MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sun Mar 7 00:19:00 2010
Length of input sequence	247 amino acids
Number of nanomers from input sequence	239
Number of nanomers with obligatory P1 anchor residue	89
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	24

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	YIFMGPLFT	7	2.6000	43.33
2	YVDIYAASV	211	1.6000	26.67
3	YIPSSGPAI	27	1.1700	19.50
4	VRFGKPMDF	171	0.7900	13.17
5	WYYLFKYIF	1	0.7000	11.67
6	YYLFKYIFM	2	0.6600	11.00
7	VVLLGQGKL	104	0.6000	10.00
8	FEGLAGNHF	182	0.6000	10.00

9	FTLLGRPKV	14	0.4700	7.83
10	VLLGQGKLL	105	0.3000	5.00
11	WFLAKSEYF	58	0.2000	3.33
12	LMGLSGQEY	203	0.2000	3.33
13	YLPLVVRRR	48	0.1900	3.17
14	VAMIGTNVV	148	0.1000	1.67
15	MLRFGRVTV	163	-0.0200	0
16	FYSVSGQVP	79	-0.1500	0
17	LAVADSFYL	41	-0.3000	0
18	FSRFEGLAG	179	-0.3200	0
19	VVNPPGRKM	155	-0.4300	0
20	WFYSVSGQV	78	-0.5000	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	VRFGKPMDF	171	1.7900	29.83
2	YIFMGPLFT	7	1.6000	26.67
3	VVLLGQGKL	104	1.6000	26.67
4	VLLGQGKLL	105	1.3000	21.67
5	LMGLSGQEY	203	1.2000	20.00
6	VAMIGTNVV	148	1.1000	18.33
7	LLGMYPEGT	112	1.0000	16.67
8	LALHTGVPV	137	1.0000	16.67
9	MLRFGRVTV	163	0.9800	16.33
10	LAVADSFYL	41	0.7000	11.67
11	FEGLAGNHF	182	0.6000	10.00
12	YVDIYAASV	211	0.6000	10.00
13	VVNPPGRKM	155	0.5700	9.50
14	FTLLGRPKV	14	0.4700	7.83
15	IFMGPLFTL	8	0.3000	5.00
16	LRFGRVTVR	164	0.2900	4.83
17	YIPSSGPAI	27	0.1700	2.83

18	VPVIPVAMI	143	0.1000	1.67
19	VIPVAMIGT	145	-0.0500	0
20	FYSVSGQVP	79	-0.1500	0
21	IYELMGLSG	200	-0.2000	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	VRFGKPMDF	171	6.0000	63.16
2	LRFGRVTVR	164	5.1000	53.68
3	LVVRRRIWF	51	3.9000	41.05
4	VPIDRTNAD	86	3.4100	35.89
5	IFMGPLFTL	8	3.3600	35.37
6	LLGQGKLLG	106	3.1000	32.63
7	LQTAVVLLG	100	3.0000	31.58
8	VAMIGTNVV	148	2.9100	30.63
9	VVLLGQGKL	104	2.8600	30.11
10	WYYLFKYIF	1	2.8500	30.00
11	LGQGKLLGM	107	2.5000	26.32
12	IWFLAKSEY	57	2.3700	24.95
13	LYKGKTGLA	127	2.3000	24.21
14	VPVIPVAMI	143	2.3000	24.21
15	MGPLFTLLG	10	2.2000	23.16
16	MLRFGRVTV	163	2.2000	23.16
17	LLGRPKVEG	16	2.1000	22.11
18	ILASNHLAV	35	2.1000	22.11
19	FTLLGRPKV	14	2.0000	21.05
20	MGLSGQEYV	204	2.0000	21.05
21	VVRRRIWFL	52	1.8600	19.58
22	FYLPLVVRR	47	1.8000	18.95
23	YIPSSGPAI	27	1.7000	17.89
24	LHTGVPVIP	139	1.7000	17.89

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	VRFGKPMDF	171	3.1000	34.07
2	LRFGRVTVR	164	2.6000	28.57
3	FTLLGRPKV	14	2.0000	21.98
4	WYYLFKYIF	1	1.9500	21.43
5	YELMGLSGQ	201	1.8700	20.55
6	YIPSSGPAI	27	1.8000	19.78
7	WFYSVSGQV	78	1.6000	17.58
8	YIFMGPLFT	7	1.4000	15.38
9	IFMGPLFTL	8	1.4000	15.38
10	VPIDRTNAD	86	1.3100	14.40
11	FYLPLVVRR	47	1.3000	14.29
12	LYKGKTGLA	127	1.3000	14.29
13	YLFKYIFMG	3	1.0000	10.99
14	LVVRRRIWF	51	1.0000	10.99
15	VAMIGTNVV	148	0.9100	10.00
16	VVLLGQGKL	104	0.9000	9.89
17	LLGQGKLLG	106	0.7000	7.69
18	FKYIFMGPL	5	0.6000	6.59
19	YLPLVVRRR	48	0.6000	6.59
20	LQTAVVLLG	100	0.6000	6.59
21	YVDIYAASV	211	0.6000	6.59
22	WFLAKSEYF	58	0.5000	5.49
23	YSVSGQVPI	80	0.5000	5.49
24	FGRVTVRFG	166	0.5000	5.49

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	VRFGKPMDF	171	3.8000	43.18
2	LRFGRVTVR	164	3.6000	40.91
3	VPIDRTNAD	86	3.0000	34.09
4	VAMIGTNVV	148	2.6000	29.55
5	LLGQGKLLG	106	2.2000	25.00
6	LQTAVVLLG	100	2.1000	23.86
7	LVVRRRIWF	51	1.6800	19.09
8	ILASNHLAV	35	1.6000	18.18
9	LGQGKLLGM	107	1.5000	17.05
10	VPVIPVAMI	143	1.4000	15.91
11	MGLSGQEYV	204	1.4000	15.91
12	MGPLFTLLG	10	1.3000	14.77
13	IGTNVVNPP	151	1.2000	13.64
14	MLRFGRVTV	163	1.0800	12.27
15	YIFMGPLFT	7	0.9000	10.23
16	IFMGPLFTL	8	0.9000	10.23
17	LYKGKTGLA	127	0.9000	10.23
18	IWFLAKSEY	57	0.8000	9.09
19	IYAASVKDG	214	0.8000	9.09
20	LLGMYPEGT	112	0.7000	7.95
21	LGRPKVEGL	17	0.6000	6.82
22	LASNHLAVA	36	0.6000	6.82
23	IERAVTDEV	191	0.6000	6.82
24	YELMGLSGQ	201	0.6000	6.82

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	VRFGKPMDF	171	3.8000	43.18
2	LRFGRVTVR	164	3.6000	40.91
3	VPIDRTNAD	86	3.0000	34.09
4	VAMIGTNVV	148	2.6000	29.55
5	LLGQGKLLG	106	2.2000	25.00

6	LQTAVVLLG	100	2.1000	23.86
7	LVVRRRIWF	51	1.6800	19.09
8	ILASNHLAV	35	1.6000	18.18
9	LGQGKLLGM	107	1.5000	17.05
10	VPVIPVAMI	143	1.4000	15.91
11	MGLSGQEYV	204	1.4000	15.91
12	MGPLFTLLG	10	1.3000	14.77
13	IGTNVVNPP	151	1.2000	13.64
14	MLRFGRVTV	163	1.0800	12.27
15	YIFMGPLFT	7	0.9000	10.23
16	IFMGPLFTL	8	0.9000	10.23
17	LYKGKTGLA	127	0.9000	10.23
18	IWFLAKSEY	57	0.8000	9.09
19	IYAASVKDG	214	0.8000	9.09
20	LLGMYPEGT	112	0.7000	7.95
21	LGRPKVEGL	17	0.6000	6.82
22	LASNHLAVA	36	0.6000	6.82
23	IERAVTDEV	191	0.6000	6.82
24	YELMGLSGQ	201	0.6000	6.82

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	VRFGKPMDF	171	3.8000	43.18
2	LRFGRVTVR	164	3.6000	40.91
3	VPIDRTNAD	86	3.0000	34.09
4	VAMIGTNVV	148	2.6000	29.55
5	LLGQGKLLG	106	2.2000	25.00
6	LQTAVVLLG	100	2.1000	23.86
7	LVVRRRIWF	51	1.6800	19.09
8	ILASNHLAV	35	1.6000	18.18
9	LGQGKLLGM	107	1.5000	17.05
10	VPVIPVAMI	143	1.4000	15.91

11	MGLSGQEYV	204	1.4000	15.91
12	MGPLFTLLG	10	1.3000	14.77
13	IGTNVVNPP	151	1.2000	13.64
14	MLRFGRVTV	163	1.0800	12.27
15	YIFMGPLFT	7	0.9000	10.23
16	IFMGPLFTL	8	0.9000	10.23
17	LYKGKTGLA	127	0.9000	10.23
18	IWFLAKSEY	57	0.8000	9.09
19	IYAASVKDG	214	0.8000	9.09
20	LLGMYPEGT	112	0.7000	7.95
21	LGRPKVEGL	17	0.6000	6.82
22	LASNHLAVA	36	0.6000	6.82
23	IERAVTDEV	191	0.6000	6.82
24	YELMGLSGQ	201	0.6000	6.82

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	VRFGKPMDF	171	5.0000	52.63
2	LRFGRVTVR	164	4.1000	43.16
3	WYYLFKYIF	1	3.8500	40.53
4	FTLLGRPKV	14	3.0000	31.58
5	LVVRRRIWF	51	2.9000	30.53
6	FYLPLVVRR	47	2.8000	29.47
7	YIPSSGPAI	27	2.7000	28.42
8	WFYSVSGQV	78	2.6000	27.37
9	VPIDRTNAD	86	2.4100	25.37
10	YLFKYIFMG	3	2.4000	25.26
11	WFLAKSEYF	58	2.4000	25.26
12	IFMGPLFTL	8	2.3600	24.84
13	YIFMGPLFT	7	2.1000	22.11
14	YLPLVVRRR	48	2.1000	22.11
15	LLGQGKLLG	106	2.1000	22.11

16	LQTAVVLLG	100	2.0000	21.05
17	VAMIGTNVV	148	1.9100	20.11
18	FGRVTVRFG	166	1.9000	20.00
19	YAASVKDGR	215	1.9000	20.00
20	VVLLGQGKL	104	1.8600	19.58
21	YVDIYAASV	211	1.6000	16.84
22	FKYIFMGPL	5	1.5600	16.42
23	LGQGKLLGM	107	1.5000	15.79
24	YSVSGQVPI	80	1.4000	14.74

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	VRFGKPMDF	171	3.8000	43.18
2	LRFGRVTVR	164	3.6000	40.91
3	VPIDRTNAD	86	3.0000	34.09
4	VAMIGTNVV	148	2.6000	29.55
5	LLGQGKLLG	106	2.2000	25.00
6	LQTAVVLLG	100	2.1000	23.86
7	LVVRRRIWF	51	1.6800	19.09
8	ILASNHLAV	35	1.6000	18.18
9	LGQGKLLGM	107	1.5000	17.05
10	VPVIPVAMI	143	1.4000	15.91
11	MGLSGQEYV	204	1.4000	15.91
12	MGPLFTLLG	10	1.3000	14.77
13	IGTNVVNPP	151	1.2000	13.64
14	MLRFGRVTV	163	1.0800	12.27
15	YIFMGPLFT	7	0.9000	10.23
16	IFMGPLFTL	8	0.9000	10.23
17	LYKGKTGLA	127	0.9000	10.23
18	IWFLAKSEY	57	0.8000	9.09
19	IYAASVKDG	214	0.8000	9.09
20	LLGMYPEGT	112	0.7000	7.95

21	LGRPKVEGL	17	0.6000	6.82
22	LASNHLAVA	36	0.6000	6.82
23	IERAVTDEV	191	0.6000	6.82
24	YELMGLSGQ	201	0.6000	6.82

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	VAMIGTNVV	148	3.0000	34.88
2	YIFMGPLFT	7	2.3000	26.74
3	MGPLFTLLG	10	2.2000	25.58
4	VPIDRTNAD	86	2.2000	25.58
5	WFLAKSEYF	58	2.0000	23.26
6	WFYSVSGQV	78	1.4000	16.28
7	YELMGLSGQ	201	1.2000	13.95
8	MYPEGTRSP	115	1.1000	12.79
9	YVDIYAASV	211	0.9000	10.47
10	YLPLVVRRR	48	0.8000	9.30
11	LQTAVVLLG	100	0.8000	9.30
12	IERAVTDEV	191	0.7000	8.14
13	VIYELMGLS	199	0.7000	8.14
14	MIGTNVVNP	150	0.6800	7.91
15	IGTNVVNPP	151	0.6000	6.98
16	VPVIPVAMI	143	0.4000	4.65
17	FYLPLVVRR	47	0.2800	3.26
18	LEYIPSSGP	25	0.2000	2.33
19	LRFGRVTVR	164	0.2000	2.33
20	VRFGKPMDF	171	0.2000	2.33
21	LLGMYPEGT	112	0.1000	1.16
22	YIPSSGPAI	27	-0.3000	0
23	IYAASVKDG	214	-0.5000	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	LKGWINRWF	71	4.9000	51.04
2	VVRRRIWFL	52	4.1000	42.71
3	VRRRIWFLA	53	3.4000	35.42
4	VAMIGTNVV	148	3.2800	34.17
5	LRFGRVTVR	164	2.3000	23.96
6	MGPLFTLLG	10	2.1000	21.88
7	LQTAVVLLG	100	2.1000	21.88
8	VRFGKPMDF	171	2.1000	21.88
9	INRWFYSVS	75	1.9000	19.79
10	YIFMGPLFT	7	1.3000	13.54
11	YLPLVVRRR	48	1.3000	13.54
12	MYPEGTRSP	115	1.2000	12.50
13	VVNPPGRKM	155	1.1000	11.46
14	FGRVTVRFG	166	1.1000	11.46
15	LAVADSFYL	41	1.0000	10.42
16	IYAASVKDG	214	0.8000	8.33
17	LVVRRRIWF	51	0.7000	7.29
18	WINRWFYSV	74	0.7000	7.29
19	VPVIPVAMI	143	0.6800	7.08
20	MIGTNVVNP	150	0.6000	6.25
21	YLFKYIFMG	3	0.3000	3.12
22	IGTNVVNPP	151	0.3000	3.12
23	LEYIPSSGP	25	0.2800	2.92
24	LALHTGVPV	137	0.2000	2.08

ALLELE: DRB1_0404	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VAMIGTNVV	148	4.4000	50.00

2	MGPLFTLLG	10	3.0000	34.09
3	LEYIPSSGP	25	2.2000	25.00
4	YIFMGPLFT	7	1.8000	20.45
5	YELMGLSGQ	201	1.8000	20.45
6	VPVIPVAMI	143	1.7000	19.32
7	LQTAVVLLG	100	1.4000	15.91
8	INRWFYSVS	75	1.1500	13.07
9	LLGMYPEGT	112	1.1000	12.50
10	LRFGRVTVR	164	0.9000	10.23
11	VPIDRTNAD	86	0.8000	9.09
12	IERAVTDEV	191	0.8000	9.09
13	LKGWINRWF	71	0.6500	7.39
14	VEGLEYIPS	22	0.5800	6.59
15	LAVADSFYL	41	0.4500	5.11
16	VVLLGQGKL	104	0.4000	4.55
17	YLPLVVRRR	48	0.3000	3.41
18	VRFGKPMDF	171	0.3000	3.41
19	YVDIYAASV	211	0.2000	2.27
20	WFLAKSEYF	58	0.1000	1.14
21	IGTNVVNPP	151	0.1000	1.14
22	YYLFKYIFM	2	0.0800	0.91

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	YIFMGPLFT	7	3.7000	39.36
2	VAMIGTNVV	148	3.7000	39.36
3	YELMGLSGQ	201	3.6000	38.30
4	MGPLFTLLG	10	3.3000	35.11
5	VPIDRTNAD	86	2.5000	26.60
6	YYLFKYIFM	2	2.1800	23.19
7	WFLAKSEYF	58	2.0000	21.28
8	FGRVTVRFG	166	2.0000	21.28

9	LQTAVVLLG	100	1.7000	18.09
10	LEYIPSSGP	25	1.6000	17.02
11	YVDIYAASV	211	1.5000	15.96
12	YLPLVVRRR	48	1.3000	13.83
13	LLGMYPEGT	112	1.0000	10.64
14	VPVIPVAMI	143	0.9000	9.57
15	FKYIFMGPL	5	0.7000	7.45
16	LKGWINRWF	71	0.5500	5.85
17	FSRFEGLAG	179	0.5000	5.32
18	YLFKYIFMG	3	0.4500	4.79
19	LAVADSFYL	41	0.4500	4.79
20	FYLPLVVRR	47	0.4000	4.26
21	VVLLGQGKL	104	0.4000	4.26
22	FEGLAGNHF	182	0.4000	4.26
23	WFYSVSGQV	78	0.3000	3.19
24	VRFGKPMDF	171	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	VAMIGTNVV	148	3.4000	38.64
2	YIFMGPLFT	7	2.8000	31.82
3	YELMGLSGQ	201	2.8000	31.82
4	MGPLFTLLG	10	2.0000	22.73
5	YLPLVVRRR	48	1.3000	14.77
6	LEYIPSSGP	25	1.2000	13.64
7	YVDIYAASV	211	1.2000	13.64
8	WFLAKSEYF	58	1.1000	12.50
9	YYLFKYIFM	2	1.0800	12.27
10	VPVIPVAMI	143	0.7000	7.95
11	FGRVTVRFG	166	0.7000	7.95
12	FYLPLVVRR	47	0.4000	4.55
13	LQTAVVLLG	100	0.4000	4.55

14	INRWFYSVS	75	0.1500	1.70
15	LLGMYPEGT	112	0.1000	1.14
16	LRFGRVTVR	164	-0.1000	0
17	VPIDRTNAD	86	-0.2000	0
18	IERAVTDEV	191	-0.2000	0
19	FKYIFMGPL	5	-0.3000	0
20	LKGWINRWF	71	-0.3500	0
21	VEGLEYIPS	22	-0.4200	0
22	FEGLAGNHF	182	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VAMIGTNVV	148	4.7000	50.00
2	MGPLFTLLG	10	4.3000	45.74
3	VPIDRTNAD	86	3.5000	37.23
4	YIFMGPLFT	7	2.7000	28.72
5	LQTAVVLLG	100	2.7000	28.72
6	LEYIPSSGP	25	2.6000	27.66
7	YELMGLSGQ	201	2.6000	27.66
8	LLGMYPEGT	112	2.0000	21.28
9	VPVIPVAMI	143	1.9000	20.21
10	LKGWINRWF	71	1.5500	16.49
11	LAVADSFYL	41	1.4500	15.43
12	VVLLGQGKL	104	1.4000	14.89
13	VRFGKPMDF	171	1.2000	12.77
14	YYLFKYIFM	2	1.1800	12.55
15	INRWFYSVS	75	1.1500	12.23
16	IERAVTDEV	191	1.1000	11.70
17	WFLAKSEYF	58	1.0000	10.64
18	FGRVTVRFG	166	1.0000	10.64
19	LRFGRVTVR	164	0.9000	9.57
20	IYAASVKDG	214	0.8000	8.51

21	LMGLSGQEY	203	0.7000	7.45
22	VEGLEYIPS	22	0.5800	6.17
23	VIPVAMIGT	145	0.5800	6.17
24	LARLALHTG	134	0.5000	5.32

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	VAMIGTNVV	148	4.0000	44.44
2	WFLAKSEYF	58	3.9000	43.33
3	MGPLFTLLG	10	3.6000	40.00
4	VPIDRTNAD	86	3.3000	36.67
5	YIFMGPLFT	7	3.0000	33.33
6	WFYSVSGQV	78	2.4000	26.67
7	YLPLVVRRR	48	2.3000	25.56
8	LQTAVVLLG	100	2.2000	24.44
9	MYPEGTRSP	115	2.1000	23.33
10	VRFGKPMDF	171	2.1000	23.33
11	YVDIYAASV	211	1.9000	21.11
12	FYLPLVVRR	47	1.7800	19.78
13	LRFGRVTVR	164	1.7000	18.89
14	IERAVTDEV	191	1.7000	18.89
15	MIGTNVVNP	150	1.6800	18.67
16	IGTNVVNPP	151	1.6000	17.78
17	VPVIPVAMI	143	1.3000	14.44
18	LEYIPSSGP	25	1.2000	13.33
19	FEGLAGNHF	182	1.1000	12.22
20	VIYELMGLS	199	1.1000	12.22
21	IYAASVKDG	214	0.9000	10.00
22	LLGMYPEGT	112	0.8000	8.89
23	YYLFKYIFM	2	0.6800	7.56
24	YIPSSGPAI	27	0.6000	6.67

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	VAMIGTNVV	148	4.4000	50.00
2	MGPLFTLLG	10	3.0000	34.09
3	LEYIPSSGP	25	2.2000	25.00
4	YIFMGPLFT	7	1.8000	20.45
5	YELMGLSGQ	201	1.8000	20.45
6	VPVIPVAMI	143	1.7000	19.32
7	LQTAVVLLG	100	1.4000	15.91
8	INRWFYSVS	75	1.1500	13.07
9	LLGMYPEGT	112	1.1000	12.50
10	LRFGRVTVR	164	0.9000	10.23
11	VPIDRTNAD	86	0.8000	9.09
12	IERAVTDEV	191	0.8000	9.09
13	LKGWINRWF	71	0.6500	7.39
14	VEGLEYIPS	22	0.5800	6.59
15	LAVADSFYL	41	0.4500	5.11
16	VVLLGQGKL	104	0.4000	4.55
17	YLPLVVRRR	48	0.3000	3.41
18	VRFGKPMDF	171	0.3000	3.41
19	YVDIYAASV	211	0.2000	2.27
20	WFLAKSEYF	58	0.1000	1.14
21	IGTNVVNPP	151	0.1000	1.14
22	YYLFKYIFM	2	0.0800	0.91

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	VAMIGTNVV	148	3.0000	34.88
2	YIFMGPLFT	7	2.3000	26.74

3	MGPLFTLLG	10	2.2000	25.58
4	VPIDRTNAD	86	2.2000	25.58
5	WFLAKSEYF	58	2.0000	23.26
6	WFYSVSGQV	78	1.4000	16.28
7	YELMGLSGQ	201	1.2000	13.95
8	MYPEGTRSP	115	1.1000	12.79
9	YVDIYAASV	211	0.9000	10.47
10	YLPLVVRRR	48	0.8000	9.30
11	LQTAVVLLG	100	0.8000	9.30
12	IERAVTDEV	191	0.7000	8.14
13	VIYELMGLS	199	0.7000	8.14
14	MIGTNVVNP	150	0.6800	7.91
15	IGTNVVNPP	151	0.6000	6.98
16	VPVIPVAMI	143	0.4000	4.65
17	FYLPLVVRR	47	0.2800	3.26
18	LEYIPSSGP	25	0.2000	2.33
19	LRFGRVTVR	164	0.2000	2.33
20	VRFGKPMDF	171	0.2000	2.33
21	LLGMYPEGT	112	0.1000	1.16
22	YIPSSGPAI	27	-0.3000	0
23	IYAASVKDG	214	-0.5000	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	WFYSVSGQV	78	5.7000	49.14
2	FKYIFMGPL	5	5.6000	48.28
3	LAVADSFYL	41	5.6000	48.28
4	YSVSGQVPI	80	5.6000	48.28
5	YYLFKYIFM	2	5.5000	47.41
6	YIPSSGPAI	27	5.5000	47.41
7	WFLAKSEYF	58	5.4000	46.55
8	VVRRRIWFL	52	5.0000	43.10

9	ILASNHLAV	35	4.9000	42.24
10	VAMIGTNVV	148	4.8200	41.55
11	IFMGPLFTL	8	4.7000	40.52
12	VRFGKPMDF	171	4.3000	37.07
13	LVVRRRIWF	51	3.9000	33.62
14	YVDIYAASV	211	3.9000	33.62
15	VADSFYLPL	43	3.8000	32.76
16	MGLSGQEYV	204	3.8000	32.76
17	WYYLFKYIF	1	3.6000	31.03
18	YIFMGPLFT	7	3.6000	31.03
19	FMGPLFTLL	9	3.6000	31.03
20	VVLLGQGKL	104	3.6000	31.03
21	VPVIPVAMI	143	3.6000	31.03
22	MDFSRFEGL	177	3.5000	30.17
23	LGRPKVEGL	17	3.4000	29.31
24	LPLVVRRRI	49	3.4000	29.31

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	WFYSVSGQV	78	5.7000	49.14
2	FKYIFMGPL	5	5.6000	48.28
3	LAVADSFYL	41	5.6000	48.28
4	YSVSGQVPI	80	5.6000	48.28
5	YYLFKYIFM	2	5.5000	47.41
6	YIPSSGPAI	27	5.5000	47.41
7	WFLAKSEYF	58	5.4000	46.55
8	VVRRRIWFL	52	5.0000	43.10
9	ILASNHLAV	35	4.9000	42.24
10	VAMIGTNVV	148	4.8200	41.55
11	IFMGPLFTL	8	4.7000	40.52
12	VRFGKPMDF	171	4.3000	37.07
13	LVVRRRIWF	51	3.9000	33.62

14	YVDIYAASV	211	3.9000	33.62
15	VADSFYLPL	43	3.8000	32.76
16	MGLSGQEYV	204	3.8000	32.76
17	WYYLFKYIF	1	3.6000	31.03
18	YIFMGPLFT	7	3.6000	31.03
19	FMGPLFTLL	9	3.6000	31.03
20	VVLLGQGKL	104	3.6000	31.03
21	VPVIPVAMI	143	3.6000	31.03
22	MDFSRFEGL	177	3.5000	30.17
23	LGRPKVEGL	17	3.4000	29.31
24	LPLVVRRRI	49	3.4000	29.31

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	YLFKYIFMG	3	4.2000	48.84
2	LVVRRRIWF	51	4.0000	46.51
3	VVRRRIWFL	52	3.6000	41.86
4	YIFMGPLFT	7	3.2000	37.21
5	LLGRPKVEG	16	3.0000	34.88
6	YELMGLSGQ	201	2.7000	31.40
7	WYYLFKYIF	1	2.5000	29.07
8	FGRVTVRFG	166	2.4000	27.91
9	FIERAVTDE	190	2.3000	26.74
10	VVLLGQGKL	104	2.0000	23.26
11	VRRRIWFLA	53	1.9000	22.09
12	YLPLVVRRR	48	1.6000	18.60
13	YKGKTGLAR	128	1.6000	18.60
14	LQTAVVLLG	100	1.4000	16.28
15	MGPLFTLLG	10	1.3000	15.12
16	FTLLGRPKV	14	1.1000	12.79
17	VRFGKPMDF	171	1.1000	12.79
18	WINRWFYSV	74	1.0000	11.63

19	VTVRFGKPM	169	1.0000	11.63
20	YYLFKYIFM	2	0.9000	10.47
21	FKYIFMGPL	5	0.8000	9.30
22	MLRFGRVTV	163	0.7000	8.14
23	YVDIYAASV	211	0.7000	8.14
24	IYAASVKDG	214	0.6000	6.98

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	LVVRRRIWF	51	3.1000	38.75
2	YLFKYIFMG	3	2.9000	36.25
3	VVRRRIWFL	52	2.6000	32.50
4	YIFMGPLFT	7	2.3000	28.75
5	VRRRIWFLA	53	1.9000	23.75
6	YELMGLSGQ	201	1.9000	23.75
7	LLGRPKVEG	16	1.7000	21.25
8	WYYLFKYIF	1	1.6000	20.00
9	YLPLVVRRR	48	1.6000	20.00
10	YKGKTGLAR	128	1.6000	20.00
11	FGRVTVRFG	166	1.1000	13.75
12	VVLLGQGKL	104	1.0000	12.50
13	FTLLGRPKV	14	0.8000	10.00
14	WINRWFYSV	74	0.7000	8.75
15	MLRFGRVTV	163	0.4000	5.00
16	YVDIYAASV	211	0.4000	5.00
17	LGMYPEGTR	113	0.2000	2.50
18	VPVIPVAMI	143	0.2000	2.50
19	VRFGKPMDF	171	0.2000	2.50
20	LQTAVVLLG	100	0.1000	1.25
21	LPLVVRRRI	49	-0.1000	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	LVVRRRIWF	51	4.1000	51.25
2	VVRRRIWFL	52	3.6000	45.00
3	VRRRIWFLA	53	2.9000	36.25
4	LLGRPKVEG	16	2.7000	33.75
5	VVLLGQGKL	104	2.0000	25.00
6	YLFKYIFMG	3	1.9000	23.75
7	MLRFGRVTV	163	1.4000	17.50
8	YIFMGPLFT	7	1.3000	16.25
9	LGMYPEGTR	113	1.2000	15.00
10	VPVIPVAMI	143	1.2000	15.00
11	VRFGKPMDF	171	1.2000	15.00
12	LQTAVVLLG	100	1.1000	13.75
13	MGPLFTLLG	10	1.0000	12.50
14	LPLVVRRRI	49	0.9000	11.25
15	VTVRFGKPM	169	0.9000	11.25
16	YELMGLSGQ	201	0.9000	11.25
17	VDIYAASVK	212	0.8000	10.00
18	WYYLFKYIF	1	0.6000	7.50
19	YLPLVVRRR	48	0.6000	7.50
20	YKGKTGLAR	128	0.6000	7.50
21	VAMIGTNVV	148	0.5000	6.25
22	MWYYLFKYI	0	0.4000	5.00
23	LASNHLAVA	36	0.4000	5.00
24	IWFLAKSEY	57	0.4000	5.00

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	LVVRRRIWF	51	5.0000	58.14

2	VVRRRIWFL	52	4.6000	53.49
3	LLGRPKVEG	16	4.0000	46.51
4	YLFKYIFMG	3	3.2000	37.21
5	VVLLGQGKL	104	3.0000	34.88
6	VRRRIWFLA	53	2.9000	33.72
7	LQTAVVLLG	100	2.4000	27.91
8	MGPLFTLLG	10	2.3000	26.74
9	YIFMGPLFT	7	2.2000	25.58
10	VRFGKPMDF	171	2.1000	24.42
11	VTVRFGKPM	169	2.0000	23.26
12	MLRFGRVTV	163	1.7000	19.77
13	YELMGLSGQ	201	1.7000	19.77
14	IYAASVKDG	214	1.6000	18.60
15	WYYLFKYIF	1	1.5000	17.44
16	IWFLAKSEY	57	1.5000	17.44
17	LLGQGKLLG	106	1.5000	17.44
18	VPVIPVAMI	143	1.4000	16.28
19	FGRVTVRFG	166	1.4000	16.28
20	FIERAVTDE	190	1.3000	15.12
21	LGMYPEGTR	113	1.2000	13.95
22	LPLVVRRRI	49	1.1000	12.79
23	LARLALHTG	134	1.0000	11.63
24	VVNPPGRKM	155	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	LVVRRRIWF	51	3.9800	45.75
2	YLFKYIFMG	3	3.7500	43.10
3	YELMGLSGQ	201	3.7000	42.53
4	VVRRRIWFL	52	3.1000	35.63
5	YIFMGPLFT	7	2.9000	33.33
6	VRRRIWFLA	53	2.7500	31.61

7	LLGRPKVEG	16	2.7000	31.03
8	WYYLFKYIF	1	2.5000	28.74
9	YKGKTGLAR	128	2.2000	25.29
10	FIERAVTDE	190	2.1000	24.14
11	WINRWFYSV	74	1.6000	18.39
12	LRFGRVTVR	164	1.6000	18.39
13	VDIYAASVK	212	1.6000	18.39
14	VAMIGTNVV	148	1.5000	17.24
15	MLRFGRVTV	163	1.4000	16.09
16	YLPLVVRRR	48	1.3000	14.94
17	IWFLAKSEY	57	1.2000	13.79
18	VRFGKPMDF	171	1.2000	13.79
19	FTLLGRPKV	14	1.0000	11.49
20	FYLPLVVRR	47	1.0000	11.49
21	FGRVTVRFG	166	0.8000	9.20
22	LQTAVVLLG	100	0.7000	8.05
23	YYLFKYIFM	2	0.6800	7.82
24	MGPLFTLLG	10	0.6000	6.90

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	LVVRRRIWF	51	5.6000	55.45
2	YIFMGPLFT	7	5.0000	49.50
3	YLFKYIFMG	3	4.7000	46.53
4	VVRRRIWFL	52	4.4000	43.56
5	LLGRPKVEG	16	3.5000	34.65
6	YKGKTGLAR	128	3.4000	33.66
7	FIERAVTDE	190	3.4000	33.66
8	WYYLFKYIF	1	3.2000	31.68
9	LQTAVVLLG	100	3.2000	31.68
10	MGPLFTLLG	10	3.1000	30.69
11	VRFGKPMDF	171	2.7000	26.73

12	YELMGLSGQ	201	2.7000	26.73
13	FGRVTVRFG	166	2.6000	25.74
14	YYLFKYIFM	2	2.5000	24.75
15	VRRRIWFLA	53	2.4000	23.76
16	LLGQGKLLG	106	2.3000	22.77
17	FTLLGRPKV	14	2.2500	22.28
18	VVLLGQGKL	104	2.1000	20.79
19	FSRFEGLAG	179	2.0000	19.80
20	YLPLVVRRR	48	1.8000	17.82
21	WINRWFYSV	74	1.7000	16.83
22	VTVRFGKPM	169	1.6000	15.84
23	FLAKSEYFT	59	1.2000	11.88
24	MLRFGRVTV	163	1.2000	11.88

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	YIFMGPLFT	7	3.7000	44.58
2	WYYLFKYIF	1	2.7000	32.53
3	FTLLGRPKV	14	2.3500	28.31
4	MGPLFTLLG	10	2.2000	26.51
5	YLPLVVRRR	48	2.2000	26.51
6	LQTAVVLLG	100	1.9000	22.89
7	LVVRRRIWF	51	1.7000	20.48
8	LLGQGKLLG	106	1.6000	19.28
9	VVLLGQGKL	104	1.5000	18.07
10	YELMGLSGQ	201	1.5000	18.07
11	FGRVTVRFG	166	1.4000	16.87
12	YYLFKYIFM	2	1.3000	15.66
13	VRFGKPMDF	171	1.1000	13.25
14	YVDIYAASV	211	1.0000	12.05
15	VPVIPVAMI	143	0.8000	9.64
16	MLRFGRVTV	163	0.8000	9.64

17	YLFKYIFMG	3	0.6000	7.23
18	YKGKTGLAR	128	0.6000	7.23
19	FSRFEGLAG	179	0.6000	7.23
20	FKYIFMGPL	5	0.5000	6.02
21	VEGLEYIPS	22	0.5000	6.02
22	VVRRRIWFL	52	0.4000	4.82
23	VAMIGTNVV	148	0.4000	4.82
24	LPLVVRRRI	49	0.2000	2.41

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	VVRRRIWFL	52	3.1000	36.90
2	MLRFGRVTV	163	2.7000	32.14
3	LLGQGKLLG	106	2.5000	29.76
4	LVVRRRIWF	51	2.3000	27.38
5	VRRRIWFLA	53	2.3000	27.38
6	YLPLVVRRR	48	2.1000	25.00
7	YLFKYIFMG	3	1.9000	22.62
8	LQTAVVLLG	100	1.8000	21.43
9	LLGRPKVEG	16	1.6000	19.05
10	LKGWINRWF	71	1.6000	19.05
11	LPLVVRRRI	49	1.5000	17.86
12	YIFMGPLFT	7	1.4000	16.67
13	MGPLFTLLG	10	1.4000	16.67
14	LFTLLGRPK	13	1.4000	16.67
15	WYYLFKYIF	1	1.2000	14.29
16	VVNPPGRKM	155	1.2000	14.29
17	IYAASVKDG	214	1.1000	13.10
18	LALHTGVPV	137	1.0000	11.90
19	VAMIGTNVV	148	1.0000	11.90
20	VRFGKPMDF	171	1.0000	11.90
21	MYPEGTRSP	115	0.8000	9.52

22	LRFGRVTVR	164	0.8000	9.52
23	VVLLGQGKL	104	0.7000	8.33
24	FGRVTVRFG	166	0.7000	8.33

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	MGPLFTLLG	10	3.2000	38.55
2	LQTAVVLLG	100	2.9000	34.94
3	YIFMGPLFT	7	2.7000	32.53
4	LVVRRRIWF	51	2.7000	32.53
5	LLGQGKLLG	106	2.6000	31.33
6	VVLLGQGKL	104	2.5000	30.12
7	VRFGKPMDF	171	2.1000	25.30
8	VPVIPVAMI	143	1.8000	21.69
9	MLRFGRVTV	163	1.8000	21.69
10	WYYLFKYIF	1	1.7000	20.48
11	VEGLEYIPS	22	1.5000	18.07
12	VVRRRIWFL	52	1.4000	16.87
13	VAMIGTNVV	148	1.4000	16.87
14	FTLLGRPKV	14	1.3500	16.27
15	YLPLVVRRR	48	1.2000	14.46
16	LPLVVRRRI	49	1.2000	14.46
17	ILASNHLAV	35	1.0000	12.05
18	IYAASVKDG	214	0.9000	10.84
19	IWFLAKSEY	57	0.8000	9.64
20	LARLALHTG	134	0.8000	9.64
21	IYELMGLSG	200	0.6000	7.23
22	LFTLLGRPK	13	0.5000	6.02
23	VIPVAMIGT	145	0.5000	6.02
24	YELMGLSGQ	201	0.5000	6.02

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	MGPLFTLLG	10	3.2000	38.55
2	LQTAVVLLG	100	2.9000	34.94
3	YIFMGPLFT	7	2.7000	32.53
4	LVVRRRIWF	51	2.7000	32.53
5	LLGQGKLLG	106	2.6000	31.33
6	VVLLGQGKL	104	2.5000	30.12
7	VRFGKPMDF	171	2.1000	25.30
8	VPVIPVAMI	143	1.8000	21.69
9	MLRFGRVTV	163	1.8000	21.69
10	WYYLFKYIF	1	1.7000	20.48
11	VEGLEYIPS	22	1.5000	18.07
12	VVRRRIWFL	52	1.4000	16.87
13	VAMIGTNVV	148	1.4000	16.87
14	FTLLGRPKV	14	1.3500	16.27
15	YLPLVVRRR	48	1.2000	14.46
16	LPLVVRRRI	49	1.2000	14.46
17	ILASNHLAV	35	1.0000	12.05
18	IYAASVKDG	214	0.9000	10.84
19	IWFLAKSEY	57	0.8000	9.64
20	LARLALHTG	134	0.8000	9.64
21	IYELMGLSG	200	0.6000	7.23
22	LFTLLGRPK	13	0.5000	6.02
23	VIPVAMIGT	145	0.5000	6.02
24	YELMGLSGQ	201	0.5000	6.02

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	VRFGKPMDF	171	4.1000	45.05

2	LRFGRVTVR	164	3.6000	39.56
3	IFMGPLFTL	8	2.4000	26.37
4	VPIDRTNAD	86	2.3100	25.38
5	LYKGKTGLA	127	2.3000	25.27
6	LVVRRRIWF	51	2.0000	21.98
7	VAMIGTNVV	148	1.9100	20.99
8	VVLLGQGKL	104	1.9000	20.88
9	LLGQGKLLG	106	1.7000	18.68
10	LQTAVVLLG	100	1.6000	17.58
11	VPVIPVAMI	143	1.4000	15.38
12	MLRFGRVTV	163	1.2000	13.19
13	ILASNHLAV	35	1.1000	12.09
14	IWFLAKSEY	57	1.0700	11.76
15	FTLLGRPKV	14	1.0000	10.99
16	VRRRIWFLA	53	1.0000	10.99
17	LGQGKLLGM	107	1.0000	10.99
18	MGLSGQEYV	204	1.0000	10.99
19	WYYLFKYIF	1	0.9500	10.44
20	VVRRRIWFL	52	0.9000	9.89
21	YELMGLSGQ	201	0.8700	9.56
22	MGPLFTLLG	10	0.8000	8.79
23	YIPSSGPAI	27	0.8000	8.79
24	VIYELMGLS	199	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	YLPLVVRRR	48	3.1000	36.90
2	YLFKYIFMG	3	2.9000	34.52
3	YIFMGPLFT	7	2.4000	28.57
4	WYYLFKYIF	1	2.2000	26.19
5	VVRRRIWFL	52	2.1000	25.00
6	MLRFGRVTV	163	1.7000	20.24

7	FGRVTVRFG	166	1.7000	20.24
8	YELMGLSGQ	201	1.7000	20.24
9	LLGQGKLLG	106	1.5000	17.86
10	LVVRRRIWF	51	1.3000	15.48
11	VRRRIWFLA	53	1.3000	15.48
12	FTLLGRPKV	14	1.2000	14.29
13	LQTAVVLLG	100	0.8000	9.52
14	YKGKTGLAR	128	0.8000	9.52
15	LLGRPKVEG	16	0.6000	7.14
16	LKGWINRWF	71	0.6000	7.14
17	FYLPLVVRR	47	0.5000	5.95
18	LPLVVRRRI	49	0.5000	5.95
19	YYLFKYIFM	2	0.4000	4.76
20	MGPLFTLLG	10	0.4000	4.76
21	LFTLLGRPK	13	0.4000	4.76
22	VVNPPGRKM	155	0.2000	2.38
23	IYAASVKDG	214	0.1000	1.19

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	YLPLVVRRR	48	4.6000	52.27
2	YLFKYIFMG	3	4.3000	48.86
3	WYYLFKYIF	1	4.1000	46.59
4	LVVRRRIWF	51	3.2000	36.36
5	YIFMGPLFT	7	3.1000	35.23
6	FGRVTVRFG	166	3.1000	35.23
7	VVRRRIWFL	52	3.0600	34.77
8	LLGQGKLLG	106	2.9000	32.95
9	MLRFGRVTV	163	2.7000	30.68
10	LKGWINRWF	71	2.5000	28.41
11	YKGKTGLAR	128	2.3000	26.14
12	FTLLGRPKV	14	2.2000	25.00

13	LQTAVVLLG	100	2.2000	25.00
14	LLGRPKVEG	16	2.0000	22.73
15	FYLPLVVRR	47	2.0000	22.73
16	YYLFKYIFM	2	1.9000	21.59
17	VRFGKPMDF	171	1.9000	21.59
18	MGPLFTLLG	10	1.8000	20.45
19	VVNPPGRKM	155	1.7000	19.32
20	WFLAKSEYF	58	1.6000	18.18
21	IYAASVKDG	214	1.5000	17.05
22	LPLVVRRRI	49	1.4000	15.91
23	VRRRIWFLA	53	1.3000	14.77
24	LRFGRVTVR	164	1.3000	14.77

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	VVRRRIWFL	52	3.1000	36.90
2	MLRFGRVTV	163	2.7000	32.14
3	LLGQGKLLG	106	2.5000	29.76
4	LVVRRRIWF	51	2.3000	27.38
5	VRRRIWFLA	53	2.3000	27.38
6	YLPLVVRRR	48	2.1000	25.00
7	YLFKYIFMG	3	1.9000	22.62
8	LQTAVVLLG	100	1.8000	21.43
9	LLGRPKVEG	16	1.6000	19.05
10	LKGWINRWF	71	1.6000	19.05
11	LPLVVRRRI	49	1.5000	17.86
12	YIFMGPLFT	7	1.4000	16.67
13	MGPLFTLLG	10	1.4000	16.67
14	LFTLLGRPK	13	1.4000	16.67
15	WYYLFKYIF	1	1.2000	14.29
16	VVNPPGRKM	155	1.2000	14.29
17	IYAASVKDG	214	1.1000	13.10

18	LALHTGVPV	137	1.0000	11.90
19	VAMIGTNVV	148	1.0000	11.90
20	VRFGKPMDF	171	1.0000	11.90
21	MYPEGTRSP	115	0.8000	9.52
22	LRFGRVTVR	164	0.8000	9.52
23	VVLLGQGKL	104	0.7000	8.33
24	FGRVTVRFG	166	0.7000	8.33

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	WYYLFKYIF	1	4.6000	52.87
2	YIFMGPLFT	7	4.4000	50.57
3	YLPLVVRRR	48	3.7000	42.53
4	MGPLFTLLG	10	3.6000	41.38
5	LVVRRRIWF	51	3.6000	41.38
6	FTLLGRPKV	14	3.3500	38.51
7	LQTAVVLLG	100	3.3000	37.93
8	LLGQGKLLG	106	3.0000	34.48
9	VRFGKPMDF	171	3.0000	34.48
10	YYLFKYIFM	2	2.8000	32.18
11	FGRVTVRFG	166	2.8000	32.18
12	VVLLGQGKL	104	2.4600	28.28
13	YKGKTGLAR	128	2.1000	24.14
14	YLFKYIFMG	3	2.0000	22.99
15	FSRFEGLAG	179	2.0000	22.99
16	YVDIYAASV	211	2.0000	22.99
17	MLRFGRVTV	163	1.8000	20.69
18	VPVIPVAMI	143	1.7000	19.54
19	FKYIFMGPL	5	1.4600	16.78
20	VAMIGTNVV	148	1.4000	16.09
21	VVRRRIWFL	52	1.3600	15.63
22	FYLPLVVRR	47	1.3000	14.94

23	WFLAKSEYF	58	1.3000	14.94
24	IYAASVKDG	214	1.3000	14.94

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	LVVRRRIWF	51	4.2000	47.73
2	VVRRRIWFL	52	4.0600	46.14
3	LLGQGKLLG	106	3.9000	44.32
4	MLRFGRVTV	163	3.7000	42.05
5	YLPLVVRRR	48	3.6000	40.91
6	LKGWINRWF	71	3.5000	39.77
7	YLFKYIFMG	3	3.3000	37.50
8	LQTAVVLLG	100	3.2000	36.36
9	WYYLFKYIF	1	3.1000	35.23
10	LLGRPKVEG	16	3.0000	34.09
11	VRFGKPMDF	171	2.9000	32.95
12	MGPLFTLLG	10	2.8000	31.82
13	VVNPPGRKM	155	2.7000	30.68
14	IYAASVKDG	214	2.5000	28.41
15	LPLVVRRRI	49	2.4000	27.27
16	VRRRIWFLA	53	2.3000	26.14
17	LRFGRVTVR	164	2.3000	26.14
18	YIFMGPLFT	7	2.1000	23.86
19	FGRVTVRFG	166	2.1000	23.86
20	LARLALHTG	134	2.0000	22.73
21	LALHTGVPV	137	2.0000	22.73
22	VAMIGTNVV	148	2.0000	22.73
23	IWFLAKSEY	57	1.8000	20.45
24	MYPEGTRSP	115	1.8000	20.45

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	YLPLVVRRR	48	4.6000	52.27
2	YLFKYIFMG	3	4.3000	48.86
3	WYYLFKYIF	1	4.1000	46.59
4	LVVRRRIWF	51	3.2000	36.36
5	YIFMGPLFT	7	3.1000	35.23
6	FGRVTVRFG	166	3.1000	35.23
7	VVRRRIWFL	52	3.0600	34.77
8	LLGQGKLLG	106	2.9000	32.95
9	MLRFGRVTV	163	2.7000	30.68
10	LKGWINRWF	71	2.5000	28.41
11	YKGKTGLAR	128	2.3000	26.14
12	FTLLGRPKV	14	2.2000	25.00
13	LQTAVVLLG	100	2.2000	25.00
14	LLGRPKVEG	16	2.0000	22.73
15	FYLPLVVRR	47	2.0000	22.73
16	YYLFKYIFM	2	1.9000	21.59
17	VRFGKPMDF	171	1.9000	21.59
18	MGPLFTLLG	10	1.8000	20.45
19	VVNPPGRKM	155	1.7000	19.32
20	WFLAKSEYF	58	1.6000	18.18
21	IYAASVKDG	214	1.5000	17.05
22	LPLVVRRRI	49	1.4000	15.91
23	VRRRIWFLA	53	1.3000	14.77
24	LRFGRVTVR	164	1.3000	14.77

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	VVRRRIWFL	52	4.1000	45.56

2	LLGQGKLLG	106	3.8000	42.22
3	YLFKYIFMG	3	3.2000	35.56
4	LVVRRRIWF	51	3.2000	35.56
5	LQTAVVLLG	100	3.1000	34.44
6	MLRFGRVTV	163	3.0000	33.33
7	LLGRPKVEG	16	2.9000	32.22
8	MGPLFTLLG	10	2.7000	30.00
9	LKGWINRWF	71	2.5000	27.78
10	IYAASVKDG	214	2.4000	26.67
11	YIFMGPLFT	7	2.3000	25.56
12	VRRRIWFLA	53	2.3000	25.56
13	VVNPPGRKM	155	2.3000	25.56
14	WYYLFKYIF	1	2.1000	23.33
15	YLPLVVRRR	48	2.1000	23.33
16	FGRVTVRFG	166	2.0000	22.22
17	LARLALHTG	134	1.9000	21.11
18	VRFGKPMDF	171	1.9000	21.11
19	LPLVVRRRI	49	1.7000	18.89
20	VVLLGQGKL	104	1.7000	18.89
21	IWFLAKSEY	57	1.6000	17.78
22	IFMGPLFTL	8	1.5000	16.67
23	VPIDRTNAD	86	1.5000	16.67
24	YELMGLSGQ	201	1.5000	16.67

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	WYYLFKYIF	1	4.6000	52.87
2	YIFMGPLFT	7	4.4000	50.57
3	YLPLVVRRR	48	3.7000	42.53
4	MGPLFTLLG	10	3.6000	41.38
5	LVVRRRIWF	51	3.6000	41.38
6	FTLLGRPKV	14	3.3500	38.51

7	LQTAVVLLG	100	3.3000	37.93
8	LLGQGKLLG	106	3.0000	34.48
9	VRFGKPMDF	171	3.0000	34.48
10	YYLFKYIFM	2	2.8000	32.18
11	FGRVTVRFG	166	2.8000	32.18
12	VVLLGQGKL	104	2.4600	28.28
13	YKGKTGLAR	128	2.1000	24.14
14	YLFKYIFMG	3	2.0000	22.99
15	FSRFEGLAG	179	2.0000	22.99
16	YVDIYAASV	211	2.0000	22.99
17	MLRFGRVTV	163	1.8000	20.69
18	VPVIPVAMI	143	1.7000	19.54
19	FKYIFMGPL	5	1.4600	16.78
20	VAMIGTNVV	148	1.4000	16.09
21	VVRRRIWFL	52	1.3600	15.63
22	FYLPLVVRR	47	1.3000	14.94
23	WFLAKSEYF	58	1.3000	14.94
24	IYAASVKDG	214	1.3000	14.94

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	WYYLFKYIF	1	2.0000	29.41
2	YLPLVVRRR	48	2.0000	29.41
3	YIFMGPLFT	7	1.9000	27.94
4	YELMGLSGQ	201	1.5000	22.06
5	VVLLGQGKL	104	1.4000	20.59
6	FTLLGRPKV	14	1.2000	17.65
7	FGRVTVRFG	166	1.2000	17.65
8	YVDIYAASV	211	1.0000	14.71
9	VPVIPVAMI	143	0.8000	11.76
10	FKYIFMGPL	5	0.4000	5.88
11	MGPLFTLLG	10	0.4000	5.88

12	MLRFGRVTV	163	0.3000	4.41
13	YLFKYIFMG	3	0.1000	1.47
14	LVVRRRIWF	51	0.1000	1.47
15	LQTAVVLLG	100	0.1000	1.47
16	VAMIGTNVV	148	0.1000	1.47
17	IWFLAKSEY	57	-0.2000	0
18	LLGQGKLLG	106	-0.2000	0
19	YYLFKYIFM	2	-0.3000	0
20	VVRRRIWFL	52	-0.4000	0
21	WFYSVSGQV	78	-0.4000	0
22	VRFGKPMDF	171	-0.5000	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	MGPLFTLLG	10	3.2000	38.55
2	LQTAVVLLG	100	2.9000	34.94
3	YIFMGPLFT	7	2.7000	32.53
4	LVVRRRIWF	51	2.7000	32.53
5	LLGQGKLLG	106	2.6000	31.33
6	VVLLGQGKL	104	2.5000	30.12
7	VRFGKPMDF	171	2.1000	25.30
8	VPVIPVAMI	143	1.8000	21.69
9	MLRFGRVTV	163	1.8000	21.69
10	WYYLFKYIF	1	1.7000	20.48
11	VEGLEYIPS	22	1.5000	18.07
12	VVRRRIWFL	52	1.4000	16.87
13	VAMIGTNVV	148	1.4000	16.87
14	FTLLGRPKV	14	1.3500	16.27
15	YLPLVVRRR	48	1.2000	14.46
16	LPLVVRRRI	49	1.2000	14.46
17	ILASNHLAV	35	1.0000	12.05
18	IYAASVKDG	214	0.9000	10.84

19	IWFLAKSEY	57	0.8000	9.64
20	LARLALHTG	134	0.8000	9.64
21	IYELMGLSG	200	0.6000	7.23
22	LFTLLGRPK	13	0.5000	6.02
23	VIPVAMIGT	145	0.5000	6.02
24	YELMGLSGQ	201	0.5000	6.02

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	YIFMGPLFT	7	4.6000	51.69
2	WYYLFKYIF	1	3.6000	40.45
3	MGPLFTLLG	10	3.5000	39.33
4	LQTAVVLLG	100	3.2000	35.96
5	LLGQGKLLG	106	2.9000	32.58
6	FGRVTVRFG	166	2.7000	30.34
7	FTLLGRPKV	14	2.6500	29.78
8	LVVRRRIWF	51	2.6000	29.21
9	VVLLGQGKL	104	2.5000	28.09
10	YYLFKYIFM	2	2.4000	26.97
11	YELMGLSGQ	201	2.3000	25.84
12	YLPLVVRRR	48	2.2000	24.72
13	VRFGKPMDF	171	2.0000	22.47
14	YLFKYIFMG	3	1.9000	21.35
15	FSRFEGLAG	179	1.9000	21.35
16	FKYIFMGPL	5	1.5000	16.85
17	VVRRRIWFL	52	1.4000	15.73
18	YVDIYAASV	211	1.3000	14.61
19	IYAASVKDG	214	1.2000	13.48
20	LARLALHTG	134	1.1000	12.36
21	MLRFGRVTV	163	1.1000	12.36
22	VPVIPVAMI	143	1.0000	11.24
23	IWFLAKSEY	57	0.9000	10.11

24	IYELMGLSG	200	0.9000	10.11

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	VVRRRIWFL	52	3.1000	36.90
2	MLRFGRVTV	163	2.7000	32.14
3	LLGQGKLLG	106	2.5000	29.76
4	LVVRRRIWF	51	2.3000	27.38
5	VRRRIWFLA	53	2.3000	27.38
6	YLPLVVRRR	48	2.1000	25.00
7	YLFKYIFMG	3	1.9000	22.62
8	LQTAVVLLG	100	1.8000	21.43
9	LLGRPKVEG	16	1.6000	19.05
10	LKGWINRWF	71	1.6000	19.05
11	LPLVVRRRI	49	1.5000	17.86
12	YIFMGPLFT	7	1.4000	16.67
13	MGPLFTLLG	10	1.4000	16.67
14	LFTLLGRPK	13	1.4000	16.67
15	WYYLFKYIF	1	1.2000	14.29
16	VVNPPGRKM	155	1.2000	14.29
17	IYAASVKDG	214	1.1000	13.10
18	LALHTGVPV	137	1.0000	11.90
19	VAMIGTNVV	148	1.0000	11.90
20	VRFGKPMDF	171	1.0000	11.90
21	MYPEGTRSP	115	0.8000	9.52
22	LRFGRVTVR	164	0.8000	9.52
23	VVLLGQGKL	104	0.7000	8.33
24	FGRVTVRFG	166	0.7000	8.33

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	YLPLVVRRR	48	3.1000	36.90
2	YLFKYIFMG	3	2.9000	34.52
3	YIFMGPLFT	7	2.4000	28.57
4	WYYLFKYIF	1	2.2000	26.19
5	VVRRRIWFL	52	2.1000	25.00
6	MLRFGRVTV	163	1.7000	20.24
7	FGRVTVRFG	166	1.7000	20.24
8	YELMGLSGQ	201	1.7000	20.24
9	LLGQGKLLG	106	1.5000	17.86
10	LVVRRRIWF	51	1.3000	15.48
11	VRRRIWFLA	53	1.3000	15.48
12	FTLLGRPKV	14	1.2000	14.29
13	LQTAVVLLG	100	0.8000	9.52
14	YKGKTGLAR	128	0.8000	9.52
15	LLGRPKVEG	16	0.6000	7.14
16	LKGWINRWF	71	0.6000	7.14
17	FYLPLVVRR	47	0.5000	5.95
18	LPLVVRRRI	49	0.5000	5.95
19	YYLFKYIFM	2	0.4000	4.76
20	MGPLFTLLG	10	0.4000	4.76
21	LFTLLGRPK	13	0.4000	4.76
22	VVNPPGRKM	155	0.2000	2.38
23	IYAASVKDG	214	0.1000	1.19

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	LVVRRRIWF	51	4.2000	47.73
2	VVRRRIWFL	52	4.0600	46.14
3	LLGQGKLLG	106	3.9000	44.32
4	MLRFGRVTV	163	3.7000	42.05
5	YLPLVVRRR	48	3.6000	40.91

6	LKGWINRWF	71	3.5000	39.77
7	YLFKYIFMG	3	3.3000	37.50
8	LQTAVVLLG	100	3.2000	36.36
9	WYYLFKYIF	1	3.1000	35.23
10	LLGRPKVEG	16	3.0000	34.09
11	VRFGKPMDF	171	2.9000	32.95
12	MGPLFTLLG	10	2.8000	31.82
13	VVNPPGRKM	155	2.7000	30.68
14	IYAASVKDG	214	2.5000	28.41
15	LPLVVRRRI	49	2.4000	27.27
16	VRRRIWFLA	53	2.3000	26.14
17	LRFGRVTVR	164	2.3000	26.14
18	YIFMGPLFT	7	2.1000	23.86
19	FGRVTVRFG	166	2.1000	23.86
20	LARLALHTG	134	2.0000	22.73
21	LALHTGVPV	137	2.0000	22.73
22	VAMIGTNVV	148	2.0000	22.73
23	IWFLAKSEY	57	1.8000	20.45
24	MYPEGTRSP	115	1.8000	20.45

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	LVVRRRIWF	51	4.2000	47.73
2	VVRRRIWFL	52	4.0600	46.14
3	LLGQGKLLG	106	3.9000	44.32
4	MLRFGRVTV	163	3.7000	42.05
5	YLPLVVRRR	48	3.6000	40.91
6	LKGWINRWF	71	3.5000	39.77
7	YLFKYIFMG	3	3.3000	37.50
8	LQTAVVLLG	100	3.2000	36.36
9	WYYLFKYIF	1	3.1000	35.23
10	LLGRPKVEG	16	3.0000	34.09

11	VRFGKPMDF	171	2.9000	32.95
12	MGPLFTLLG	10	2.8000	31.82
13	VVNPPGRKM	155	2.7000	30.68
14	IYAASVKDG	214	2.5000	28.41
15	LPLVVRRRI	49	2.4000	27.27
16	VRRRIWFLA	53	2.3000	26.14
17	LRFGRVTVR	164	2.3000	26.14
18	YIFMGPLFT	7	2.1000	23.86
19	FGRVTVRFG	166	2.1000	23.86
20	LARLALHTG	134	2.0000	22.73
21	LALHTGVPV	137	2.0000	22.73
22	VAMIGTNVV	148	2.0000	22.73
23	IWFLAKSEY	57	1.8000	20.45
24	MYPEGTRSP	115	1.8000	20.45

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	MLRFGRVTV	163	5.7000	58.16
2	YYLFKYIFM	2	5.2800	53.88
3	LVVRRRIWF	51	4.9000	50.00
4	IFMGPLFTL	8	4.3000	43.88
5	VVRRRIWFL	52	4.1500	42.35
6	VRRRIWFLA	53	4.1000	41.84
7	VRFGKPMDF	171	4.1000	41.84
8	LFKYIFMGP	4	3.6000	36.73
9	YIFMGPLFT	7	3.4000	34.69
10	FSRFEGLAG	179	3.4000	34.69
11	MWYYLFKYI	0	3.3000	33.67
12	VVLLGQGKL	104	3.3000	33.67
13	LALHTGVPV	137	3.2000	32.65
14	LAVADSFYL	41	3.0000	30.61
15	VIPVAMIGT	145	3.0000	30.61

16	VAMIGTNVV	148	2.9600	30.20
17	VLLGQGKLL	105	2.7000	27.55
18	LGQGKLLGM	107	2.6800	27.35
19	VEGLEYIPS	22	2.4000	24.49
20	ILASNHLAV	35	2.4000	24.49
21	LGMYPEGTR	113	2.4000	24.49
22	VVNPPGRKM	155	2.3800	24.29
23	MGPLFTLLG	10	2.3600	24.08
24	INRWFYSVS	75	2.3000	23.47

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	YYLFKYIFM	2	6.2800	64.08
2	MLRFGRVTV	163	4.7000	47.96
3	YIFMGPLFT	7	4.4000	44.90
4	FSRFEGLAG	179	4.4000	44.90
5	LVVRRRIWF	51	3.9000	39.80
6	IFMGPLFTL	8	3.3000	33.67
7	VVRRRIWFL	52	3.1500	32.14
8	FKYIFMGPL	5	3.1000	31.63
9	FTLLGRPKV	14	3.1000	31.63
10	VRRRIWFLA	53	3.1000	31.63
11	VRFGKPMDF	171	3.1000	31.63
12	LFKYIFMGP	4	2.6000	26.53
13	YIPSSGPAI	27	2.6000	26.53
14	WINRWFYSV	74	2.5000	25.51
15	YFTGTGLKG	65	2.4000	24.49
16	MWYYLFKYI	0	2.3000	23.47
17	VVLLGQGKL	104	2.3000	23.47
18	WYYLFKYIF	1	2.2000	22.45
19	WFYSVSGQV	78	2.2000	22.45
20	LALHTGVPV	137	2.2000	22.45

21	LAVADSFYL	41	2.0000	20.41
22	YKGKTGLAR	128	2.0000	20.41
23	VIPVAMIGT	145	2.0000	20.41
24	VAMIGTNVV	148	1.9600	20.00

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	MLRFGRVTV	163	5.7000	58.16
2	YYLFKYIFM	2	5.2800	53.88
3	LVVRRRIWF	51	4.9000	50.00
4	IFMGPLFTL	8	4.3000	43.88
5	VVRRRIWFL	52	4.1500	42.35
6	VRRRIWFLA	53	4.1000	41.84
7	VRFGKPMDF	171	4.1000	41.84
8	LFKYIFMGP	4	3.6000	36.73
9	YIFMGPLFT	7	3.4000	34.69
10	FSRFEGLAG	179	3.4000	34.69
11	MWYYLFKYI	0	3.3000	33.67
12	VVLLGQGKL	104	3.3000	33.67
13	LALHTGVPV	137	3.2000	32.65
14	LAVADSFYL	41	3.0000	30.61
15	VIPVAMIGT	145	3.0000	30.61
16	VAMIGTNVV	148	2.9600	30.20
17	VLLGQGKLL	105	2.7000	27.55
18	LGQGKLLGM	107	2.6800	27.35
19	VEGLEYIPS	22	2.4000	24.49
20	ILASNHLAV	35	2.4000	24.49
21	LGMYPEGTR	113	2.4000	24.49
22	VVNPPGRKM	155	2.3800	24.29
23	MGPLFTLLG	10	2.3600	24.08
24	INRWFYSVS	75	2.3000	23.47

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	YLPLVVRRR	48	4.4000	44.90
2	YIFMGPLFT	7	4.2000	42.86
3	LFTLLGRPK	13	4.1000	41.84
4	FKYIFMGPL	5	3.6000	36.73
5	WYYLFKYIF	1	3.2000	32.65
6	VVLLGQGKL	104	3.2000	32.65
7	FGRVTVRFG	166	2.7000	27.55
8	LMGLSGQEY	203	2.6000	26.53
9	YKGKTGLAR	128	2.4000	24.49
10	FEGLAGNHF	182	2.3000	23.47
11	YELMGLSGQ	201	2.3000	23.47
12	VRFGKPMDF	171	2.2000	22.45
13	VSGQVPIDR	82	2.1000	21.43
14	YYLFKYIFM	2	2.0000	20.41
15	LRFGRVTVR	164	1.9000	19.39
16	YVDIYAASV	211	1.9000	19.39
17	LAVADSFYL	41	1.8000	18.37
18	LPLVVRRRI	49	1.8000	18.37
19	FYSVSGQVP	79	1.8000	18.37
20	WFLAKSEYF	58	1.6000	16.33
21	VVNPPGRKM	155	1.6000	16.33
22	IFMGPLFTL	8	1.4000	14.29
23	LGMYPEGTR	113	1.4000	14.29
24	FYLPLVVRR	47	1.3000	13.27

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	YLPLVVRRR	48	4.4000	44.90
2	YIFMGPLFT	7	4.2000	42.86
3	LFTLLGRPK	13	4.1000	41.84
4	FKYIFMGPL	5	3.6000	36.73
5	WYYLFKYIF	1	3.2000	32.65
6	VVLLGQGKL	104	3.2000	32.65
7	FGRVTVRFG	166	2.7000	27.55
8	LMGLSGQEY	203	2.6000	26.53
9	YKGKTGLAR	128	2.4000	24.49
10	FEGLAGNHF	182	2.3000	23.47
11	YELMGLSGQ	201	2.3000	23.47
12	VRFGKPMDF	171	2.2000	22.45
13	VSGQVPIDR	82	2.1000	21.43
14	YYLFKYIFM	2	2.0000	20.41
15	LRFGRVTVR	164	1.9000	19.39
16	YVDIYAASV	211	1.9000	19.39
17	LAVADSFYL	41	1.8000	18.37
18	LPLVVRRRI	49	1.8000	18.37
19	FYSVSGQVP	79	1.8000	18.37
20	WFLAKSEYF	58	1.6000	16.33
21	VVNPPGRKM	155	1.6000	16.33
22	IFMGPLFTL	8	1.4000	14.29
23	LGMYPEGTR	113	1.4000	14.29
24	FYLPLVVRR	47	1.3000	13.27