MHC Class-II Binding Peptide Prediction Results

HELP HOME MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Thu Feb 25 01:27:35 2010
Length of input sequence	174 amino acids
Number of nanomers from input sequence	166
Number of nanomers with obligatory P1 anchor residue	63
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	17

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	VVGCGALHV	61	1.9000	31.67
2	LQLQRVFVL	106	1.0000	16.67
3	VRRARTSDV	11	0.8000	13.33
4	YGKVVGCGA	58	0.1500	2.50
5	LSYVKPNIL	156	-0.1500	0
6	LQRVFVLTF	108	-0.3500	0
7	ILLEKNLVT	33	-0.4000	0
8	YDIGVAEFL	146	-0.6000	0

9	FVLTFETEF	112	-0.6100	0
10	FTEIEGTPV	126	-0.6100	0
11	ILGNSRMLL	163	-0.9700	0
12	LQVARDLQL	100	-1.2000	0
13	FWVAEHPDL	49	-1.2300	0
14	IGVAEFLDL	148	-1.3000	0
15	FARHGFTEI	121	-1.3100	0
16	WVAEHPDLY	50	-1.4000	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	VVGCGALHV	61	2.9000	48.33
2	LQLQRVFVL	106	2.0000	33.33
3	VRRARTSDV	11	1.8000	30.00
4	LSYVKPNIL	156	0.8500	14.17
5	LQRVFVLTF	108	0.6500	10.83
6	ILLEKNLVT	33	0.6000	10.00
7	ILGNSRMLL	163	0.0300	0.50
8	LQVARDLQL	100	-0.2000	0
9	IGVAEFLDL	148	-0.3000	0
10	LGEIRTVAV	74	-0.4000	0
11	LVDTYAGKI	25	-0.6000	0
12	IKQLVDTYA	22	-0.6100	0
13	FVLTFETEF	112	-0.6100	0
14	FTEIEGTPV	126	-0.6100	0
15	YGKVVGCGA	58	-0.8500	0
16	LGNSRMLLV	164	-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	VAVDPAMTG	80	4.3000	45.26
2	LQRVFVLTF	108	4.2000	44.21
3	VRRARTSDV	11	4.0700	42.84
4	LQLQRVFVL	106	3.8600	40.63
5	ILGNSRMLL	163	3.4600	36.42
6	VARDLQLQR	102	3.4000	35.79
7	VKPNILGNS	159	3.0000	31.58
8	VVGCGALHV	61	2.8000	29.47
9	IRTVAVDPA	77	2.8000	29.47
10	VLWSDLGEI	69	2.6000	27.37
11	VVRRARTSD	10	2.1000	22.11
12	LWSDLGEIR	70	2.0000	21.05
13	LYGKVVGCG	57	1.8000	18.95
14	LEKNLVTLY	35	1.7000	17.89
15	VLTFETEFF	113	1.5000	15.79
16	LGNSRMLLV	164	1.3000	13.68
17	IGHAIVDRL	91	1.2600	13.26

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	VRRARTSDV	11	2.0700	22.75
2	VAVDPAMTG	80	1.9000	20.88
3	LQLQRVFVL	106	1.9000	20.88
4	IRTVAVDPA	77	1.8000	19.78
5	VKPNILGNS	159	1.6000	17.58
6	ILGNSRMLL	163	1.5000	16.48
7	LQRVFVLTF	108	1.3000	14.29
8	LLQVARDLQ	99	0.9000	9.89
9	VARDLQLQR	102	0.9000	9.89
10	VVGCGALHV	61	0.8000	8.79
11	VLWSDLGEI	69	0.7000	7.69

12	YVKPNILGN	158	0.6000	6.59
13	LVTLYEAVQ	39	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	IRTVAVDPA	77	3.1000	35.23
2	VRRARTSDV	11	2.8000	31.82
3	LQRVFVLTF	108	2.8000	31.82
4	VAVDPAMTG	80	2.6000	29.55
5	VARDLQLQR	102	2.4000	27.27
6	VVGCGALHV	61	2.3000	26.14
7	LLQVARDLQ	99	2.2000	25.00
8	ILGNSRMLL	163	2.2000	25.00
9	LQLQRVFVL	106	1.4000	15.91
10	LVTLYEAVQ	39	1.2000	13.64
11	VKPNILGNS	159	1.2000	13.64
12	VVRRARTSD	10	1.0000	11.36
13	LWSDLGEIR	70	0.9000	10.23
14	LGNSRMLLV	164	0.8000	9.09
15	IGHAIVDRL	91	0.6000	6.82
16	LSYVKPNIL	156	0.6000	6.82
17	LEKNLVTLY	35	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	IRTVAVDPA	77	3.1000	35.23
2	VRRARTSDV	11	2.8000	31.82
3	LQRVFVLTF	108	2.8000	31.82
4	VAVDPAMTG	80	2.6000	29.55

5	VARDLQLQR	102	2.4000	27.27
6	VVGCGALHV	61	2.3000	26.14
7	LLQVARDLQ	99	2.2000	25.00
8	ILGNSRMLL	163	2.2000	25.00
9	LQLQRVFVL	106	1.4000	15.91
10	LVTLYEAVQ	39	1.2000	13.64
11	VKPNILGNS	159	1.2000	13.64
12	VVRRARTSD	10	1.0000	11.36
13	LWSDLGEIR	70	0.9000	10.23
14	LGNSRMLLV	164	0.8000	9.09
15	IGHAIVDRL	91	0.6000	6.82
16	LSYVKPNIL	156	0.6000	6.82
17	LEKNLVTLY	35	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	IRTVAVDPA	77	3.1000	35.23
2	VRRARTSDV	11	2.8000	31.82
3	LQRVFVLTF	108	2.8000	31.82
4	VAVDPAMTG	80	2.6000	29.55
5	VARDLQLQR	102	2.4000	27.27
6	VVGCGALHV	61	2.3000	26.14
7	LLQVARDLQ	99	2.2000	25.00
8	ILGNSRMLL	163	2.2000	25.00
9	LQLQRVFVL	106	1.4000	15.91
10	LVTLYEAVQ	39	1.2000	13.64
11	VKPNILGNS	159	1.2000	13.64
12	VVRRARTSD	10	1.0000	11.36
13	LWSDLGEIR	70	0.9000	10.23
14	LGNSRMLLV	164	0.8000	9.09
15	IGHAIVDRL	91	0.6000	6.82
16	LSYVKPNIL	156	0.6000	6.82

17	LEKNLVTLY	35	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	VAVDPAMTG	80	3.3000	34.74
2	LQRVFVLTF	108	3.2000	33.68
3	VRRARTSDV	11	3.0700	32.32
4	LQLQRVFVL	106	2.8600	30.11
5	ILGNSRMLL	163	2.4600	25.89
6	VARDLQLQR	102	2.4000	25.26
7	VKPNILGNS	159	2.0000	21.05
8	VVGCGALHV	61	1.8000	18.95
9	IRTVAVDPA	77	1.8000	18.95
10	VLWSDLGEI	69	1.6000	16.84
11	FVLTFETEF	112	1.5000	15.79
12	YVKPNILGN	158	1.4000	14.74
13	WVAEHPDLY	50	1.3000	13.68
14	VVRRARTSD	10	1.1000	11.58
15	LWSDLGEIR	70	1.0000	10.53
16	FWVAEHPDL	49	0.9600	10.11
17	LYGKVVGCG	57	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	IRTVAVDPA	77	3.1000	35.23
2	VRRARTSDV	11	2.8000	31.82
3	LQRVFVLTF	108	2.8000	31.82
4	VAVDPAMTG	80	2.6000	29.55
5	VARDLQLQR	102	2.4000	27.27

6	VVGCGALHV	61	2.3000	26.14
7	LLQVARDLQ	99	2.2000	25.00
8	ILGNSRMLL	163	2.2000	25.00
9	LQLQRVFVL	106	1.4000	15.91
10	LVTLYEAVQ	39	1.2000	13.64
11	VKPNILGNS	159	1.2000	13.64
12	VVRRARTSD	10	1.0000	11.36
13	LWSDLGEIR	70	0.9000	10.23
14	LGNSRMLLV	164	0.8000	9.09
15	IGHAIVDRL	91	0.6000	6.82
16	LSYVKPNIL	156	0.6000	6.82
17	LEKNLVTLY	35	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	ILLEKNLVT	33	3.3000	38.37
2	VRRARTSDV	11	2.9000	33.72
3	WVAEHPDLY	50	2.3000	26.74
4	VVGCGALHV	61	1.3000	15.12
5	IRTVAVDPA	77	0.9000	10.47
6	LQLQRVFVL	106	0.9000	10.47
7	LHVLWSDLG	67	0.8000	9.30
8	VAVDPAMTG	80	0.7000	8.14
9	LQRVFVLTF	108	0.6000	6.98
10	FETEFFARH	116	0.5800	6.74
11	LGEIRTVAV	74	0.3800	4.42
12	FVLTFETEF	112	0.3000	3.49
13	FARHGFTEI	121	0.3000	3.49
14	VLTFETEFF	113	0.2000	2.33
15	LEKNLVTLY	35	-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	VRRARTSDV	11	3.7000	38.54
2	VVGCGALHV	61	2.6000	27.08
3	LQLQRVFVL	106	2.2000	22.92
4	LQRVFVLTF	108	2.1000	21.88
5	IVDRLLQVA	95	1.8000	18.75
6	VQEFWVAEH	46	1.2800	13.33
7	VLTFETEFF	113	1.0000	10.42
8	ILLEKNLVT	33	0.8000	8.33
9	LGEIRTVAV	74	0.7800	8.12
10	LQVARDLQL	100	0.6000	6.25
11	IRTVAVDPA	77	0.3000	3.12
12	IGVAEFLDL	148	-0.1000	0
13	VVRRARTSD	10	-0.2000	0
14	LEKNLVTLY	35	-0.3000	0
15	LVTLYEAVQ	39	-0.4000	0
16	FARHGFTEI	121	-0.4000	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	VRRARTSDV	11	4.6000	52.27
2	LQRVFVLTF	108	2.6000	29.55
3	IRTVAVDPA	77	2.4000	27.27
4	VLTFETEFF	113	2.2000	25.00
5	LQLQRVFVL	106	2.0500	23.30
6	VQEFWVAEH	46	1.9800	22.50
7	VVGCGALHV	61	1.9000	21.59
8	LGEIRTVAV	74	1.5000	17.05
9	IKQLVDTYA	22	1.4000	15.91

10	ILLEKNLVT	33	1.3000	14.77
11	LVTLYEAVQ	39	1.2000	13.64
12	LHVLWSDLG	67	1.1000	12.50
13	LSYVKPNIL	156	0.7000	7.95
14	LQVARDLQL	100	-0.1000	0
15	LEKNLVTLY	35	-0.3000	0
16	IGHAIVDRL	91	-0.6000	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	VRRARTSDV	11	3.9000	41.49
2	LQRVFVLTF	108	2.5000	26.60
3	VQEFWVAEH	46	2.2000	23.40
4	VLTFETEFF	113	2.1000	22.34
5	LQLQRVFVL	106	2.0500	21.81
6	YVKPNILGN	158	1.6000	17.02
7	LHVLWSDLG	67	1.4000	14.89
8	IRTVAVDPA	77	1.4000	14.89
9	ILLEKNLVT	33	1.2000	12.77
10	VVGCGALHV	61	1.2000	12.77
11	LVTLYEAVQ	39	1.0000	10.64
12	IEGTPVTAE	129	1.0000	10.64
13	VTLYEAVQE	40	0.8000	8.51
14	LGEIRTVAV	74	0.8000	8.51
15	VFVLTFETE	111	0.8000	8.51
16	LSYVKPNIL	156	0.7000	7.45
17	IKQLVDTYA	22	0.4000	4.26

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	VRRARTSDV	11	3.6000	40.91
2	LQRVFVLTF	108	1.6000	18.18
3	IRTVAVDPA	77	1.4000	15.91
4	VLTFETEFF	113	1.2000	13.64
5	LQLQRVFVL	106	1.0500	11.93
6	VQEFWVAEH	46	0.9800	11.14
7	VVGCGALHV	61	0.9000	10.23
8	LGEIRTVAV	74	0.5000	5.68
9	IKQLVDTYA	22	0.4000	4.55
10	ILLEKNLVT	33	0.3000	3.41
11	LVTLYEAVQ	39	0.2000	2.27
12	LHVLWSDLG	67	0.1000	1.14
13	LSYVKPNIL	156	-0.3000	0
14	YVKPNILGN	158	-0.4000	0
15	YGKVVGCGA	58	-0.5000	0
16	FVLTFETEF	112	-0.8000	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	VRRARTSDV	11	4.9000	52.13
2	LQRVFVLTF	108	3.5000	37.23
3	VQEFWVAEH	46	3.2000	34.04
4	VLTFETEFF	113	3.1000	32.98
5	LQLQRVFVL	106	3.0500	32.45
6	LHVLWSDLG	67	2.4000	25.53
7	IRTVAVDPA	77	2.4000	25.53
8	ILLEKNLVT	33	2.2000	23.40
9	VVGCGALHV	61	2.2000	23.40
10	LVTLYEAVQ	39	2.0000	21.28
11	IEGTPVTAE	129	2.0000	21.28
12	VTLYEAVQE	40	1.8000	19.15

13	LGEIRTVAV	74	1.8000	19.15
14	VFVLTFETE	111	1.8000	19.15
15	LSYVKPNIL	156	1.7000	18.09
16	IKQLVDTYA	22	1.4000	14.89
17	LQVARDLQL	100	0.9000	9.57

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	ILLEKNLVT	33	4.0000	44.44
2	VRRARTSDV	11	3.9000	43.33
3	WVAEHPDLY	50	3.6000	40.00
4	LQRVFVLTF	108	2.5000	27.78
5	VVGCGALHV	61	2.3000	25.56
6	LHVLWSDLG	67	2.2000	24.44
7	FVLTFETEF	112	2.2000	24.44
8	VAVDPAMTG	80	2.1000	23.33
9	VLTFETEFF	113	2.1000	23.33
10	LQLQRVFVL	106	1.8600	20.67
11	LGEIRTVAV	74	1.3800	15.33
12	FARHGFTEI	121	1.2000	13.33
13	LEKNLVTLY	35	1.1000	12.22
14	IRTVAVDPA	77	0.9000	10.00
15	VARDLQLQR	102	0.8000	8.89
16	LGNSRMLLV	164	0.7000	7.78
17	IEGTPVTAE	129	0.5000	5.56

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	VRRARTSDV	11	4.6000	52.27

2	LQRVFVLTF	108	2.6000	29.55
3	IRTVAVDPA	77	2.4000	27.27
4	VLTFETEFF	113	2.2000	25.00
5	LQLQRVFVL	106	2.0500	23.30
6	VQEFWVAEH	46	1.9800	22.50
7	VVGCGALHV	61	1.9000	21.59
8	LGEIRTVAV	74	1.5000	17.05
9	IKQLVDTYA	22	1.4000	15.91
10	ILLEKNLVT	33	1.3000	14.77
11	LVTLYEAVQ	39	1.2000	13.64
12	LHVLWSDLG	67	1.1000	12.50
13	LSYVKPNIL	156	0.7000	7.95
14	LQVARDLQL	100	-0.1000	0
15	LEKNLVTLY	35	-0.3000	0
16	IGHAIVDRL	91	-0.6000	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	ILLEKNLVT	33	3.3000	38.37
2	VRRARTSDV	11	2.9000	33.72
3	WVAEHPDLY	50	2.3000	26.74
4	VVGCGALHV	61	1.3000	15.12
5	IRTVAVDPA	77	0.9000	10.47
6	LQLQRVFVL	106	0.9000	10.47
7	LHVLWSDLG	67	0.8000	9.30
8	VAVDPAMTG	80	0.7000	8.14
9	LQRVFVLTF	108	0.6000	6.98
10	FETEFFARH	116	0.5800	6.74
11	LGEIRTVAV	74	0.3800	4.42
12	FVLTFETEF	112	0.3000	3.49
13	FARHGFTEI	121	0.3000	3.49
14	VLTFETEFF	113	0.2000	2.33

15	LEKNLVTLY	35	-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	LQRVFVLTF	108	6.2000	53.45
2	VVGCGALHV	61	5.5000	47.41
3	LQLQRVFVL	106	5.3000	45.69
4	FVLTFETEF	112	5.0000	43.10
5	LGNSRMLLV	164	4.9000	42.24
6	IGVAEFLDL	148	4.8000	41.38
7	LSYVKPNIL	156	4.7000	40.52
8	LVDTYAGKI	25	4.6000	39.66
9	FARHGFTEI	121	4.3000	37.07
10	VRRARTSDV	11	4.2200	36.38
11	VLWSDLGEI	69	4.0000	34.48
12	LQVARDLQL	100	3.8000	32.76
13	YDIGVAEFL	146	3.4000	29.31
14	ILGNSRMLL	163	3.2000	27.59
15	VLTFETEFF	113	3.1200	26.90
16	MCRSYDIGV	142	3.1000	26.72
17	LGEIRTVAV	74	2.9200	25.17

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	LQRVFVLTF	108	6.2000	53.45
2	VVGCGALHV	61	5.5000	47.41
3	LQLQRVFVL	106	5.3000	45.69
4	FVLTFETEF	112	5.0000	43.10
5	LGNSRMLLV	164	4.9000	42.24

6	IGVAEFLDL	148	4.8000	41.38
7	LSYVKPNIL	156	4.7000	40.52
8	LVDTYAGKI	25	4.6000	39.66
9	FARHGFTEI	121	4.3000	37.07
10	VRRARTSDV	11	4.2200	36.38
11	VLWSDLGEI	69	4.0000	34.48
12	LQVARDLQL	100	3.8000	32.76
13	YDIGVAEFL	146	3.4000	29.31
14	ILGNSRMLL	163	3.2000	27.59
15	VLTFETEFF	113	3.1200	26.90
16	MCRSYDIGV	142	3.1000	26.72
17	LGEIRTVAV	74	2.9200	25.17

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	VVRRARTSD	10	3.7000	43.02
2	LYGKVVGCG	57	3.4000	39.53
3	FFARHGFTE	120	2.8000	32.56
4	VTLYEAVQE	40	2.4000	27.91
5	YVKPNILGN	158	2.1000	24.42
6	VQEFWVAEH	46	2.0000	23.26
7	LQRVFVLTF	108	2.0000	23.26
8	LVTLYEAVQ	39	1.7000	19.77
9	YAGKILLEK	29	1.4000	16.28
10	IVDRLLQVA	95	1.1000	12.79
11	VRRARTSDV	11	1.0000	11.63
12	ILGNSRMLL	163	0.9000	10.47
13	VKPNILGNS	159	0.8000	9.30
14	VVGCGALHV	61	0.6000	6.98
15	LQLQRVFVL	106	0.5000	5.81
16	IRTVAVDPA	77	0.3000	3.49
17	LLEKNLVTL	34	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	YAGKILLEK	29	2.1000	26.25
2	LYGKVVGCG	57	2.1000	26.25
3	IVDRLLQVA	95	1.1000	13.75
4	LQRVFVLTF	108	1.1000	13.75
5	VVRRARTSD	10	1.0000	12.50
6	LVTLYEAVQ	39	0.9000	11.25
7	VKPNILGNS	159	0.8000	10.00
8	VQEFWVAEH	46	0.7800	9.75
9	VRRARTSDV	11	0.7000	8.75
10	VVGCGALHV	61	0.3000	3.75
11	IRTVAVDPA	77	0.3000	3.75
12	YGKVVGCGA	58	0.1000	1.25
13	YVKPNILGN	158	0.1000	1.25
14	ILGNSRMLL	163	-0.1000	0
15	FFARHGFTE	120	-0.2000	0
16	LQLQRVFVL	106	-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	LYGKVVGCG	57	3.1000	38.75
2	IVDRLLQVA	95	2.1000	26.25
3	LQRVFVLTF	108	2.1000	26.25
4	VVRRARTSD	10	2.0000	25.00
5	LVTLYEAVQ	39	1.9000	23.75
6	VKPNILGNS	159	1.8000	22.50
7	VQEFWVAEH	46	1.7800	22.25
8	VRRARTSDV	11	1.7000	21.25

9	VVGCGALHV	61	1.3000	16.25
10	IRTVAVDPA	77	1.3000	16.25
11	YAGKILLEK	29	1.1000	13.75
12	ILGNSRMLL	163	0.9000	11.25
13	LQLQRVFVL	106	0.5000	6.25
14	VTLYEAVQE	40	0.4000	5.00
15	LLQVARDLQ	99	0.4000	5.00
16	LLEKNLVTL	34	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	VVRRARTSD	10	4.7000	54.65
2	LYGKVVGCG	57	4.4000	51.16
3	VTLYEAVQE	40	3.4000	39.53
4	VQEFWVAEH	46	3.0000	34.88
5	LQRVFVLTF	108	3.0000	34.88
6	LVTLYEAVQ	39	2.7000	31.40
7	IVDRLLQVA	95	2.1000	24.42
8	VRRARTSDV	11	2.0000	23.26
9	ILGNSRMLL	163	1.9000	22.09
10	FFARHGFTE	120	1.8000	20.93
11	VKPNILGNS	159	1.8000	20.93
12	VVGCGALHV	61	1.6000	18.60
13	LQLQRVFVL	106	1.5000	17.44
14	IRTVAVDPA	77	1.3000	15.12
15	LLEKNLVTL	34	1.2000	13.95
16	LLQVARDLQ	99	1.2000	13.95
17	YVKPNILGN	158	1.1000	12.79

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	VVRRARTSD	10	3.8000	43.68
2	YAGKILLEK	29	2.7000	31.03
3	VRRARTSDV	11	2.5000	28.74
4	IVDRLLQVA	95	2.1000	24.14
5	LQRVFVLTF	108	1.7000	19.54
6	IRTVAVDPA	77	1.5000	17.24
7	LYGKVVGCG	57	1.4000	16.09
8	LVTLYEAVQ	39	0.9000	10.34
9	VVGCGALHV	61	0.9000	10.34
10	ILGNSRMLL	163	0.9000	10.34
11	VQEFWVAEH	46	0.7800	8.97
12	YVKPNILGN	158	0.7000	8.05
13	FFARHGFTE	120	0.6500	7.47
14	LLQVARDLQ	99	0.6000	6.90
15	VTLYEAVQE	40	0.4000	4.60
16	LQLQRVFVL	106	0.3500	4.02
17	LLEKNLVTL	34	0.2000	2.30

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	VVRRARTSD	10	4.8000	47.52
2	YVKPNILGN	158	3.9000	38.61
3	LQRVFVLTF	108	3.8000	37.62
4	LYGKVVGCG	57	3.5000	34.65
5	FFARHGFTE	120	3.3000	32.67
6	YAGKILLEK	29	3.2000	31.68
7	VTLYEAVQE	40	2.9000	28.71
8	ILGNSRMLL	163	2.5000	24.75
9	VVGCGALHV	61	2.4000	23.76
10	VQEFWVAEH	46	2.0000	19.80
11	LVTLYEAVQ	39	1.7000	16.83

12	IVDRLLQVA	95	1.2000	11.88
13	VRRARTSDV	11	1.0000	9.90
14	VPAIKQLVD	19	1.0000	9.90
15	LQLQRVFVL	106	1.0000	9.90
16	VKPNILGNS	159	0.9000	8.91
17	LLEKNLVTL	34	0.7000	6.93

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	LQRVFVLTF	108	3.0000	36.14
2	VVGCGALHV	61	2.1000	25.30
3	ILGNSRMLL	163	1.5000	18.07
4	LVTLYEAVQ	39	1.3000	15.66
5	YVKPNILGN	158	1.2000	14.46
6	YAGKILLEK	29	1.1000	13.25
7	VKPNILGNS	159	0.9000	10.84
8	VRRARTSDV	11	0.7000	8.43
9	VQEFWVAEH	46	0.6800	8.19
10	LQLQRVFVL	106	0.6000	7.23
11	YGKVVGCGA	58	0.2000	2.41
12	IRTVAVDPA	77	0.1000	1.20
13	LYGKVVGCG	57	-0.6000	0
14	FWVAEHPDL	49	-0.7500	0
15	LLQVARDLQ	99	-0.8000	0
16	LGNSRMLLV	164	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LQLQRVFVL	106	3.6000	42.86

2	VRRARTSDV	11	2.1000	25.00
3	VQEFWVAEH	46	2.0800	24.76
4	VVGCGALHV	61	2.0000	23.81
5	LVTLYEAVQ	39	1.6000	19.05
6	LQRVFVLTF	108	1.6000	19.05
7	VVRRARTSD	10	1.4000	16.67
8	ILGNSRMLL	163	1.3000	15.48
9	IRTVAVDPA	77	1.0000	11.90
10	MTGHGIGHA	86	0.9000	10.71
11	VKPNILGNS	159	0.9000	10.71
12	IVDRLLQVA	95	0.8000	9.52
13	LYGKVVGCG	57	0.6000	7.14
14	VLTFETEFF	113	0.6000	7.14
15	YAGKILLEK	29	0.3000	3.57
16	LLQVARDLQ	99	0.1000	1.19

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	LQRVFVLTF	108	4.0000	48.19
2	VVGCGALHV	61	3.1000	37.35
3	ILGNSRMLL	163	2.5000	30.12
4	LVTLYEAVQ	39	2.3000	27.71
5	VKPNILGNS	159	1.9000	22.89
6	VRRARTSDV	11	1.7000	20.48
7	VQEFWVAEH	46	1.6800	20.24
8	LQLQRVFVL	106	1.6000	19.28
9	IRTVAVDPA	77	1.1000	13.25
10	LYGKVVGCG	57	0.4000	4.82
11	LLQVARDLQ	99	0.2000	2.41
12	YVKPNILGN	158	0.2000	2.41
13	LGNSRMLLV	164	0.2000	2.41
14	VVRRARTSD	10	0.1000	1.20

15	YAGKILLEK	29	0.1000	1.20
16	IGVAEFLDL	148	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	LQRVFVLTF	108	4.0000	48.19
2	VVGCGALHV	61	3.1000	37.35
3	ILGNSRMLL	163	2.5000	30.12
4	LVTLYEAVQ	39	2.3000	27.71
5	VKPNILGNS	159	1.9000	22.89
6	VRRARTSDV	11	1.7000	20.48
7	VQEFWVAEH	46	1.6800	20.24
8	LQLQRVFVL	106	1.6000	19.28
9	IRTVAVDPA	77	1.1000	13.25
10	LYGKVVGCG	57	0.4000	4.82
11	LLQVARDLQ	99	0.2000	2.41
12	YVKPNILGN	158	0.2000	2.41
13	LGNSRMLLV	164	0.2000	2.41
14	VVRRARTSD	10	0.1000	1.20
15	YAGKILLEK	29	0.1000	1.20
16	IGVAEFLDL	148	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	VRRARTSDV	11	3.0700	33.74
2	VAVDPAMTG	80	2.9000	31.87
3	LQLQRVFVL	106	2.9000	31.87
4	IRTVAVDPA	77	2.8000	30.77
5	VKPNILGNS	159	2.6000	28.57

6	ILGNSRMLL	163	2.5000	27.47
7	LQRVFVLTF	108	2.3000	25.27
8	LLQVARDLQ	99	1.9000	20.88
9	VARDLQLQR	102	1.9000	20.88
10	VVGCGALHV	61	1.8000	19.78
11	VLWSDLGEI	69	1.7000	18.68
12	LVTLYEAVQ	39	1.2000	13.19
13	VVRRARTSD	10	1.0000	10.99
14	MTGHGIGHA	86	1.0000	10.99
15	LWSDLGEIR	70	0.5000	5.49
16	LEKNLVTLY	35	0.4000	4.40
17	LYGKVVGCG	57	0.4000	4.40

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	LQLQRVFVL	106	2.6000	30.95
2	YAGKILLEK	29	1.3000	15.48
3	VRRARTSDV	11	1.1000	13.10
4	VQEFWVAEH	46	1.0800	12.86
5	VVGCGALHV	61	1.0000	11.90
6	LVTLYEAVQ	39	0.6000	7.14
7	LQRVFVLTF	108	0.6000	7.14
8	VVRRARTSD	10	0.4000	4.76
9	YVKPNILGN	158	0.3000	3.57
10	ILGNSRMLL	163	0.3000	3.57
11	MTGHGIGHA	86	-0.1000	0
12	VKPNILGNS	159	-0.1000	0
13	IVDRLLQVA	95	-0.2000	0
14	LYGKVVGCG	57	-0.4000	0
15	VLTFETEFF	113	-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	LQLQRVFVL	106	3.5600	40.45
2	LQRVFVLTF	108	2.5000	28.41
3	VRRARTSDV	11	2.1000	23.86
4	VVGCGALHV	61	2.0000	22.73
5	VVRRARTSD	10	1.5000	17.05
6	VLTFETEFF	113	1.5000	17.05
7	YAGKILLEK	29	1.4000	15.91
8	ILGNSRMLL	163	1.2600	14.32
9	YVKPNILGN	158	1.1000	12.50
10	LYGKVVGCG	57	1.0000	11.36
11	FVLTFETEF	112	0.6000	6.82
12	FFARHGFTE	120	0.6000	6.82
13	VQEFWVAEH	46	0.5000	5.68
14	FARHGFTEI	121	0.5000	5.68
15	WVAEHPDLY	50	0.3000	3.41
16	VKPNILGNS	159	0.3000	3.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LQLQRVFVL	106	3.6000	42.86
2	VRRARTSDV	11	2.1000	25.00
3	VQEFWVAEH	46	2.0800	24.76
4	VVGCGALHV	61	2.0000	23.81
5	LVTLYEAVQ	39	1.6000	19.05
6	LQRVFVLTF	108	1.6000	19.05
7	VVRRARTSD	10	1.4000	16.67
8	ILGNSRMLL	163	1.3000	15.48
9	IRTVAVDPA	77	1.0000	11.90

10	MTGHGIGHA	86	0.9000	10.71
11	VKPNILGNS	159	0.9000	10.71
12	IVDRLLQVA	95	0.8000	9.52
13	LYGKVVGCG	57	0.6000	7.14
14	VLTFETEFF	113	0.6000	7.14
15	YAGKILLEK	29	0.3000	3.57
16	LLQVARDLQ	99	0.1000	1.19

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	LQRVFVLTF	108	4.9000	56.32
2	VVGCGALHV	61	3.1000	35.63
3	ILGNSRMLL	163	2.4600	28.28
4	YVKPNILGN	158	2.0000	22.99
5	VRRARTSDV	11	1.7000	19.54
6	LQLQRVFVL	106	1.5600	17.93
7	VKPNILGNS	159	1.3000	14.94
8	YAGKILLEK	29	1.2000	13.79
9	LYGKVVGCG	57	0.8000	9.20
10	VLTFETEFF	113	0.8000	9.20
11	FVLTFETEF	112	0.7000	8.05
12	LVTLYEAVQ	39	0.6000	6.90
13	FWVAEHPDL	49	0.2100	2.41
14	VVRRARTSD	10	0.2000	2.30
15	YGKVVGCGA	58	0.2000	2.30
16	LGNSRMLLV	164	0.2000	2.30
17	VQEFWVAEH	46	0.1000	1.15

ALLELE: DRB1_1301	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LQLQRVFVL	106	4.5600	51.82
2	LQRVFVLTF	108	3.5000	39.77
3	VRRARTSDV	11	3.1000	35.23
4	VVGCGALHV	61	3.0000	34.09
5	VVRRARTSD	10	2.5000	28.41
6	VLTFETEFF	113	2.5000	28.41
7	ILGNSRMLL	163	2.2600	25.68
8	LYGKVVGCG	57	2.0000	22.73
9	VQEFWVAEH	46	1.5000	17.05
10	VKPNILGNS	159	1.3000	14.77
11	VTLYEAVQE	40	1.0000	11.36
12	IRTVAVDPA	77	1.0000	11.36
13	LVTLYEAVQ	39	0.9000	10.23
14	MTGHGIGHA	86	0.9000	10.23
15	LEKNLVTLY	35	0.8000	9.09
16	IVDRLLQVA	95	0.8000	9.09
17	LLEKNLVTL	34	0.6600	7.50

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	LQLQRVFVL	106	3.5600	40.45
2	LQRVFVLTF	108	2.5000	28.41
3	VRRARTSDV	11	2.1000	23.86
4	VVGCGALHV	61	2.0000	22.73
5	VVRRARTSD	10	1.5000	17.05
6	VLTFETEFF	113	1.5000	17.05
7	YAGKILLEK	29	1.4000	15.91
8	ILGNSRMLL	163	1.2600	14.32
9	YVKPNILGN	158	1.1000	12.50
10	LYGKVVGCG	57	1.0000	11.36
11	FVLTFETEF	112	0.6000	6.82

12	FFARHGFTE	120	0.6000	6.82
13	VQEFWVAEH	46	0.5000	5.68
14	FARHGFTEI	121	0.5000	5.68
15	WVAEHPDLY	50	0.3000	3.41
16	VKPNILGNS	159	0.3000	3.41

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LQLQRVFVL	106	4.6000	51.11
2	VVRRARTSD	10	4.1000	45.56
3	VQEFWVAEH	46	3.3000	36.67
4	VTLYEAVQE	40	2.6000	28.89
5	LQRVFVLTF	108	2.5000	27.78
6	VRRARTSDV	11	2.4000	26.67
7	LVTLYEAVQ	39	2.4000	26.67
8	VVGCGALHV	61	2.3000	25.56
9	ILGNSRMLL	163	2.3000	25.56
10	LYGKVVGCG	57	1.9000	21.11
11	VLTFETEFF	113	1.5000	16.67
12	YVKPNILGN	158	1.3000	14.44
13	FFARHGFTE	120	1.2000	13.33
14	IRTVAVDPA	77	1.0000	11.11
15	MTGHGIGHA	86	0.9000	10.00
16	LLQVARDLQ	99	0.9000	10.00
17	LDLSYVKPN	154	0.9000	10.00

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	LQRVFVLTF	108	4.9000	56.32

2	VVGCGALHV	61	3.1000	35.63
3	ILGNSRMLL	163	2.4600	28.28
4	YVKPNILGN	158	2.0000	22.99
5	VRRARTSDV	11	1.7000	19.54
6	LQLQRVFVL	106	1.5600	17.93
7	VKPNILGNS	159	1.3000	14.94
8	YAGKILLEK	29	1.2000	13.79
9	LYGKVVGCG	57	0.8000	9.20
10	VLTFETEFF	113	0.8000	9.20
11	FVLTFETEF	112	0.7000	8.05
12	LVTLYEAVQ	39	0.6000	6.90
13	FWVAEHPDL	49	0.2100	2.41
14	VVRRARTSD	10	0.2000	2.30
15	YGKVVGCGA	58	0.2000	2.30
16	LGNSRMLLV	164	0.2000	2.30
17	VQEFWVAEH	46	0.1000	1.15

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8

Rank	Sequence	At Position	Score	% of Highest Score
1	LVTLYEAVQ	39	1.3000	19.12
2	LQRVFVLTF	108	1.2000	17.65
3	VKPNILGNS	159	0.8000	11.76
4	VRRARTSDV	11	0.7000	10.29
5	VQEFWVAEH	46	0.6800	10.00
6	IRTVAVDPA	77	0.4000	5.88
7	VVGCGALHV	61	0.3000	4.41
8	YGKVVGCGA	58	0.2000	2.94
9	LQLQRVFVL	106	0.1000	1.47
10	ILGNSRMLL	163	-0.1000	0
11	LLQVARDLQ	99	-0.5000	0
12	YVKPNILGN	158	-0.6000	0
13	YAGKILLEK	29	-0.7000	0

14	LYGKVVGCG	57	-0.7000	0
15	MTGHGIGHA	86	-1.2000	0
16	VLWSDLGEI	69	-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	LQRVFVLTF	108	4.0000	48.19
2	VVGCGALHV	61	3.1000	37.35
3	ILGNSRMLL	163	2.5000	30.12
4	LVTLYEAVQ	39	2.3000	27.71
5	VKPNILGNS	159	1.9000	22.89
6	VRRARTSDV	11	1.7000	20.48
7	VQEFWVAEH	46	1.6800	20.24
8	LQLQRVFVL	106	1.6000	19.28
9	IRTVAVDPA	77	1.1000	13.25
10	LYGKVVGCG	57	0.4000	4.82
11	LLQVARDLQ	99	0.2000	2.41
12	YVKPNILGN	158	0.2000	2.41
13	LGNSRMLLV	164	0.2000	2.41
14	VVRRARTSD	10	0.1000	1.20
15	YAGKILLEK	29	0.1000	1.20
16	IGVAEFLDL	148	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	LQRVFVLTF	108	3.9000	43.82
2	YVKPNILGN	158	3.2000	35.96
3	ILGNSRMLL	163	2.5000	28.09
4	VVGCGALHV	61	2.4000	26.97

5	LVTLYEAVQ	39	2.1000	23.60
6	VQEFWVAEH	46	1.9000	21.35
7	VVRRARTSD	10	1.8000	20.22
8	VPAIKQLVD	19	1.6000	17.98
9	LQLQRVFVL	106	1.6000	17.98
10	VRRARTSDV	11	1.0000	11.24
11	VKPNILGNS	159	0.9000	10.11
12	LYGKVVGCG	57	0.7000	7.87
13	YAGKILLEK	29	0.4000	4.49
14	FFARHGFTE	120	0.3000	3.37
15	FWVAEHPDL	49	0.2500	2.81
16	YGKVVGCGA	58	0.2000	2.25
17	IRTVAVDPA	77	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	LQLQRVFVL	106	3.6000	42.86
2	VRRARTSDV	11	2.1000	25.00
3	VQEFWVAEH	46	2.0800	24.76
4	VVGCGALHV	61	2.0000	23.81
5	LVTLYEAVQ	39	1.6000	19.05
6	LQRVFVLTF	108	1.6000	19.05
7	VVRRARTSD	10	1.4000	16.67
8	ILGNSRMLL	163	1.3000	15.48
9	IRTVAVDPA	77	1.0000	11.90
10	MTGHGIGHA	86	0.9000	10.71
11	VKPNILGNS	159	0.9000	10.71
12	IVDRLLQVA	95	0.8000	9.52
13	LYGKVVGCG	57	0.6000	7.14
14	VLTFETEFF	113	0.6000	7.14
15	YAGKILLEK	29	0.3000	3.57
16	LLQVARDLQ	99	0.1000	1.19

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	LQLQRVFVL	106	2.6000	30.95
2	YAGKILLEK	29	1.3000	15.48
3	VRRARTSDV	11	1.1000	13.10
4	VQEFWVAEH	46	1.0800	12.86
5	VVGCGALHV	61	1.0000	11.90
6	LVTLYEAVQ	39	0.6000	7.14
7	LQRVFVLTF	108	0.6000	7.14
8	VVRRARTSD	10	0.4000	4.76
9	YVKPNILGN	158	0.3000	3.57
10	ILGNSRMLL	163	0.3000	3.57
11	MTGHGIGHA	86	-0.1000	0
12	VKPNILGNS	159	-0.1000	0
13	IVDRLLQVA	95	-0.2000	0
14	LYGKVVGCG	57	-0.4000	0
15	VLTFETEFF	113	-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	LQLQRVFVL	106	4.5600	51.82
2	LQRVFVLTF	108	3.5000	39.77
3	VRRARTSDV	11	3.1000	35.23
4	VVGCGALHV	61	3.0000	34.09
5	VVRRARTSD	10	2.5000	28.41
6	VLTFETEFF	113	2.5000	28.41
7	ILGNSRMLL	163	2.2600	25.68
8	LYGKVVGCG	57	2.0000	22.73
9	VQEFWVAEH	46	1.5000	17.05

10	VKPNILGNS	159	1.3000	14.77
11	VTLYEAVQE	40	1.0000	11.36
12	IRTVAVDPA	77	1.0000	11.36
13	LVTLYEAVQ	39	0.9000	10.23
14	MTGHGIGHA	86	0.9000	10.23
15	LEKNLVTLY	35	0.8000	9.09
16	IVDRLLQVA	95	0.8000	9.09
17	LLEKNLVTL	34	0.6600	7.50

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	LQLQRVFVL	106	4.5600	51.82
2	LQRVFVLTF	108	3.5000	39.77
3	VRRARTSDV	11	3.1000	35.23
4	VVGCGALHV	61	3.0000	34.09
5	VVRRARTSD	10	2.5000	28.41
6	VLTFETEFF	113	2.5000	28.41
7	ILGNSRMLL	163	2.2600	25.68
8	LYGKVVGCG	57	2.0000	22.73
9	VQEFWVAEH	46	1.5000	17.05
10	VKPNILGNS	159	1.3000	14.77
11	VTLYEAVQE	40	1.0000	11.36
12	IRTVAVDPA	77	1.0000	11.36
13	LVTLYEAVQ	39	0.9000	10.23
14	MTGHGIGHA	86	0.9000	10.23
15	LEKNLVTLY	35	0.8000	9.09
16	IVDRLLQVA	95	0.8000	9.09
17	LLEKNLVTL	34	0.6600	7.50

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	VVGCGALHV	61	4.5000	45.92
2	ILGNSRMLL	163	4.2000	42.86
3	ILLEKNLVT	33	3.8000	38.78
4	LQVARDLQL	100	3.7000	37.76
5	VRRARTSDV	11	3.4600	35.31
6	LQRVFVLTF	108	3.3000	33.67
7	IGVAEFLDL	148	3.1000	31.63
8	LQLQRVFVL	106	3.0000	30.61
9	LGNSRMLLV	164	3.0000	30.61
10	VVRRARTSD	10	2.3000	23.47
11	VLTFETEFF	113	2.2600	23.06
12	VDTYAGKIL	26	1.9000	19.39
13	VTLYEAVQE	40	1.9000	19.39
14	VGCGALHVL	62	1.8000	18.37
15	MCRSYDIGV	142	1.8000	18.37
16	VAEFLDLSY	150	1.8000	18.37
17	LSYVKPNIL	156	1.7000	17.35

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	VVGCGALHV	61	3.5000	35.71
2	ILGNSRMLL	163	3.2000	32.65
3	ILLEKNLVT	33	2.8000	28.57
4	LQVARDLQL	100	2.7000	27.55
5	YVKPNILGN	158	2.5500	26.02
6	VRRARTSDV	11	2.4600	25.10
7	FARHGFTEI	121	2.4000	24.49
8	LQRVFVLTF	108	2.3000	23.47
9	IGVAEFLDL	148	2.1000	21.43
10	LQLQRVFVL	106	2.0000	20.41
11	LGNSRMLLV	164	2.0000	20.41

12	FVLTFETEF	112	1.6000	16.33
13	VVRRARTSD	10	1.3000	13.27
14	VLTFETEFF	113	1.2600	12.86
15	YGKVVGCGA	58	1.2000	12.24
16	YEAVQEFWV	43	1.0000	10.20
17	FFARHGFTE	120	1.0000	10.20

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	VVGCGALHV	61	4.5000	45.92
2	ILGNSRMLL	163	4.2000	42.86
3	ILLEKNLVT	33	3.8000	38.78
4	LQVARDLQL	100	3.7000	37.76
5	VRRARTSDV	11	3.4600	35.31
6	LQRVFVLTF	108	3.3000	33.67
7	IGVAEFLDL	148	3.1000	31.63
8	LQLQRVFVL	106	3.0000	30.61
9	LGNSRMLLV	164	3.0000	30.61
10	VVRRARTSD	10	2.3000	23.47
11	VLTFETEFF	113	2.2600	23.06
12	VDTYAGKIL	26	1.9000	19.39
13	VTLYEAVQE	40	1.9000	19.39
14	VGCGALHVL	62	1.8000	18.37
15	MCRSYDIGV	142	1.8000	18.37
16	VAEFLDLSY	150	1.8000	18.37
17	LSYVKPNIL	156	1.7000	17.35

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	FVLTFETEF	112	2.9000	29.59
2	LSYVKPNIL	156	2.6000	26.53
3	LQRVFVLTF	108	2.5000	25.51
4	LQLQRVFVL	106	2.0000	20.41
5	LVDTYAGKI	25	1.9000	19.39
6	VVGCGALHV	61	1.7000	17.35
7	YGKVVGCGA	58	1.3000	13.27
8	YAGKILLEK	29	0.8000	8.16
9	WVAEHPDLY	50	0.8000	8.16
10	VRRARTSDV	11	0.7000	7.14
11	LQVARDLQL	100	0.6000	6.12
12	YEAVQEFWV	43	0.5000	5.10
13	LVTLYEAVQ	39	0.4000	4.08
14	VLWSDLGEI	69	0.3000	3.06
15	IGVAEFLDL	148	0.2000	2.04
16	FWVAEHPDL	49	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FVLTFETEF	112	2.9000	29.59
2	LSYVKPNIL	156	2.6000	26.53
3	LQRVFVLTF	108	2.5000	25.51
4	LQLQRVFVL	106	2.0000	20.41
5	LVDTYAGKI	25	1.9000	19.39
6	VVGCGALHV	61	1.7000	17.35
7	YGKVVGCGA	58	1.3000	13.27
8	YAGKILLEK	29	0.8000	8.16
9	WVAEHPDLY	50	0.8000	8.16
10	VRRARTSDV	11	0.7000	7.14
11	LQVARDLQL	100	0.6000	6.12
12	YEAVQEFWV	43	0.5000	5.10
13	LVTLYEAVQ	39	0.4000	4.08

14	VLWSDLGEI	69	0.3000	3.06
15	IGVAEFLDL	148	0.2000	2.04
16	FWVAEHPDL	49	-0.1000	0