MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sat Feb 20 00:25:02 2010
Length of input sequence	168 amino acids
Number of nanomers from input sequence	160
Number of nanomers with obligatory P1 anchor residue	53
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	16

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	LRVLEPFGI	137	3.4000	56.67
2	VNLFRANVI	107	1.6800	28.00
3	LFRANVIDV	109	0.3000	5.00
4	LARVAALFS	18	-0.3500	0
5	VVSAEDTPL	51	-0.8100	0
6	FNIESLAVG	30	-0.9000	0
7	LFSRRGFNI	24	-1.4000	0
8	LNKLINVIK	66	-1.4000	0
9	VAALFSRRG	21	-1.4100	0

10	IREIAQSGM	145	-1.4200	0
11	ITKQLNKLI	62	-1.5000	0
12	VLVEDKPGV	9	-1.5300	0
13	VIDVSPESL	114	-1.5500	0
14	LEPFGIREI	140	-1.6300	0
15	MVSLSRGPR	153	-1.7000	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	LRVLEPFGI	137	4.4000	73.33
2	VNLFRANVI	107	2.6800	44.67
3	LFRANVIDV	109	1.3000	21.67
4	LARVAALFS	18	0.6500	10.83
5	VVSAEDTPL	51	0.1900	3.17
6	LFSRRGFNI	24	-0.4000	0
7	LNKLINVIK	66	-0.4000	0
8	VAALFSRRG	21	-0.4100	0
9	IREIAQSGM	145	-0.4200	0
10	ITKQLNKLI	62	-0.5000	0
11	VLVEDKPGV	9	-0.5300	0
12	VIDVSPESL	114	-0.5500	0
13	LEPFGIREI	140	-0.6300	0
14	MVSLSRGPR	153	-0.7000	0
15	FNIESLAVG	30	-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	LRVLEPFGI	137	4.3000	45.26
2	VQADAGSRS	93	3.9700	41.79
3	MVSLSRGPR	153	3.9000	41.05
4	LVEDKPGVL	10	3.7600	39.58

5	LFRANVIDV	109	3.4000	35.79
6	LINVIKIVE	69	3.0000	31.58
7	VLVEDKPGV	9	2.8000	29.47
8	FRANVIDVS	110	2.6000	27.37
9	INVIKIVEQ	70	2.5000	26.32
10	LSRGPRGIG	156	2.4000	25.26
11	IREIAQSGM	145	2.3700	24.95
12	LARVAALFS	18	2.0000	21.05
13	LALIKVQAD	88	2.0000	21.05
14	FGIREIAQS	143	1.8000	18.95
15	VSLSRGPRG	154	1.8000	18.95
16	LAVGATECK	35	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	FRANVIDVS	110	3.2000	35.16
2	VQADAGSRS	93	2.5700	28.24
3	LRVLEPFGI	137	2.4000	26.37
4	FGIREIAQS	143	2.4000	26.37
5	INVIKIVEQ	70	2.2000	24.18
6	LVEDKPGVL	10	1.8000	19.78
7	LFRANVIDV	109	1.4000	15.38
8	MVSLSRGPR	153	1.4000	15.38
9	VLVEDKPGV	9	0.8000	8.79
10	LARVAALFS	18	0.6000	6.59
11	LINVIKIVE	69	0.6000	6.59
12	FNIESLAVG	30	0.5000	5.49
13	LAVGATECK	35	0.3000	3.30
14	LALIKVQAD	88	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VQADAGSRS	93	3.3000	37.50
2	INVIKIVEQ	70	3.0800	35.00
3	FRANVIDVS	110	2.5000	28.41
4	LARVAALFS	18	2.1000	23.86
5	LFRANVIDV	109	2.0800	23.64
6	LRVLEPFGI	137	1.9000	21.59
7	LAVGATECK	35	1.7000	19.32
8	LVEDKPGVL	10	1.4000	15.91
9	FGIREIAQS	143	1.4000	15.91
10	LINVIKIVE	69	1.2800	14.55
11	VNLFRANVI	107	1.1000	12.50
12	LALIKVQAD	88	1.0000	11.36
13	MVSLSRGPR	153	1.0000	11.36
14	IREIAQSGM	145	0.6000	6.82
15	LEQITKQLN	59	0.5000	5.68
16	VLVEDKPGV	9	0.4000	4.55

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	VQADAGSRS	93	3.3000	37.50
2	INVIKIVEQ	70	3.0800	35.00
3	FRANVIDVS	110	2.5000	28.41
4	LARVAALFS	18	2.1000	23.86
5	LFRANVIDV	109	2.0800	23.64
6	LRVLEPFGI	137	1.9000	21.59
7	LAVGATECK	35	1.7000	19.32
8	LVEDKPGVL	10	1.4000	15.91
9	FGIREIAQS	143	1.4000	15.91
10	LINVIKIVE	69	1.2800	14.55
11	VNLFRANVI	107	1.1000	12.50
12	LALIKVQAD	88	1.0000	11.36

13	MVSLSRGPR	153	1.0000	11.36
14	IREIAQSGM	145	0.6000	6.82
15	LEQITKQLN	59	0.5000	5.68
16	VLVEDKPGV	9	0.4000	4.55

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	VQADAGSRS	93	3.3000	37.50
2	INVIKIVEQ	70	3.0800	35.00
3	FRANVIDVS	110	2.5000	28.41
4	LARVAALFS	18	2.1000	23.86
5	LFRANVIDV	109	2.0800	23.64
6	LRVLEPFGI	137	1.9000	21.59
7	LAVGATECK	35	1.7000	19.32
8	LVEDKPGVL	10	1.4000	15.91
9	FGIREIAQS	143	1.4000	15.91
10	LINVIKIVE	69	1.2800	14.55
11	VNLFRANVI	107	1.1000	12.50
12	LALIKVQAD	88	1.0000	11.36
13	MVSLSRGPR	153	1.0000	11.36
14	IREIAQSGM	145	0.6000	6.82
15	LEQITKQLN	59	0.5000	5.68
16	VLVEDKPGV	9	0.4000	4.55

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	FRANVIDVS	110	3.6000	37.89
2	LRVLEPFGI	137	3.3000	34.74
3	VQADAGSRS	93	2.9700	31.26
4	MVSLSRGPR	153	2.9000	30.53
5	FGIREIAQS	143	2.8000	29.47

6	LVEDKPGVL	10	2.7600	29.05
7	LFRANVIDV	109	2.4000	25.26
8	LINVIKIVE	69	2.0000	21.05
9	FNIESLAVG	30	1.9000	20.00
10	VLVEDKPGV	9	1.8000	18.95
11	INVIKIVEQ	70	1.5000	15.79
12	LSRGPRGIG	156	1.4000	14.74
13	IREIAQSGM	145	1.3700	14.42
14	LARVAALFS	18	1.0000	10.53
15	LALIKVQAD	88	1.0000	10.53
16	VSLSRGPRG	154	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	VQADAGSRS	93	3.3000	37.50
2	INVIKIVEQ	70	3.0800	35.00
3	FRANVIDVS	110	2.5000	28.41
4	LARVAALFS	18	2.1000	23.86
5	LFRANVIDV	109	2.0800	23.64
6	LRVLEPFGI	137	1.9000	21.59
7	LAVGATECK	35	1.7000	19.32
8	LVEDKPGVL	10	1.4000	15.91
9	FGIREIAQS	143	1.4000	15.91
10	LINVIKIVE	69	1.2800	14.55
11	VNLFRANVI	107	1.1000	12.50
12	LALIKVQAD	88	1.0000	11.36
13	MVSLSRGPR	153	1.0000	11.36
14	IREIAQSGM	145	0.6000	6.82
15	LEQITKQLN	59	0.5000	5.68
16	VLVEDKPGV	9	0.4000	4.55

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	FRANVIDVS	110	3.4000	39.53
2	FNIESLAVG	30	1.7000	19.77
3	LNKLINVIK	66	1.6800	19.53
4	INVIKIVEQ	70	1.5800	18.37
5	VSRELALIK	84	1.3000	15.12
6	LRVLEPFGI	137	1.2000	13.95
7	IKVQADAGS	91	1.0000	11.63
8	LFRANVIDV	109	0.7800	9.07
9	FGIREIAQS	143	0.7000	8.14
10	VQADAGSRS	93	0.6000	6.98
11	LTVEATGNR	122	0.6000	6.98
12	ITKQLNKLI	62	0.5000	5.81
13	IVEQDDEHS	75	0.5000	5.81
14	LARVAALFS	18	0.2000	2.33
15	VNLFRANVI	107	0.2000	2.33

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	FGIREIAQS	143	2.6000	27.08
2	VNLFRANVI	107	2.4000	25.00
3	VEATGNRGK	124	2.3000	23.96
4	LRVLEPFGI	137	2.3000	23.96
5	LFRANVIDV	109	2.2000	22.92
6	LEPFGIREI	140	2.0000	20.83
7	INVIKIVEQ	70	1.9800	20.62
8	LARVAALFS	18	1.7000	17.71
9	LNKLINVIK	66	1.4000	14.58
10	LALIKVQAD	88	1.3800	14.37
11	VIEAVNLFR	103	1.2000	12.50
12	VAALFSRRG	21	1.1000	11.46

13	VLARVAALF	17	1.0000	10.42
14	IKVQADAGS	91	0.8000	8.33
15	LFSRRGFNI	24	0.7000	7.29
16	ITKQLNKLI	62	0.6000	6.25

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	LRVLEPFGI	137	3.3500	38.07
2	VNLFRANVI	107	3.2000	36.36
3	LNKLINVIK	66	2.7000	30.68
4	INVIKIVEQ	70	2.7000	30.68
5	LARVAALFS	18	2.2000	25.00
6	LFRANVIDV	109	1.7800	20.23
7	MTIVVSAED	48	1.3000	14.77
8	IKVQADAGS	91	1.2000	13.64
9	LALIKVQAD	88	1.1000	12.50
10	IREIAQSGM	145	0.7000	7.95
11	VVSAEDTPL	51	0.6000	6.82
12	VIEAVNLFR	103	0.5000	5.68
13	VAALFSRRG	21	0.1000	1.14
14	LEPFGIREI	140	0.1000	1.14
15	FRANVIDVS	110	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MTIVVSAED	48	3.0000	31.91
2	LALIKVQAD	88	2.8000	29.79
3	LRVLEPFGI	137	2.5500	27.13
4	INVIKIVEQ	70	2.5000	26.60
5	VNLFRANVI	107	2.4000	25.53
6	LARVAALFS	18	1.2000	12.77

7	LFRANVIDV	109	1.0800	11.49
8	LNKLINVIK	66	1.0000	10.64
9	FRANVIDVS	110	0.9000	9.57
10	IREIAQSGM	145	0.8000	8.51
11	IKIVEQDDE	73	0.7000	7.45
12	VVSAEDTPL	51	0.6000	6.38
13	VAALFSRRG	21	0.4000	4.26
14	FNIESLAVG	30	0.4000	4.26
15	IKVQADAGS	91	0.2000	2.13
16	FGIREIAQS	143	0.2000	2.13

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	LRVLEPFGI	137	2.3500	26.70
2	VNLFRANVI	107	2.2000	25.00
3	LNKLINVIK	66	1.7000	19.32
4	INVIKIVEQ	70	1.7000	19.32
5	LARVAALFS	18	1.2000	13.64
6	FRANVIDVS	110	0.9000	10.23
7	LFRANVIDV	109	0.7800	8.86
8	MTIVVSAED	48	0.3000	3.41
9	IKVQADAGS	91	0.2000	2.27
10	FGIREIAQS	143	0.2000	2.27
11	LALIKVQAD	88	0.1000	1.14
12	IREIAQSGM	145	-0.3000	0
13	VVSAEDTPL	51	-0.4000	0
14	VIEAVNLFR	103	-0.5000	0
15	VAALFSRRG	21	-0.9000	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	MTIVVSAED	48	4.0000	42.55
2	LALIKVQAD	88	3.8000	40.43
3	LRVLEPFGI	137	3.5500	37.77
4	INVIKIVEQ	70	3.5000	37.23
5	VNLFRANVI	107	3.4000	36.17
6	LARVAALFS	18	2.2000	23.40
7	LFRANVIDV	109	2.0800	22.13
8	LNKLINVIK	66	2.0000	21.28
9	IREIAQSGM	145	1.8000	19.15
10	IKIVEQDDE	73	1.7000	18.09
11	VVSAEDTPL	51	1.6000	17.02
12	VAALFSRRG	21	1.4000	14.89
13	IKVQADAGS	91	1.2000	12.77
14	LINVIKIVE	69	1.0800	11.49
15	VSAEDTPLE	52	0.8000	8.51
16	IESLAVGAT	32	0.7000	7.45

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	FRANVIDVS	110	3.8000	42.22
2	FNIESLAVG	30	3.1000	34.44
3	LTVEATGNR	122	2.1000	23.33
4	LRVLEPFGI	137	2.1000	23.33
5	LNKLINVIK	66	1.7800	19.78
6	LFRANVIDV	109	1.7800	19.78
7	ITKQLNKLI	62	1.4000	15.56
8	VSRELALIK	84	1.4000	15.56
9	IKVQADAGS	91	1.4000	15.56
10	VIEAVNLFR	103	1.4000	15.56
11	VSAEDTPLE	52	1.1000	12.22
12	LALIKVQAD	88	1.1000	12.22
13	VNLFRANVI	107	1.1000	12.22
14	FGIREIAQS	143	1.1000	12.22

15	VQADAGSRS	93	1.0000	11.11
16	IVEQDDEHS	75	0.9000	10.00

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	LRVLEPFGI	137	3.3500	38.07
2	VNLFRANVI	107	3.2000	36.36
3	LNKLINVIK	66	2.7000	30.68
4	INVIKIVEQ	70	2.7000	30.68
5	LARVAALFS	18	2.2000	25.00
6	LFRANVIDV	109	1.7800	20.23
7	MTIVVSAED	48	1.3000	14.77
8	IKVQADAGS	91	1.2000	13.64
9	LALIKVQAD	88	1.1000	12.50
10	IREIAQSGM	145	0.7000	7.95
11	VVSAEDTPL	51	0.6000	6.82
12	VIEAVNLFR	103	0.5000	5.68
13	VAALFSRRG	21	0.1000	1.14
14	LEPFGIREI	140	0.1000	1.14
15	FRANVIDVS	110	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FRANVIDVS	110	3.4000	39.53
2	FNIESLAVG	30	1.7000	19.77
3	LNKLINVIK	66	1.6800	19.53
4	INVIKIVEQ	70	1.5800	18.37
5	VSRELALIK	84	1.3000	15.12
6	LRVLEPFGI	137	1.2000	13.95
7	IKVQADAGS	91	1.0000	11.63
8	LFRANVIDV	109	0.7800	9.07

9	FGIREIAQS	143	0.7000	8.14
10	VQADAGSRS	93	0.6000	6.98
11	LTVEATGNR	122	0.6000	6.98
12	ITKQLNKLI	62	0.5000	5.81
13	IVEQDDEHS	75	0.5000	5.81
14	LARVAALFS	18	0.2000	2.33
15	VNLFRANVI	107	0.2000	2.33

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	LRVLEPFGI	137	5.9000	50.86
2	VNLFRANVI	107	5.8000	50.00
3	LFRANVIDV	109	5.0000	43.10
4	IAQSGMVSL	148	4.7000	40.52
5	LFSRRGFNI	24	3.8000	32.76
6	VIDVSPESL	114	3.5000	30.17
7	LEPFGIREI	140	3.2000	27.59
8	VVSAEDTPL	51	3.1000	26.72
9	LARVAALFS	18	2.5000	21.55
10	LINVIKIVE	69	2.5000	21.55
11	IREIAQSGM	145	2.4000	20.69
12	INVIKIVEQ	70	1.6000	13.79
13	LVEDKPGVL	10	1.2000	10.34
14	IEAVNLFRA	104	1.2000	10.34
15	LALIKVQAD	88	1.1000	9.48
16	VLARVAALF	17	1.0000	8.62

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	LRVLEPFGI	137	5.9000	50.86
2	VNLFRANVI	107	5.8000	50.00

3	LFRANVIDV	109	5.0000	43.10
4	IAQSGMVSL	148	4.7000	40.52
5	LFSRRGFNI	24	3.8000	32.76
6	VIDVSPESL	114	3.5000	30.17
7	LEPFGIREI	140	3.2000	27.59
8	VVSAEDTPL	51	3.1000	26.72
9	LARVAALFS	18	2.5000	21.55
10	LINVIKIVE	69	2.5000	21.55
11	IREIAQSGM	145	2.4000	20.69
12	INVIKIVEQ	70	1.6000	13.79
13	LVEDKPGVL	10	1.2000	10.34
14	IEAVNLFRA	104	1.2000	10.34
15	LALIKVQAD	88	1.1000	9.48
16	VLARVAALF	17	1.0000	8.62

ALLELE: DRB1_0801	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	FGIREIAQS	143	5.7000	66.28
2	LINVIKIVE	69	2.7000	31.40
3	VLARVAALF	17	2.2000	25.58
4	LRVLEPFGI	137	1.9000	22.09
5	FNIESLAVG	30	1.8000	20.93
6	MTIVVSAED	48	1.7000	19.77
7	INVIKIVEQ	70	1.5000	17.44
8	MVSLSRGPR	153	1.5000	17.44
9	FSRRGFNIE	25	1.3000	15.12
10	LALIKVQAD	88	1.3000	15.12
11	FRANVIDVS	110	1.2000	13.95
12	LEALLRVLE	133	1.0000	11.63
13	LFSRRGFNI	24	0.6000	6.98
14	IKIVEQDDE	73	0.5000	5.81
15	LFRANVIDV	109	0.5000	5.81

16	LARVAALFS	18	0.4000	4.65

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	FGIREIAQS	143	5.7000	71.25
2	LRVLEPFGI	137	1.7000	21.25
3	MVSLSRGPR	153	1.5000	18.75
4	VLARVAALF	17	1.3000	16.25
5	FRANVIDVS	110	1.2000	15.00
6	INVIKIVEQ	70	0.7000	8.75
7	FNIESLAVG	30	0.5000	6.25
8	LARVAALFS	18	0.4000	5.00
9	LFSRRGFNI	24	0.4000	5.00
10	LFRANVIDV	109	0.2000	2.50
11	LINVIKIVE	69	-0.3000	0
12	VNLFRANVI	107	-0.3000	0
13	LEPFGIREI	140	-0.3000	0
14	MSPKTHTLS	0	-0.5000	0
15	IESLAVGAT	32	-0.5000	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	FGIREIAQS	143	4.7000	58.75
2	LRVLEPFGI	137	2.7000	33.75
3	MVSLSRGPR	153	2.5000	31.25
4	VLARVAALF	17	2.3000	28.75
5	INVIKIVEQ	70	1.7000	21.25
6	LARVAALFS	18	1.4000	17.50
7	LFSRRGFNI	24	1.4000	17.50
8	LFRANVIDV	109	1.2000	15.00
9	LINVIKIVE	69	0.7000	8.75

10	VNLFRANVI	107	0.7000	8.75
11	LEPFGIREI	140	0.7000	8.75
12	MSPKTHTLS	0	0.5000	6.25
13	IESLAVGAT	32	0.5000	6.25
14	FRANVIDVS	110	0.2000	2.50

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	FGIREIAQS	143	4.7000	54.65
2	LINVIKIVE	69	3.7000	43.02
3	VLARVAALF	17	3.2000	37.21
4	LRVLEPFGI	137	2.9000	33.72
5	MTIVVSAED	48	2.7000	31.40
6	INVIKIVEQ	70	2.5000	29.07
7	MVSLSRGPR	153	2.5000	29.07
8	LALIKVQAD	88	2.3000	26.74
9	LEALLRVLE	133	2.0000	23.26
10	LFSRRGFNI	24	1.6000	18.60
11	IKIVEQDDE	73	1.5000	17.44
12	LFRANVIDV	109	1.5000	17.44
13	LARVAALFS	18	1.4000	16.28
14	IESLAVGAT	32	1.4000	16.28
15	LEQITKQLN	59	1.1000	12.79
16	VNLFRANVI	107	0.9000	10.47

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	FGIREIAQS	143	5.7000	65.52
2	LRVLEPFGI	137	2.5500	29.31
3	FRANVIDVS	110	2.4000	27.59
4	MSPKTHTLS	0	2.3000	26.44

5	INVIKIVEQ	70	1.7000	19.54
6	VNLFRANVI	107	1.7000	19.54
7	VLARVAALF	17	1.3000	14.94
8	LFSRRGFNI	24	1.2500	14.37
9	LFRANVIDV	109	1.0800	12.41
10	LARVAALFS	18	1.0000	11.49
11	MVSLSRGPR	153	0.8000	9.20
12	LINVIKIVE	69	0.5800	6.67
13	FNIESLAVG	30	0.5000	5.75
14	FSRRGFNIE	25	0.3000	3.45
15	IREIAQSGM	145	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	FGIREIAQS	143	5.7000	56.44
2	LINVIKIVE	69	4.3000	42.57
3	LRVLEPFGI	137	2.4000	23.76
4	VLARVAALF	17	2.2000	21.78
5	LARVAALFS	18	2.2000	21.78
6	LFRANVIDV	109	2.1000	20.79
7	INVIKIVEQ	70	2.0000	19.80
8	FNIESLAVG	30	1.8000	17.82
9	MTIVVSAED	48	1.7000	16.83
10	FSRRGFNIE	25	1.6000	15.84
11	MVSLSRGPR	153	1.6000	15.84
12	LEALLRVLE	133	1.5000	14.85
13	LALIKVQAD	88	1.4000	13.86
14	LFSRRGFNI	24	1.1000	10.89
15	FRANVIDVS	110	0.9000	8.91
16	MSPKTHTLS	0	0.6000	5.94

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FGIREIAQS	143	2.7000	32.53
2	LRVLEPFGI	137	2.6000	31.33
3	LARVAALFS	18	2.3000	27.71
4	MVSLSRGPR	153	2.0000	24.10
5	INVIKIVEQ	70	1.8000	21.69
6	LFRANVIDV	109	1.8000	21.69
7	LINVIKIVE	69	1.4000	16.87
8	FRANVIDVS	110	0.9000	10.84
9	VNLFRANVI	107	-0.1000	0
10	FNIESLAVG	30	-0.2000	0
11	LEPFGIREI	140	-0.2000	0
12	LNKLINVIK	66	-0.6000	0
13	VLVEDKPGV	9	-0.6500	0
14	LALIKVQAD	88	-0.7000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRVLEPFGI	137	3.9000	46.43
2	LEPFGIREI	140	2.8000	33.33
3	FGIREIAQS	143	2.6000	30.95
4	VNLFRANVI	107	2.4000	28.57
5	INVIKIVEQ	70	1.8000	21.43
6	LFRANVIDV	109	1.5000	17.86
7	FRANVIDVS	110	1.2000	14.29
8	MVSLSRGPR	153	1.2000	14.29
9	LARVAALFS	18	0.9000	10.71
10	LFSRRGFNI	24	0.8000	9.52
11	MSPKTHTLS	0	0.5000	5.95
12	VLVEDKPGV	9	0.5000	5.95
13	VAALFSRRG	21	0.5000	5.95

14	IKVQADAGS	91	0.5000	5.95
15	VLARVAALF	17	0.2000	2.38
16	LNKLINVIK	66	0.2000	2.38

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	LRVLEPFGI	137	3.6000	43.37
2	LARVAALFS	18	3.3000	39.76
3	MVSLSRGPR	153	3.0000	36.14
4	INVIKIVEQ	70	2.8000	33.73
5	LFRANVIDV	109	2.8000	33.73
6	LINVIKIVE	69	2.4000	28.92
7	FGIREIAQS	143	1.7000	20.48
8	IESLAVGAT	32	1.0000	12.05
9	VNLFRANVI	107	0.9000	10.84
10	LEPFGIREI	140	0.8000	9.64
11	LNKLINVIK	66	0.4000	4.82
12	VLVEDKPGV	9	0.3500	4.22
13	LALIKVQAD	88	0.3000	3.61
14	IEAVNLFRA	104	0.3000	3.61
15	MTIVVSAED	48	0.1000	1.20

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	LRVLEPFGI	137	3.6000	43.37
2	LARVAALFS	18	3.3000	39.76
3	MVSLSRGPR	153	3.0000	36.14
4	INVIKIVEQ	70	2.8000	33.73
5	LFRANVIDV	109	2.8000	33.73
6	LINVIKIVE	69	2.4000	28.92
7	FGIREIAQS	143	1.7000	20.48

8	IESLAVGAT	32	1.0000	12.05
9	VNLFRANVI	107	0.9000	10.84
10	LEPFGIREI	140	0.8000	9.64
11	LNKLINVIK	66	0.4000	4.82
12	VLVEDKPGV	9	0.3500	4.22
13	LALIKVQAD	88	0.3000	3.61
14	IEAVNLFRA	104	0.3000	3.61
15	MTIVVSAED	48	0.1000	1.20

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	VQADAGSRS	93	3.5700	39.23
2	LRVLEPFGI	137	3.4000	37.36
3	INVIKIVEQ	70	3.2000	35.16
4	LVEDKPGVL	10	2.8000	30.77
5	LFRANVIDV	109	2.4000	26.37
6	MVSLSRGPR	153	2.4000	26.37
7	FRANVIDVS	110	2.2000	24.18
8	VLVEDKPGV	9	1.8000	19.78
9	LARVAALFS	18	1.6000	17.58
10	LINVIKIVE	69	1.6000	17.58
11	FGIREIAQS	143	1.4000	15.38
12	LAVGATECK	35	1.3000	14.29
13	LSRGPRGIG	156	1.0000	10.99
14	LALIKVQAD	88	0.9000	9.89
15	IREIAQSGM	145	0.8700	9.56
16	IEAVNLFRA	104	0.8000	8.79

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	FGIREIAQS	143	3.6000	42.86

2	LRVLEPFGI	137	2.9000	34.52
3	FRANVIDVS	110	2.2000	26.19
4	LEPFGIREI	140	1.8000	21.43
5	VNLFRANVI	107	1.4000	16.67
6	INVIKIVEQ	70	0.8000	9.52
7	LFRANVIDV	109	0.5000	5.95
8	FNIESLAVG	30	0.4000	4.76
9	MVSLSRGPR	153	0.2000	2.38
10	LARVAALFS	18	-0.1000	0
11	LFSRRGFNI	24	-0.2000	0
12	MSPKTHTLS	0	-0.5000	0
13	VLVEDKPGV	9	-0.5000	0
14	VAALFSRRG	21	-0.5000	0
15	IKVQADAGS	91	-0.5000	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	FGIREIAQS	143	4.0000	45.45
2	LRVLEPFGI	137	3.8000	43.18
3	LEPFGIREI	140	2.7000	30.68
4	FRANVIDVS	110	2.6000	29.55
5	VNLFRANVI	107	2.3000	26.14
6	FNIESLAVG	30	1.8000	20.45
7	MVSLSRGPR	153	1.7000	19.32
8	LFRANVIDV	109	1.5000	17.05
9	VLARVAALF	17	1.1000	12.50
10	VAALFSRRG	21	0.9000	10.23
11	LFSRRGFNI	24	0.7000	7.95
12	VLVEDKPGV	9	0.5000	5.68
13	LARVAALFS	18	0.3000	3.41
14	LINVIKIVE	69	0.2000	2.27
15	INVIKIVEQ	70	0.1000	1.14

16	LEALLRVLE	133	0.1000	1.14

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	LRVLEPFGI	137	3.9000	46.43
2	LEPFGIREI	140	2.8000	33.33
3	FGIREIAQS	143	2.6000	30.95
4	VNLFRANVI	107	2.4000	28.57
5	INVIKIVEQ	70	1.8000	21.43
6	LFRANVIDV	109	1.5000	17.86
7	FRANVIDVS	110	1.2000	14.29
8	MVSLSRGPR	153	1.2000	14.29
9	LARVAALFS	18	0.9000	10.71
10	LFSRRGFNI	24	0.8000	9.52
11	MSPKTHTLS	0	0.5000	5.95
12	VLVEDKPGV	9	0.5000	5.95
13	VAALFSRRG	21	0.5000	5.95
14	IKVQADAGS	91	0.5000	5.95
15	VLARVAALF	17	0.2000	2.38
16	LNKLINVIK	66	0.2000	2.38

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	LRVLEPFGI	137	3.5000	40.23
2	MVSLSRGPR	153	3.5000	40.23
3	FGIREIAQS	143	3.1000	35.63
4	LINVIKIVE	69	2.8000	32.18
5	LFRANVIDV	109	2.8000	32.18
6	LARVAALFS	18	2.7000	31.03
7	FRANVIDVS	110	1.3000	14.94
8	FNIESLAVG	30	1.2000	13.79

9	INVIKIVEQ	70	1.1000	12.64
10	VNLFRANVI	107	0.8000	9.20
11	IESLAVGAT	32	0.7000	8.05
12	LEPFGIREI	140	0.7000	8.05
13	LALIKVQAD	88	0.4000	4.60
14	IREIAQSGM	145	0.4000	4.60
15	VLVEDKPGV	9	0.3500	4.02
16	VIEAVNLFR	103	0.3000	3.45

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	LRVLEPFGI	137	4.8000	54.55
2	LEPFGIREI	140	3.7000	42.05
3	VNLFRANVI	107	3.3000	37.50
4	FGIREIAQS	143	3.0000	34.09
5	MVSLSRGPR	153	2.7000	30.68
6	LFRANVIDV	109	2.5000	28.41
7	VLARVAALF	17	2.1000	23.86
8	VAALFSRRG	21	1.9000	21.59
9	LFSRRGFNI	24	1.7000	19.32
10	FRANVIDVS	110	1.6000	18.18
11	VLVEDKPGV	9	1.5000	17.05
12	LARVAALFS	18	1.3000	14.77
13	LINVIKIVE	69	1.2000	13.64
14	INVIKIVEQ	70	1.1000	12.50
15	LEALLRVLE	133	1.1000	12.50
16	MSPKTHTLS	0	0.9000	10.23

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	FGIREIAQS	143	4.0000	45.45

2	LRVLEPFGI	137	3.8000	43.18
3	LEPFGIREI	140	2.7000	30.68
4	FRANVIDVS	110	2.6000	29.55
5	VNLFRANVI	107	2.3000	26.14
6	FNIESLAVG	30	1.8000	20.45
7	MVSLSRGPR	153	1.7000	19.32
8	LFRANVIDV	109	1.5000	17.05
9	VLARVAALF	17	1.1000	12.50
10	VAALFSRRG	21	0.9000	10.23
11	LFSRRGFNI	24	0.7000	7.95
12	VLVEDKPGV	9	0.5000	5.68
13	LARVAALFS	18	0.3000	3.41
14	LINVIKIVE	69	0.2000	2.27
15	INVIKIVEQ	70	0.1000	1.14
16	LEALLRVLE	133	0.1000	1.14

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	LRVLEPFGI	137	4.1000	45.56
2	LEPFGIREI	140	3.0000	33.33
3	LINVIKIVE	69	2.8000	31.11
4	LEALLRVLE	133	2.7000	30.00
5	INVIKIVEQ	70	2.6000	28.89
6	VNLFRANVI	107	2.6000	28.89
7	FGIREIAQS	143	2.6000	28.89
8	LALIKVQAD	88	2.2000	24.44
9	VAALFSRRG	21	1.8000	20.00
10	LFRANVIDV	109	1.8000	20.00
11	MTIVVSAED	48	1.5000	16.67
12	IKIVEQDDE	73	1.2000	13.33
13	FRANVIDVS	110	1.2000	13.33
14	MVSLSRGPR	153	1.2000	13.33
15	VLARVAALF	17	1.1000	12.22

16	LFSRRGFNI	24	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	LRVLEPFGI	137	3.5000	40.23
2	MVSLSRGPR	153	3.5000	40.23
3	FGIREIAQS	143	3.1000	35.63
4	LINVIKIVE	69	2.8000	32.18
5	LFRANVIDV	109	2.8000	32.18
6	LARVAALFS	18	2.7000	31.03
7	FRANVIDVS	110	1.3000	14.94
8	FNIESLAVG	30	1.2000	13.79
9	INVIKIVEQ	70	1.1000	12.64
10	VNLFRANVI	107	0.8000	9.20
11	IESLAVGAT	32	0.7000	8.05
12	LEPFGIREI	140	0.7000	8.05
13	LALIKVQAD	88	0.4000	4.60
14	IREIAQSGM	145	0.4000	4.60
15	VLVEDKPGV	9	0.3500	4.02
16	VIEAVNLFR	103	0.3000	3.45

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	FGIREIAQS	143	2.7000	39.71
2	LRVLEPFGI	137	2.1000	30.88
3	MVSLSRGPR	153	1.9000	27.94
4	INVIKIVEQ	70	1.3000	19.12
5	FRANVIDVS	110	1.2000	17.65
6	LARVAALFS	18	0.5000	7.35
7	LFRANVIDV	109	0.2000	2.94
8	IESLAVGAT	32	-0.1000	0

9	FNIESLAVG	30	-0.2000	0
10	LINVIKIVE	69	-0.2000	0
11	VNLFRANVI	107	-0.4000	0
12	LEPFGIREI	140	-0.4000	0
13	LALIKVQAD	88	-0.8000	0
14	MTIVVSAED	48	-0.9000	0
15	LNKLINVIK	66	-1.1000	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	LRVLEPFGI	137	3.6000	43.37
2	LARVAALFS	18	3.3000	39.76
3	MVSLSRGPR	153	3.0000	36.14
4	INVIKIVEQ	70	2.8000	33.73
5	LFRANVIDV	109	2.8000	33.73
6	LINVIKIVE	69	2.4000	28.92
7	FGIREIAQS	143	1.7000	20.48
8	IESLAVGAT	32	1.0000	12.05
9	VNLFRANVI	107	0.9000	10.84
10	LEPFGIREI	140	0.8000	9.64
11	LNKLINVIK	66	0.4000	4.82
12	VLVEDKPGV	9	0.3500	4.22
13	LALIKVQAD	88	0.3000	3.61
14	IEAVNLFRA	104	0.3000	3.61
15	MTIVVSAED	48	0.1000	1.20

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	LINVIKIVE	69	4.4000	49.44
2	LRVLEPFGI	137	2.8000	31.46
3	FGIREIAQS	143	2.7000	30.34

4	INVIKIVEQ	70	2.6000	29.21
5	LARVAALFS	18	2.3000	25.84
6	LFRANVIDV	109	2.1000	23.60
7	LALIKVQAD	88	2.0000	22.47
8	MVSLSRGPR	153	2.0000	22.47
9	LEALLRVLE	133	1.9000	21.35
10	MTIVVSAED	48	1.8000	20.22
11	FNIESLAVG	30	1.1000	12.36
12	IESLAVGAT	32	0.9000	10.11
13	FRANVIDVS	110	0.9000	10.11
14	LEQITKQLN	59	0.8000	8.99
15	IKIVEQDDE	73	0.3000	3.37
16	VNLFRANVI	107	0.1000	1.12

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LRVLEPFGI	137	3.9000	46.43
2	LEPFGIREI	140	2.8000	33.33
3	FGIREIAQS	143	2.6000	30.95
4	VNLFRANVI	107	2.4000	28.57
5	INVIKIVEQ	70	1.8000	21.43
6	LFRANVIDV	109	1.5000	17.86
7	FRANVIDVS	110	1.2000	14.29
8	MVSLSRGPR	153	1.2000	14.29
9	LARVAALFS	18	0.9000	10.71
10	LFSRRGFNI	24	0.8000	9.52
11	MSPKTHTLS	0	0.5000	5.95
12	VLVEDKPGV	9	0.5000	5.95
13	VAALFSRRG	21	0.5000	5.95
14	IKVQADAGS	91	0.5000	5.95
15	VLARVAALF	17	0.2000	2.38
16	LNKLINVIK	66	0.2000	2.38

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	FGIREIAQS	143	3.6000	42.86
2	LRVLEPFGI	137	2.9000	34.52
3	FRANVIDVS	110	2.2000	26.19
4	LEPFGIREI	140	1.8000	21.43
5	VNLFRANVI	107	1.4000	16.67
6	INVIKIVEQ	70	0.8000	9.52
7	LFRANVIDV	109	0.5000	5.95
8	FNIESLAVG	30	0.4000	4.76
9	MVSLSRGPR	153	0.2000	2.38
10	LARVAALFS	18	-0.1000	0
11	LFSRRGFNI	24	-0.2000	0
12	MSPKTHTLS	0	-0.5000	0
13	VLVEDKPGV	9	-0.5000	0
14	VAALFSRRG	21	-0.5000	0
15	IKVQADAGS	91	-0.5000	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	LRVLEPFGI	137	4.8000	54.55
2	LEPFGIREI	140	3.7000	42.05
3	VNLFRANVI	107	3.3000	37.50
4	FGIREIAQS	143	3.0000	34.09
5	MVSLSRGPR	153	2.7000	30.68
6	LFRANVIDV	109	2.5000	28.41
7	VLARVAALF	17	2.1000	23.86
8	VAALFSRRG	21	1.9000	21.59
9	LFSRRGFNI	24	1.7000	19.32
10	FRANVIDVS	110	1.6000	18.18
11	VLVEDKPGV	9	1.5000	17.05

12	LARVAALFS	18	1.3000	14.77
13	LINVIKIVE	69	1.2000	13.64
14	INVIKIVEQ	70	1.1000	12.50
15	LEALLRVLE	133	1.1000	12.50
16	MSPKTHTLS	0	0.9000	10.23

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	LRVLEPFGI	137	4.8000	54.55
2	LEPFGIREI	140	3.7000	42.05
3	VNLFRANVI	107	3.3000	37.50
4	FGIREIAQS	143	3.0000	34.09
5	MVSLSRGPR	153	2.7000	30.68
6	LFRANVIDV	109	2.5000	28.41
7	VLARVAALF	17	2.1000	23.86
8	VAALFSRRG	21	1.9000	21.59
9	LFSRRGFNI	24	1.7000	19.32
10	FRANVIDVS	110	1.6000	18.18
11	VLVEDKPGV	9	1.5000	17.05
12	LARVAALFS	18	1.3000	14.77
13	LINVIKIVE	69	1.2000	13.64
14	INVIKIVEQ	70	1.1000	12.50
15	LEALLRVLE	133	1.1000	12.50
16	MSPKTHTLS	0	0.9000	10.23

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	VNLFRANVI	107	5.6000	57.14
2	LRVLEPFGI	137	5.1000	52.04
3	LFSRRGFNI	24	3.8000	38.78
4	LEPFGIREI	140	3.0500	31.12

5	LFRANVIDV	109	3.0000	30.61
6	MVSLSRGPR	153	2.8000	28.57
7	VVSAEDTPL	51	2.6000	26.53
8	LARVAALFS	18	2.5000	25.51
9	IEAVNLFRA	104	1.9000	19.39
10	VIEAVNLFR	103	1.5000	15.31
11	VQADAGSRS	93	1.3000	13.27
12	VLVEDKPGV	9	1.2000	12.24
13	IREIAQSGM	145	1.1800	12.04
14	LINVIKIVE	69	1.1000	11.22
15	FGIREIAQS	143	0.9500	9.69
16	LVEDKPGVL	10	0.8000	8.16

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	VNLFRANVI	107	4.6000	46.94
2	LRVLEPFGI	137	4.1000	41.84
3	LFSRRGFNI	24	2.8000	28.57
4	LEPFGIREI	140	2.0500	20.92
5	LFRANVIDV	109	2.0000	20.41
6	FGIREIAQS	143	1.9500	19.90
7	MVSLSRGPR	153	1.8000	18.37
8	VVSAEDTPL	51	1.6000	16.33
9	LARVAALFS	18	1.5000	15.31
10	FNIESLAVG	30	1.1000	11.22
11	FRANVIDVS	110	1.0500	10.71
12	IEAVNLFRA	104	0.9000	9.18
13	VIEAVNLFR	103	0.5000	5.10
14	VQADAGSRS	93	0.3000	3.06
15	VLVEDKPGV	9	0.2000	2.04
16	IREIAQSGM	145	0.1800	1.84

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	VNLFRANVI	107	5.6000	57.14
2	LRVLEPFGI	137	5.1000	52.04
3	LFSRRGFNI	24	3.8000	38.78
4	LEPFGIREI	140	3.0500	31.12
5	LFRANVIDV	109	3.0000	30.61
6	MVSLSRGPR	153	2.8000	28.57
7	VVSAEDTPL	51	2.6000	26.53
8	LARVAALFS	18	2.5000	25.51
9	IEAVNLFRA	104	1.9000	19.39
10	VIEAVNLFR	103	1.5000	15.31
11	VQADAGSRS	93	1.3000	13.27
12	VLVEDKPGV	9	1.2000	12.24
13	IREIAQSGM	145	1.1800	12.04
14	LINVIKIVE	69	1.1000	11.22
15	FGIREIAQS	143	0.9500	9.69
16	LVEDKPGVL	10	0.8000	8.16

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	LRVLEPFGI	137	5.2000	53.06
2	MVSLSRGPR	153	3.7000	37.76
3	VGATECKDR	37	3.2000	32.65
4	LARVAALFS	18	2.1000	21.43
5	VEATGNRGK	124	2.1000	21.43
6	VNLFRANVI	107	1.9000	19.39
7	LNKLINVIK	66	1.5000	15.31
8	VSRELALIK	84	1.4000	14.29
9	VVSAEDTPL	51	0.9000	9.18
10	VAALFSRRG	21	0.8000	8.16
11	LINVIKIVE	69	0.8000	8.16

12	LFSRRGFNI	24	0.7000	7.14
13	VIEAVNLFR	103	0.7000	7.14
14	IEAVNLFRA	104	0.7000	7.14
15	INVIKIVEQ	70	0.6000	6.12
16	VIDVSPESL	114	0.5000	5.10

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	LRVLEPFGI	137	5.2000	53.06
2	MVSLSRGPR	153	3.7000	37.76
3	VGATECKDR	37	3.2000	32.65
4	LARVAALFS	18	2.1000	21.43
5	VEATGNRGK	124	2.1000	21.43
6	VNLFRANVI	107	1.9000	19.39
7	LNKLINVIK	66	1.5000	15.31
8	VSRELALIK	84	1.4000	14.29
9	VVSAEDTPL	51	0.9000	9.18
10	VAALFSRRG	21	0.8000	8.16
11	LINVIKIVE	69	0.8000	8.16
12	LFSRRGFNI	24	0.7000	7.14
13	VIEAVNLFR	103	0.7000	7.14
14	IEAVNLFRA	104	0.7000	7.14
15	INVIKIVEQ	70	0.6000	6.12
16	VIDVSPESL	114	0.5000	5.10