATAITP	223	0.6000	6.90
22	IRLDGAVEI	133	0.5000	5.75
23	LAAIGAKAI	265	0.3000	3.45
24	LGVADAIAD	145	0.2000	2.30
25	VGSGRTLSQ	155	0.1000	1.15
26	LVAFGEPLC	166	0.0500	0.57

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	LRPKDIAIY	47	4.3000	48.86
2	LRVAVPNKG	1	3.7000	42.05
3	IRALVPRRD	249	3.7000	42.05
4	LVRKDLATK	118	3.6000	40.91
5	IGAKAILAS	268	3.5000	39.77
6	FRYAAPAGR	91	3.0000	34.09
7	VEFFFLRPK	42	2.9000	32.95
8	MRIATAYPN	109	2.9000	32.95
9	VVGSGRTLS	154	2.9000	32.95
10	VRERLALGF	78	2.5000	28.41
11	IRLDGAVEI	133	2.3000	26.14
12	VAIRALVPR	247	2.3000	26.14
13	VPRRDVNGI	253	2.3000	26.14
14	ILASDIRFC	273	2.3000	26.14
15	LSQHDLVAF	161	2.2000	25.00

16	FFFLRPKDI	44	2.1000	23.86
17	VVFGQQYLM	205	2.0000	22.73
18	LAGMRIATA	106	1.7000	19.32
19	VEISVQLGV	139	1.4000	15.91
20	MLRVAVPNK	0	1.3000	14.77
21	VIRLDGAVE	132	1.2000	13.64
22	LVAFGEPLC	166	1.0000	11.36
23	VPNKGALSE	5	0.9000	10.23
24	IATAYPNLV	111	0.9000	10.23
25	LASDIRFCR	274	0.9000	10.23
26	FFLRPKDIA	45	0.8000	9.09
27	LVARVQGVV	198	0.8000	9.09
28	MLDYDCPRS	213	0.7000	7.95

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	FRYAAPAGR	91	4.0000	45.45
2	LRPKDIAIY	47	3.3000	37.50
3	FFFLRPKDI	44	3.1000	35.23
4	LRVAVPNKG	1	2.7000	30.68
5	IRALVPRRD	249	2.7000	30.68
6	LVRKDLATK	118	2.6000	29.55
7	IGAKAILAS	268	2.5000	28.41
8	VEFFFLRPK	42	1.9000	21.59
9	MRIATAYPN	109	1.9000	21.59
10	VVGSGRTLS	154	1.9000	21.59
11	FFLRPKDIA	45	1.8000	20.45
12	YVGSGELDF	55	1.6000	18.18
13	WVAIRALVP	246	1.6000	18.18
14	VRERLALGF	78	1.5000	17.05
15	YPNLVRKDL	115	1.3600	15.45
16	WTTADLAGM	101	1.3000	14.77

17	IRLDGAVEI	133	1.3000	14.77
18	VAIRALVPR	247	1.3000	14.77
19	VPRRDVNGI	253	1.3000	14.77
20	ILASDIRFC	273	1.3000	14.77
21	LSQHDLVAF	161	1.2000	13.64
22	VVFGQQYLM	205	1.0000	11.36
23	FGITGRDLV	63	0.7000	7.95
24	LAGMRIATA	106	0.7000	7.95
25	FGQQYLMLD	207	0.7000	7.95
26	VEISVQLGV	139	0.4000	4.55
27	MLRVAVPNK	0	0.3000	3.41
28	VIRLDGAVE	132	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	IRALVPRRD	249	5.3000	58.89
2	LRPKDIAIY	47	4.1000	45.56
3	MRIATAYPN	109	4.1000	45.56
4	LRVAVPNKG	1	3.6000	40.00
5	IGAKAILAS	268	3.1000	34.44
6	LVRKDLATK	118	2.8000	31.11
7	VIRLDGAVE	132	2.8000	31.11
8	VPNKGALSE	5	2.5000	27.78
9	VVGSGRTLS	154	2.5000	27.78
10	ILASDIRFC	273	2.3000	25.56
11	VEFFFLRPK	42	2.1000	23.33
12	IEATVIRLD	128	1.9000	21.11
13	LAGMRIATA	106	1.7000	18.89
14	VGSGRTLSQ	155	1.7000	18.89
15	IAIYVGSGE	52	1.6000	17.78
16	IRLDGAVEI	133	1.6000	17.78
17	VVFGQQYLM	205	1.6000	17.78

18	VPRRDVNGI	253	1.6000	17.78
19	ITGRDLVCD	65	1.5000	16.67
20	VRERLALGF	78	1.5000	16.67
21	FRYAAPAGR	91	1.5000	16.67
22	LGVADAIAD	145	1.5000	16.67
23	FFFLRPKDI	44	1.4000	15.56
24	IERAGTDGQ	181	1.4000	15.56
25	FGQQYLMLD	207	1.3000	14.44
26	LSQHDLVAF	161	1.2000	13.33
27	VAFGEPLCD	167	1.2000	13.33
28	ISVQLGVAD	141	1.0000	11.11

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	WVAIRALVP	246	4.2000	48.28
2	FRYAAPAGR	91	4.0000	45.98
3	FFFLRPKDI	44	3.6000	41.38
4	YVGSGELDF	55	2.6000	29.89
5	IGAKAILAS	268	2.3000	26.44
6	MLRVAVPNK	0	2.0500	23.56
7	LRPKDIAIY	47	2.0000	22.99
8	YPNLVRKDL	115	1.8600	21.38
9	IRALVPRRD	249	1.8000	20.69
10	VRERLALGF	78	1.7000	19.54
11	MRIATAYPN	109	1.7000	19.54
12	LRVAVPNKG	1	1.6000	18.39
13	VEISVQLGV	139	1.4000	16.09
14	VVGSGRTLS	154	1.4000	16.09
15	WTTADLAGM	101	1.3000	14.94
16	LVRKDLATK	118	1.3000	14.94
17	FGQQYLMLD	207	1.0000	11.49
18	LAGMRIATA	106	0.9000	10.34

19	VIRLDGAVE	132	0.9000	10.34
20	VVFGQQYLM	205	0.6000	6.90
21	LKKATAITP	223	0.6000	6.90
22	IRLDGAVEI	133	0.5000	5.75
23	LAAIGAKAI	265	0.3000	3.45
24	LGVADAIAD	145	0.2000	2.30
25	VGSGRTLSQ	155	0.1000	1.15
26	LVAFGEPLC	166	0.0500	0.57

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	FRYAAPAGR	91	2.5000	36.76
2	FFFLRPKDI	44	2.1000	30.88
3	WVAIRALVP	246	1.4000	20.59
4	LVRKDLATK	118	1.2000	17.65
5	LAGMRIATA	106	0.9000	13.24
6	MLRVAVPNK	0	0.8000	11.76
7	LRPKDIAIY	47	0.7000	10.29
8	IRALVPRRD	249	0.5000	7.35
9	YPNLVRKDL	115	0.3000	4.41
10	MRIATAYPN	109	0.2000	2.94
11	IGAKAILAS	268	0.1000	1.47
12	LRVAVPNKG	1	-0.1000	0
13	VVGSGRTLS	154	-0.1000	0
14	WTTADLAGM	101	-0.2000	0
15	VEFFFLRPK	42	-0.4000	0
16	VIRLDGAVE	132	-0.5000	0
17	VQGVVFGQQ	202	-0.6000	0
18	ILASDIRFC	273	-0.6000	0
19	FGITGRDLV	63	-0.7000	0
20	IRLDGAVEI	133	-0.9000	0
21	VGSGRTLSQ	155	-1.0000	0

22	YVGSGELDF	55	-1.1000	0
23	LVAFGEPLC	166	-1.1000	0
24	LVARVQGVV	198	-1.1000	0
25	LAAIGAKAI	265	-1.2000	0
26	IERAGTDGQ	181	-1.3000	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	MLRVAVPNK	0	2.9500	35.54
2	IGAKAILAS	268	2.9000	34.94
3	LVRKDLATK	118	2.2000	26.51
4	WVAIRALVP	246	2.2000	26.51
5	VVGSGRTLS	154	2.0000	24.10
6	LAGMRIATA	106	1.9000	22.89
7	MRIATAYPN	109	1.9000	22.89
8	VGSGRTLSQ	155	1.8000	21.69
9	FFFLRPKDI	44	1.7000	20.48
10	LRPKDIAIY	47	1.7000	20.48
11	IRALVPRRD	249	1.7000	20.48
12	FRYAAPAGR	91	1.5000	18.07
13	VEISVQLGV	139	1.4000	16.87
14	LRVAVPNKG	1	1.2000	14.46
15	LVAFGEPLC	166	1.0500	12.65
16	VEFFFLRPK	42	0.8000	9.64
17	VRERLALGF	78	0.8000	9.64
18	IRLDGAVEI	133	0.6000	7.23
19	LKKATAITP	223	0.6000	7.23
20	ILASDIRFC	273	0.6000	7.23
21	VIRLDGAVE	132	0.5000	6.02
22	VQGVVFGQQ	202	0.5000	6.02
23	LAAIGAKAI	265	0.4000	4.82
24	LGVADAIAD	145	0.1000	1.20

25	VVFGQQYLM	205	0.1000	1.20
26	LTVIDPVNN	33	-0.1000	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	WVAIRALVP	246	3.6000	40.45
2	IRALVPRRD	249	3.4000	38.20
3	FFFLRPKDI	44	2.9000	32.58
4	MRIATAYPN	109	2.9000	32.58
5	FGQQYLMLD	207	2.6000	29.21
6	FRYAAPAGR	91	2.5000	28.09
7	VIRLDGAVE	132	2.5000	28.09
8	YPNLVRKDL	115	1.9000	21.35
9	IGAKAILAS	268	1.9000	21.35
10	LRPKDIAIY	47	1.8000	20.22
11	LGVADAIAD	145	1.8000	20.22
12	YVGSGELDF	55	1.6000	17.98
13	VGSGRTLSQ	155	1.6000	17.98
14	LRVAVPNKG	1	1.5000	16.85
15	VPNKGALSE	5	1.3000	14.61
16	MLRVAVPNK	0	1.2500	14.04
17	VAFGEPLCD	167	1.1000	12.36
18	VVGSGRTLS	154	1.0000	11.24
19	LTVIDPVNN	33	0.9000	10.11
20	WTTADLAGM	101	0.9000	10.11
21	LAGMRIATA	106	0.9000	10.11
22	VRERLALGF	78	0.7000	7.87
23	VEISVQLGV	139	0.7000	7.87
24	LVRKDLATK	118	0.5000	5.62
25	VLIERAGTD	179	0.4000	4.49
26	VQGVVFGQQ	202	0.3000	3.37
27	VVFGQQYLM	205	0.2000	2.25

28	LVAFGEPLC	166	0.0500	0.56

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRKDLATK	118	3.5000	41.67
2	IGAKAILAS	268	3.1000	36.90
3	LRPKDIAIY	47	3.0000	35.71
4	VEFFFLRPK	42	2.8000	33.33
5	IRALVPRRD	249	2.6000	30.95
6	VVGSGRTLS	154	2.5000	29.76
7	LRVAVPNKG	1	2.3000	27.38
8	ILASDIRFC	273	2.3000	27.38
9	MRIATAYPN	109	2.1000	25.00
10	LAGMRIATA	106	1.7000	20.24
11	FRYAAPAGR	91	1.5000	17.86
12	IRLDGAVEI	133	1.4000	16.67
13	VPRRDVNGI	253	1.4000	16.67
14	MLRVAVPNK	0	1.2000	14.29
15	FFFLRPKDI	44	1.2000	14.29
16	LVAFGEPLC	166	1.0000	11.90
17	VGSGRTLSQ	155	0.9000	10.71
18	FFLRPKDIA	45	0.8000	9.52
19	VAIRALVPR	247	0.8000	9.52
20	VRERLALGF	78	0.6000	7.14
21	IERAGTDGQ	181	0.6000	7.14
22	VVFGQQYLM	205	0.5000	5.95
23	VEISVQLGV	139	0.4000	4.76
24	LSQHDLVAF	161	0.3000	3.57
25	MLDYDCPRS	213	0.3000	3.57
26	IATAYPNLV	111	-0.1000	0
27	VIRLDGAVE	132	-0.2000	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	FRYAAPAGR	91	2.5000	29.76
2	LVRKDLATK	118	2.5000	29.76
3	FFFLRPKDI	44	2.2000	26.19
4	IGAKAILAS	268	2.1000	25.00
5	LRPKDIAIY	47	2.0000	23.81
6	VEFFFLRPK	42	1.8000	21.43
7	FFLRPKDIA	45	1.8000	21.43
8	IRALVPRRD	249	1.6000	19.05
9	VVGSGRTLS	154	1.5000	17.86
10	LRVAVPNKG	1	1.3000	15.48
11	ILASDIRFC	273	1.3000	15.48
12	MRIATAYPN	109	1.1000	13.10
13	LAGMRIATA	106	0.7000	8.33
14	WVAIRALVP	246	0.6000	7.14
15	YPNLVRKDL	115	0.4000	4.76
16	IRLDGAVEI	133	0.4000	4.76
17	VPRRDVNGI	253	0.4000	4.76
18	MLRVAVPNK	0	0.2000	2.38
19	FGSSSFRYA	86	-0.1000	0
20	VGSGRTLSQ	155	-0.1000	0
21	WTTADLAGM	101	-0.2000	0
22	VAIRALVPR	247	-0.2000	0
23	YVGSGELDF	55	-0.3000	0
24	FGITGRDLV	63	-0.3000	0
25	VRERLALGF	78	-0.4000	0
26	IERAGTDGQ	181	-0.4000	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	LRPKDIAIY	47	4.3000	48.86
2	LRVAVPNKG	1	3.7000	42.05
3	IRALVPRRD	249	3.7000	42.05
4	LVRKDLATK	118	3.6000	40.91
5	IGAKAILAS	268	3.5000	39.77
6	FRYAAPAGR	91	3.0000	34.09
7	VEFFFLRPK	42	2.9000	32.95
8	MRIATAYPN	109	2.9000	32.95
9	VVGSGRTLS	154	2.9000	32.95
10	VRERLALGF	78	2.5000	28.41
11	IRLDGAVEI	133	2.3000	26.14
12	VAIRALVPR	247	2.3000	26.14
13	VPRRDVNGI	253	2.3000	26.14
14	ILASDIRFC	273	2.3000	26.14
15	LSQHDLVAF	161	2.2000	25.00
16	FFFLRPKDI	44	2.1000	23.86
17	VVFGQQYLM	205	2.0000	22.73
18	LAGMRIATA	106	1.7000	19.32
19	VEISVQLGV	139	1.4000	15.91
20	MLRVAVPNK	0	1.3000	14.77
21	VIRLDGAVE	132	1.2000	13.64
22	LVAFGEPLC	166	1.0000	11.36
23	VPNKGALSE	5	0.9000	10.23
24	IATAYPNLV	111	0.9000	10.23
25	LASDIRFCR	274	0.9000	10.23
26	FFLRPKDIA	45	0.8000	9.09
27	LVARVQGVV	198	0.8000	9.09
28	MLDYDCPRS	213	0.7000	7.95

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	LRPKDIAIY	47	4.3000	48.86
2	LRVAVPNKG	1	3.7000	42.05
3	IRALVPRRD	249	3.7000	42.05
4	LVRKDLATK	118	3.6000	40.91
5	IGAKAILAS	268	3.5000	39.77
6	FRYAAPAGR	91	3.0000	34.09
7	VEFFFLRPK	42	2.9000	32.95
8	MRIATAYPN	109	2.9000	32.95
9	VVGSGRTLS	154	2.9000	32.95
10	VRERLALGF	78	2.5000	28.41
11	IRLDGAVEI	133	2.3000	26.14
12	VAIRALVPR	247	2.3000	26.14
13	VPRRDVNGI	253	2.3000	26.14
14	ILASDIRFC	273	2.3000	26.14
15	LSQHDLVAF	161	2.2000	25.00
16	FFFLRPKDI	44	2.1000	23.86
17	VVFGQQYLM	205	2.0000	22.73
18	LAGMRIATA	106	1.7000	19.32
19	VEISVQLGV	139	1.4000	15.91
20	MLRVAVPNK	0	1.3000	14.77
21	VIRLDGAVE	132	1.2000	13.64
22	LVAFGEPLC	166	1.0000	11.36
23	VPNKGALSE	5	0.9000	10.23
24	IATAYPNLV	111	0.9000	10.23
25	LASDIRFCR	274	0.9000	10.23
26	FFLRPKDIA	45	0.8000	9.09
27	LVARVQGVV	198	0.8000	9.09
28	MLDYDCPRS	213	0.7000	7.95

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	IRLDGAVEI	133	3.8000	38.78

2	LVAFGEPLC	166	3.8000	38.78
3	MRIATAYPN	109	3.2000	32.65
4	VNNVEFFFL	39	3.1000	31.63
5	VFGQQYLML	206	3.0000	30.61
6	IAIYVGSGE	52	2.9000	29.59
7	VVGSGRTLS	154	2.9000	29.59
8	VVFGQQYLM	205	2.8800	29.39
9	VRERLALGF	78	2.7000	27.55
10	VEISVQLGV	139	2.7000	27.55
11	LVCDSGAQV	70	2.5000	25.51
12	WVAIRALVP	246	2.5000	25.51
13	LRVAVPNKG	1	2.4000	24.49
14	FLRPKDIAI	46	2.2000	22.45
15	VQLGVADAI	143	2.2000	22.45
16	MLDYDCPRS	213	2.2000	22.45
17	LVARVQGVV	198	1.8000	18.37
18	LVPRRDVNG	252	1.7000	17.35
19	YVGSGELDF	55	1.5000	15.31
20	LALGFGSSS	82	1.5000	15.31
21	LKKATAITP	223	1.5000	15.31
22	VPRRDVNGI	253	1.5000	15.31
23	IGAKAILAS	268	1.4500	14.80
24	VEFFFLRPK	42	1.3000	13.27
25	FFFLRPKDI	44	1.3000	13.27
26	FGITGRDLV	63	1.3000	13.27
27	VARVQGVVF	199	1.3000	13.27
28	LAGMRIATA	106	1.2500	12.76

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	WVAIRALVP	246	3.5000	35.71
2	FLRPKDIAI	46	3.2000	32.65

3	IRLDGAVEI	133	2.8000	28.57
4	LVAFGEPLC	166	2.8000	28.57
5	YVGSGELDF	55	2.5000	25.51
6	FFFLRPKDI	44	2.3000	23.47
7	FGITGRDLV	63	2.3000	23.47
8	MRIATAYPN	109	2.2000	22.45
9	VNNVEFFFL	39	2.1000	21.43
10	VFGQQYLML	206	2.0000	20.41
11	IAIYVGSGE	52	1.9000	19.39
12	VVGSGRTLS	154	1.9000	19.39
13	VVFGQQYLM	205	1.8800	19.18
14	FRYAAPAGR	91	1.8000	18.37
15	VRERLALGF	78	1.7000	17.35
16	YPNLVRKDL	115	1.7000	17.35
17	VEISVQLGV	139	1.7000	17.35
18	LVCDSGAQV	70	1.5000	15.31
19	YLMLDYDCP	211	1.5000	15.31
20	LRVAVPNKG	1	1.4000	14.29
21	VQLGVADAI	143	1.2000	12.24
22	MLDYDCPRS	213	1.2000	12.24
23	YRRRTDSKD	24	1.1000	11.22
24	FFLRPKDIA	45	1.0000	10.20
25	LVARVQGVV	198	0.8000	8.16
26	LVPRRDVNG	252	0.7000	7.14
27	LALGFGSSS	82	0.5000	5.10
28	LKKATAITP	223	0.5000	5.10

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	IRLDGAVEI	133	3.8000	38.78
2	LVAFGEPLC	166	3.8000	38.78
3	MRIATAYPN	109	3.2000	32.65

4	VNNVEFFFL	39	3.1000	31.63
5	VFGQQYLML	206	3.0000	30.61
6	IAIYVGSGE	52	2.9000	29.59
7	VVGSGRTLS	154	2.9000	29.59
8	VVFGQQYLM	205	2.8800	29.39
9	VRERLALGF	78	2.7000	27.55
10	VEISVQLGV	139	2.7000	27.55
11	LVCDSGAQV	70	2.5000	25.51
12	WVAIRALVP	246	2.5000	25.51
13	LRVAVPNKG	1	2.4000	24.49
14	FLRPKDIAI	46	2.2000	22.45
15	VQLGVADAI	143	2.2000	22.45
16	MLDYDCPRS	213	2.2000	22.45
17	LVARVQGVV	198	1.8000	18.37
18	LVPRRDVNG	252	1.7000	17.35
19	YVGSGELDF	55	1.5000	15.31
20	LALGFGSSS	82	1.5000	15.31
21	LKKATAITP	223	1.5000	15.31
22	VPRRDVNGI	253	1.5000	15.31
23	IGAKAILAS	268	1.4500	14.80
24	VEFFFLRPK	42	1.3000	13.27
25	FFFLRPKDI	44	1.3000	13.27
26	FGITGRDLV	63	1.3000	13.27
27	VARVQGVVF	199	1.3000	13.27
28	LAGMRIATA	106	1.2500	12.76

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	FRYAAPAGR	91	5.7000	58.16
2	FFFLRPKDI	44	4.5000	45.92
3	MRIATAYPN	109	3.9000	39.80
4	WVAIRALVP	246	3.2000	32.65

5	LRVAVPNKG	1	2.8000	28.57
6	MLRVAVPNK	0	2.6000	26.53
7	VNNVEFFFL	39	2.5000	25.51
8	LAAIGAKAI	265	2.4000	24.49
9	VEFFFLRPK	42	2.3000	23.47
10	ILAEAGYRR	18	2.1000	21.43
11	LVRKDLATK	118	1.8000	18.37
12	IRALVPRRD	249	1.8000	18.37
13	YVGSGELDF	55	1.6000	16.33
14	YPNLVRKDL	115	1.5000	15.31
15	VARVQGVVF	199	1.4000	14.29
16	IRLDGAVEI	133	1.2000	12.24
17	VQGVVFGQQ	202	1.1000	11.22
18	IADVVGSGR	151	0.8000	8.16
19	LTVIDPVNN	33	0.7000	7.14
20	LAEAGYRRR	19	0.6000	6.12
21	FLRPKDIAI	46	0.6000	6.12
22	VVFGQQYLM	205	0.6000	6.12
23	LGFGSSSFR	84	0.5000	5.10
24	VIRLDGAVE	132	0.5000	5.10
25	VVGSGRTLS	154	0.5000	5.10
26	LKKATAITP	223	0.5000	5.10
27	VCDSGAQVR	71	0.4000	4.08
28	VFGQQYLML	206	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	FRYAAPAGR	91	5.7000	58.16
2	FFFLRPKDI	44	4.5000	45.92
3	MRIATAYPN	109	3.9000	39.80
4	WVAIRALVP	246	3.2000	32.65
5	LRVAVPNKG	1	2.8000	28.57

6	MLRVAVPNK	0	2.6000	26.53
7	VNNVEFFFL	39	2.5000	25.51
8	LAAIGAKAI	265	2.4000	24.49
9	VEFFFLRPK	42	2.3000	23.47
10	ILAEAGYRR	18	2.1000	21.43
11	LVRKDLATK	118	1.8000	18.37
12	IRALVPRRD	249	1.8000	18.37
13	YVGSGELDF	55	1.6000	16.33
14	YPNLVRKDL	115	1.5000	15.31
15	VARVQGVVF	199	1.4000	14.29
16	IRLDGAVEI	133	1.2000	12.24
17	VQGVVFGQQ	202	1.1000	11.22
18	IADVVGSGR	151	0.8000	8.16
19	LTVIDPVNN	33	0.7000	7.14
20	LAEAGYRRR	19	0.6000	6.12
21	FLRPKDIAI	46	0.6000	6.12
22	VVFGQQYLM	205	0.6000	6.12
23	LGFGSSSFR	84	0.5000	5.10
24	VIRLDGAVE	132	0.5000	5.10
25	VVGSGRTLS	154	0.5000	5.10
26	LKKATAITP	223	0.5000	5.10
27	VCDSGAQVR	71	0.4000	4.08
28	VFGQQYLML	206	0.2000	2.04