MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Mar 8 00:27:19 2010
Length of input sequence	379 amino acids
Number of nanomers from input sequence	371
Number of nanomers with obligatory P1 anchor residue	113
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	37

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	FEINEAASL	269	2.1400	35.67
2	FEPVDAVSV	344	1.3500	22.50
3	FRSADEVLL	179	1.2000	20.00
4	VVASIARKL	112	0.9900	16.50
5	VLLNGVQGI	185	0.8400	14.00
6	VVGIGGGGV	12	0.7000	11.67
7	LRGADMVFV	89	0.6000	10.00
8	LQMGDAAVS	166	0.6000	10.00
9	VSLMDAFRS	173	0.5000	8.33
10	LAVIKVVGI	7	0.3000	5.00
11	MSIAGGSDL	258	0.2000	3.33
12	MVFVTAGEG	94	-0.0500	0

13	IMSGAGTAL	213	-0.1100	0
14	MEGAQGVLM	250	-0.2200	0
15	LHTNGATLS	354	-0.3700	0
16	VNRMIEQGL	23	-0.4000	0
17	VIKVVGIGG	9	-0.4500	0
18	LKGVEFIAI	31	-0.5500	0
19	LMGIGSARG	221	-0.6000	0
20	VLMSIAGGS	256	-0.7000	0
21	YLAVIKVVG	6	-1.1500	0
22	LGLFEINEA	266	-1.2200	0
23	LINVDFADV	202	-1.2500	0
24	IAINSPLLE	239	-1.2600	0
25	IESAKAGKL	331	-1.3000	0
26	FADVKGIMS	207	-1.3500	0
27	IVIPNDRLL	158	-1.4100	0
28	LGALTVGVV	120	-1.5000	0
29	LIVIPNDRL	157	-1.5000	0
30	MGIGSARGE	222	-1.5100	0
31	LLQMGDAAV	165	-1.6000	0
32	LNGVQGITD	187	-1.6500	0
33	IGGGGVNAV	15	-1.7000	0
34	VQGITDLIT	190	-1.7000	0
35	VKGIMSGAG	210	-1.7000	0
36	VKLDVGRDS	53	-1.8100	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	FEINEAASL	269	2.1400	35.67
2	VVASIARKL	112	1.9900	33.17
3	VLLNGVQGI	185	1.8400	30.67
4	VVGIGGGGV	12	1.7000	28.33
5	LRGADMVFV	89	1.6000	26.67
6	LQMGDAAVS	166	1.6000	26.67
7	VSLMDAFRS	173	1.5000	25.00
8	FEPVDAVSV	344	1.3500	22.50
9	LAVIKVVGI	7	1.3000	21.67

10	FRSADEVLL	179	1.2000	20.00
11	MSIAGGSDL	258	1.2000	20.00
12	MVFVTAGEG	94	0.9500	15.83
13	IMSGAGTAL	213	0.8900	14.83
14	MEGAQGVLM	250	0.7800	13.00
15	LHTNGATLS	354	0.6300	10.50
16	VNRMIEQGL	23	0.6000	10.00
17	VIKVVGIGG	9	0.5500	9.17
18	LKGVEFIAI	31	0.4500	7.50
19	LMGIGSARG	221	0.4000	6.67
20	VLMSIAGGS	256	0.3000	5.00
21	LGLFEINEA	266	-0.2200	0
22	LINVDFADV	202	-0.2500	0
23	IAINSPLLE	239	-0.2600	0
24	IESAKAGKL	331	-0.3000	0
25	IVIPNDRLL	158	-0.4100	0
26	LGALTVGVV	120	-0.5000	0
27	LIVIPNDRL	157	-0.5000	0
28	MGIGSARGE	222	-0.5100	0
29	LLQMGDAAV	165	-0.6000	0
30	LNGVQGITD	187	-0.6500	0
31	IGGGGVNAV	15	-0.7000	0
32	VQGITDLIT	190	-0.7000	0
33	VKGIMSGAG	210	-0.7000	0
34	VKLDVGRDS	53	-0.8100	0
35	VRVTVIAAG	302	-1.0000	0
36	VGVVTRPFS	125	-1.0800	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	VLMSIAGGS	256	4.3000	45.26
2	LQMGDAAVS	166	4.2000	44.21
3	VKLDVGRDS	53	3.9000	41.05
4	VLLNGVQGI	185	3.9000	41.05
5	VGVVTRPFS	125	3.8000	40.00
6	IPNDRLLQM	160	3.8000	40.00

7	MVFVTAGEG	94	3.4000	35.79
8	IIFGTVIDD	288	3.4000	35.79
9	VGRDSTRGL	57	3.3600	35.37
10	LAVIKVVGI	7	3.0000	31.58
11	LVQDAAHPD	277	3.0000	31.58
12	IKVVGIGGG	10	2.8000	29.47
13	INVDFADVK	203	2.8000	29.47
14	VRVTVIAAG	302	2.8000	29.47
15	INTDAQALL	39	2.7600	29.05
16	IGGGGVNAV	15	2.6100	27.47
17	VNAVNRMIE	20	2.6000	27.37
18	VIPNDRLLQ	159	2.6000	27.37
19	VVGIGGGGV	12	2.5000	26.32
20	LLMSDADVK	46	2.3000	24.21
21	VSLMDAFRS	173	2.3000	24.21
22	VKGIMSGAG	210	2.2000	23.16
23	LGALTVGVV	120	2.1000	22.11
24	LMGIGSARG	221	2.1000	22.11
25	IAINSPLLE	239	2.1000	22.11
26	VIDDSLGDE	293	2.1000	22.11
27	LRGADMVFV	89	2.0000	21.05
28	LHTNGATLS	354	2.0000	21.05
29	YLAVIKVVG	6	1.9000	20.00
30	VVASIARKL	112	1.8600	19.58
31	LLRGADMVF	88	1.8000	18.95
32	LTVGVVTRP	123	1.8000	18.95
33	MSGAGTALM	214	1.8000	18.95
34	IEQGLKGVE	27	1.7000	17.89
35	MGDAAVSLM	168	1.5700	16.53
36	VEFIAINTD	34	1.4100	14.84
37	LMSDADVKL	47	1.3600	14.32

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	VLMSIAGGS	256	2.9000	31.87
2	LQMGDAAVS	166	2.8000	30.77

3	VKLDVGRDS	53	2.5000	27.47
4	VGVVTRPFS	125	2.4000	26.37
5	FIAINTDAQ	36	2.3000	25.27
6	VIPNDRLLQ	159	2.3000	25.27
7	VLLNGVQGI	185	2.0000	21.98
8	INVDFADVK	203	1.7000	18.68
9	YLAVIKVVG	6	1.5000	16.48
10	VGRDSTRGL	57	1.4000	15.38
11	IPNDRLLQM	160	1.3000	14.29
12	IIFGTVIDD	288	1.3000	14.29
13	LLMSDADVK	46	1.2000	13.19
14	LAVIKVVGI	7	1.1000	12.09
15	MVFVTAGEG	94	1.0000	10.99
16	VSLMDAFRS	173	0.9000	9.89
17	LVQDAAHPD	277	0.9000	9.89
18	FEGKRRSNQ	134	0.8700	9.56
19	INTDAQALL	39	0.8000	8.79
20	FEINEAASL	269	0.8000	8.79
21	IGGGGVNAV	15	0.6100	6.70
22	FSFEGKRRS	132	0.6000	6.59
23	LHTNGATLS	354	0.6000	6.59
24	VVGIGGGGV	12	0.5000	5.49
25	IKVVGIGGG	10	0.4000	4.40
26	VRVTVIAAG	302	0.4000	4.40
27	VNAVNRMIE	20	0.2000	2.20
28	FRSADEVLL	179	0.2000	2.20
29	FDVSGPGRK	311	0.2000	2.20
30	LGLFEINEA	266	0.1100	1.21
31	LGALTVGVV	120	0.1000	1.10
32	VVASIARKL	112	-0.1000	0
33	FEPVDAVSV	344	-0.1000	0
34	FVTAGEGGG	96	-0.2000	0
35	LTVGVVTRP	123	-0.2000	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	VIPNDRLLQ	159	3.8000	43.18
2	LQMGDAAVS	166	3.8000	43.18
3	VKLDVGRDS	53	3.2000	36.36
4	VLLNGVQGI	185	3.1000	35.23
5	INVDFADVK	203	3.0000	34.09
6	IPNDRLLQM	160	2.8000	31.82
7	LVQDAAHPD	277	2.7000	30.68
8	LLMSDADVK	46	2.5000	28.41
9	VLMSIAGGS	256	2.5000	28.41
10	IGGGGVNAV	15	2.3000	26.14
11	VGRDSTRGL	57	2.1000	23.86
12	VGVVTRPFS	125	2.0000	22.73
13	LAVIKVVGI	7	1.9800	22.50
14	IIFGTVIDD	288	1.9800	22.50
15	INTDAQALL	39	1.8000	20.45
16	LGLFEINEA	266	1.8000	20.45
17	FIAINTDAQ	36	1.6000	18.18
18	LHTNGATLS	354	1.6000	18.18
19	VRVTVIAAG	302	1.4000	15.91
20	IAINSPLLE	239	1.2000	13.64
21	INSPLLEAS	241	1.1000	12.50
22	IFGTVIDDS	289	1.1000	12.50
23	VEFIAINTD	34	1.0000	11.36
24	VNAVNRMIE	20	0.9000	10.23
25	LRGADMVFV	89	0.8800	10.00
26	LTVGVVTRP	123	0.8000	9.09
27	LMGIGSARG	221	0.7000	7.95
28	INEAASLVQ	271	0.7000	7.95
29	MVFVTAGEG	94	0.6000	6.82
30	VVASIARKL	112	0.6000	6.82
31	VGRKAAEDA	73	0.4000	4.55
32	VASIARKLG	113	0.4000	4.55
33	VSLMDAFRS	173	0.4000	4.55
34	LKAAEIAIN	234	0.4000	4.55
35	YLAVIKVVG	6	0.3800	4.32
36	MSGAGTALM	214	0.3000	3.41
37	LMSDADVKL	47	0.2800	3.18

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	VIPNDRLLQ	159	3.8000	43.18
2	LQMGDAAVS	166	3.8000	43.18
3	VKLDVGRDS	53	3.2000	36.36
4	VLLNGVQGI	185	3.1000	35.23
5	INVDFADVK	203	3.0000	34.09
6	IPNDRLLQM	160	2.8000	31.82
7	LVQDAAHPD	277	2.7000	30.68
8	LLMSDADVK	46	2.5000	28.41
9	VLMSIAGGS	256	2.5000	28.41
10	IGGGGVNAV	15	2.3000	26.14
11	VGRDSTRGL	57	2.1000	23.86
12	VGVVTRPFS	125	2.0000	22.73
13	LAVIKVVGI	7	1.9800	22.50
14	IIFGTVIDD	288	1.9800	22.50
15	INTDAQALL	39	1.8000	20.45
16	LGLFEINEA	266	1.8000	20.45
17	FIAINTDAQ	36	1.6000	18.18
18	LHTNGATLS	354	1.6000	18.18
19	VRVTVIAAG	302	1.4000	15.91
20	IAINSPLLE	239	1.2000	13.64
21	INSPLLEAS	241	1.1000	12.50
22	IFGTVIDDS	289	1.1000	12.50
23	VEFIAINTD	34	1.0000	11.36
24	VNAVNRMIE	20	0.9000	10.23
25	LRGADMVFV	89	0.8800	10.00
26	LTVGVVTRP	123	0.8000	9.09
27	LMGIGSARG	221	0.7000	7.95
28	INEAASLVQ	271	0.7000	7.95
29	MVFVTAGEG	94	0.6000	6.82
30	VVASIARKL	112	0.6000	6.82
31	VGRKAAEDA	73	0.4000	4.55
32	VASIARKLG	113	0.4000	4.55
33	VSLMDAFRS	173	0.4000	4.55
34	LKAAEIAIN	234	0.4000	4.55

35	YLAVIKVVG	6	0.3800	4.32
36	MSGAGTALM	214	0.3000	3.41
37	LMSDADVKL	47	0.2800	3.18

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	VIPNDRLLQ	159	3.8000	43.18
2	LQMGDAAVS	166	3.8000	43.18
3	VKLDVGRDS	53	3.2000	36.36
4	VLLNGVQGI	185	3.1000	35.23
5	INVDFADVK	203	3.0000	34.09
6	IPNDRLLQM	160	2.8000	31.82
7	LVQDAAHPD	277	2.7000	30.68
8	LLMSDADVK	46	2.5000	28.41
9	VLMSIAGGS	256	2.5000	28.41
10	IGGGGVNAV	15	2.3000	26.14
11	VGRDSTRGL	57	2.1000	23.86
12	VGVVTRPFS	125	2.0000	22.73
13	LAVIKVVGI	7	1.9800	22.50
14	IIFGTVIDD	288	1.9800	22.50
15	INTDAQALL	39	1.8000	20.45
16	LGLFEINEA	266	1.8000	20.45
17	FIAINTDAQ	36	1.6000	18.18
18	LHTNGATLS	354	1.6000	18.18
19	VRVTVIAAG	302	1.4000	15.91
20	IAINSPLLE	239	1.2000	13.64
21	INSPLLEAS	241	1.1000	12.50
22	IFGTVIDDS	289	1.1000	12.50
23	VEFIAINTD	34	1.0000	11.36
24	VNAVNRMIE	20	0.9000	10.23
25	LRGADMVFV	89	0.8800	10.00
26	LTVGVVTRP	123	0.8000	9.09
27	LMGIGSARG	221	0.7000	7.95
28	INEAASLVQ	271	0.7000	7.95
29	MVFVTAGEG	94	0.6000	6.82
30	VVASIARKL	112	0.6000	6.82

31	VGRKAAEDA	73	0.4000	4.55
32	VASIARKLG	113	0.4000	4.55
33	VSLMDAFRS	173	0.4000	4.55
34	LKAAEIAIN	234	0.4000	4.55
35	YLAVIKVVG	6	0.3800	4.32
36	MSGAGTALM	214	0.3000	3.41
37	LMSDADVKL	47	0.2800	3.18

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	VLMSIAGGS	256	3.3000	34.74
2	LQMGDAAVS	166	3.2000	33.68
3	YLAVIKVVG	6	2.9000	30.53
4	VKLDVGRDS	53	2.9000	30.53
5	VLLNGVQGI	185	2.9000	30.53
6	VGVVTRPFS	125	2.8000	29.47
7	IPNDRLLQM	160	2.8000	29.47
8	MVFVTAGEG	94	2.4000	25.26
9	IIFGTVIDD	288	2.4000	25.26
10	VGRDSTRGL	57	2.3600	24.84
11	LAVIKVVGI	7	2.0000	21.05
12	LVQDAAHPD	277	2.0000	21.05
13	IKVVGIGGG	10	1.8000	18.95
14	INVDFADVK	203	1.8000	18.95
15	VRVTVIAAG	302	1.8000	18.95
16	INTDAQALL	39	1.7600	18.53
17	FEINEAASL	269	1.7600	18.53
18	IGGGGVNAV	15	1.6100	16.95
19	VNAVNRMIE	20	1.6000	16.84
20	FIAINTDAQ	36	1.6000	16.84
21	VIPNDRLLQ	159	1.6000	16.84
22	VVGIGGGGV	12	1.5000	15.79
23	LLMSDADVK	46	1.3000	13.68
24	VSLMDAFRS	173	1.3000	13.68
25	FVTAGEGGG	96	1.2000	12.63
26	VKGIMSGAG	210	1.2000	12.63

27	FRSADEVLL	179	1.1600	12.21
28	LGALTVGVV	120	1.1000	11.58
29	LMGIGSARG	221	1.1000	11.58
30	IAINSPLLE	239	1.1000	11.58
31	VIDDSLGDE	293	1.1000	11.58
32	LRGADMVFV	89	1.0000	10.53
33	FSFEGKRRS	132	1.0000	10.53
34	LHTNGATLS	354	1.0000	10.53
35	FEPVDAVSV	344	0.9000	9.47
36	VVASIARKL	112	0.8600	9.05
37	LLRGADMVF	88	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	VIPNDRLLQ	159	3.8000	43.18
2	LQMGDAAVS	166	3.8000	43.18
3	VKLDVGRDS	53	3.2000	36.36
4	VLLNGVQGI	185	3.1000	35.23
5	INVDFADVK	203	3.0000	34.09
6	IPNDRLLQM	160	2.8000	31.82
7	LVQDAAHPD	277	2.7000	30.68
8	LLMSDADVK	46	2.5000	28.41
9	VLMSIAGGS	256	2.5000	28.41
10	IGGGGVNAV	15	2.3000	26.14
11	VGRDSTRGL	57	2.1000	23.86
12	VGVVTRPFS	125	2.0000	22.73
13	LAVIKVVGI	7	1.9800	22.50
14	IIFGTVIDD	288	1.9800	22.50
15	INTDAQALL	39	1.8000	20.45
16	LGLFEINEA	266	1.8000	20.45
17	FIAINTDAQ	36	1.6000	18.18
18	LHTNGATLS	354	1.6000	18.18
19	VRVTVIAAG	302	1.4000	15.91
20	IAINSPLLE	239	1.2000	13.64
21	INSPLLEAS	241	1.1000	12.50
22	IFGTVIDDS	289	1.1000	12.50

23	VEFIAINTD	34	1.0000	11.36
24	VNAVNRMIE	20	0.9000	10.23
25	LRGADMVFV	89	0.8800	10.00
26	LTVGVVTRP	123	0.8000	9.09
27	LMGIGSARG	221	0.7000	7.95
28	INEAASLVQ	271	0.7000	7.95
29	MVFVTAGEG	94	0.6000	6.82
30	VVASIARKL	112	0.6000	6.82
31	VGRKAAEDA	73	0.4000	4.55
32	VASIARKLG	113	0.4000	4.55
33	VSLMDAFRS	173	0.4000	4.55
34	LKAAEIAIN	234	0.4000	4.55
35	YLAVIKVVG	6	0.3800	4.32
36	MSGAGTALM	214	0.3000	3.41
37	LMSDADVKL	47	0.2800	3.18

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	FIAINTDAQ	36	4.0000	46.51
2	VLLNGVQGI	185	2.5000	29.07
3	LLMSDADVK	46	1.6000	18.60
4	VLMSIAGGS	256	1.6000	18.60
5	FEINEAASL	269	1.5000	17.44
6	LIVIPNDRL	157	1.4000	16.28
7	VGRDSTRGL	57	1.3000	15.12
8	VRVTVIAAG	302	1.3000	15.12
9	LHTNGATLS	354	1.3000	15.12
10	INVDFADVK	203	1.1000	12.79
11	LMGIGSARG	221	1.1000	12.79
12	IFGTVIDDS	289	1.0000	11.63
13	LAVIKVVGI	7	0.9800	11.40
14	INEAASLVQ	271	0.8000	9.30
15	LVQDAAHPD	277	0.8000	9.30
16	LQMGDAAVS	166	0.7000	8.14
17	VKLDVGRDS	53	0.5000	5.81
18	MSGAGTALM	214	0.4000	4.65

19	IAINSPLLE	239	0.4000	4.65
20	IAINTDAQA	37	0.3000	3.49
21	VSLMDAFRS	173	0.3000	3.49
22	VIPNDRLLQ	159	0.1000	1.16
23	LGLFEINEA	266	0.1000	1.16
24	VKGIMSGAG	210	-0.2000	0
25	VVASIARKL	112	-0.3000	0
26	LMSDADVKL	47	-0.3200	0
27	LRGADMVFV	89	-0.3200	0
28	IPNDRLLQM	160	-0.4000	0
29	VQGITDLIT	190	-0.4000	0
30	VEFIAINTD	34	-0.5000	0
31	VIAAGFDVS	306	-0.6000	0
32	VPLHTNGAT	352	-0.6000	0
33	LRESCDTLI	150	-0.7000	0
34	ITDLITTPG	193	-0.7000	0
35	LGALTVGVV	120	-0.8000	0
36	FSFEGKRRS	132	-0.9000	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VLLNGVQGI	185	3.3000	34.38
2	LQMGDAAVS	166	2.6000	27.08
3	VSLMDAFRS	173	2.5000	26.04
4	LGLFEINEA	266	2.3000	23.96
5	INEAASLVQ	271	2.1000	21.88
6	IVIPNDRLL	158	1.9000	19.79
7	VVASIARKL	112	1.8000	18.75
8	VGRDSTRGL	57	1.5000	15.62
9	MSGAGTALM	214	1.4000	14.58
10	LAVIKVVGI	7	1.3800	14.37
11	LMGIGSARG	221	1.3800	14.37
12	MGIGSARGE	222	1.3000	13.54
13	MTPPHNYLA	0	1.2000	12.50
14	LHTNGATLS	354	1.2000	12.50
15	VRVTVIAAG	302	1.1000	11.46

16	IIFGTVIDD	288	0.9000	9.38
17	IGGGGVNAV	15	0.8000	8.33
18	LRGADMVFV	89	0.8000	8.33
19	VKLDVGRDS	53	0.7000	7.29
20	FIAINTDAQ	36	0.4800	5.00
21	IAINSPLLE	239	0.4000	4.17
22	VQGITDLIT	190	0.1800	1.88
23	VGRKAAEDA	73	0.1000	1.04
24	VIPNDRLLQ	159	0.1000	1.04
25	VDFADVKGI	205	0.1000	1.04
26	VVTRPFSFE	127	-0.1000	0
27	VTRPFSFEG	128	-0.1000	0
28	LIVIPNDRL	157	-0.1200	0
29	VNRMIEQGL	23	-0.2000	0
30	LLQMGDAAV	165	-0.2000	0
31	VEFIAINTD	34	-0.2200	0
32	LKGVEFIAI	31	-0.3000	0
33	LLRGADMVF	88	-0.3000	0
34	VPLHTNGAT	352	-0.3000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VSLMDAFRS	173	3.1500	35.80
2	LGLFEINEA	266	3.1000	35.23
3	FIAINTDAQ	36	2.4000	27.27
4	LMGIGSARG	221	2.4000	27.27
5	LAVIKVVGI	7	2.1000	23.86
6	LIVIPNDRL	157	1.8000	20.45
7	VLLNGVQGI	185	1.7000	19.32
8	MSGAGTALM	214	1.4000	15.91
9	INEAASLVQ	271	1.4000	15.91
10	MVFVTAGEG	94	1.2000	13.64
11	VKGIMSGAG	210	1.2000	13.64
12	VLMSIAGGS	256	1.2000	13.64
13	LHTNGATLS	354	1.2000	13.64
14	LLQMGDAAV	165	1.0000	11.36

15	ITDLITTPG	193	1.0000	11.36
16	VEFIAINTD	34	0.9000	10.23
17	LQMGDAAVS	166	0.9000	10.23
18	VRVTVIAAG	302	0.7000	7.95
19	LRGADMVFV	89	0.5000	5.68
20	LGALTVGVV	120	0.5000	5.68
21	VQGITDLIT	190	0.5000	5.68
22	LKGVEFIAI	31	0.4800	5.45
23	LINVDFADV	202	0.3000	3.41
24	LLMSDADVK	46	0.2000	2.27
25	MGDAAVSLM	168	0.2000	2.27
26	MTPPHNYLA	0	0.1000	1.14
27	VGRDSTRGL	57	0.1000	1.14
28	IKVVGIGGG	10	-0.2000	0
29	VNRMIEQGL	23	-0.3000	0
30	IAINTDAQA	37	-0.3000	0
31	LKAAEIAIN	234	-0.4000	0
32	VVASIARKL	112	-0.5000	0
33	IFGTVIDDS	289	-0.5000	0
34	VIAAGFDVS	306	-0.5000	0
35	IAINSPLLE	239	-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	FIAINTDAQ	36	4.2000	44.68
2	LMGIGSARG	221	2.7000	28.72
3	VEFIAINTD	34	2.6000	27.66
4	VSLMDAFRS	173	2.1500	22.87
5	LGLFEINEA	266	2.1000	22.34
6	LIVIPNDRL	157	1.8000	19.15
7	MVFVTAGEG	94	1.5000	15.96
8	VKGIMSGAG	210	1.5000	15.96
9	MSGAGTALM	214	1.5000	15.96
10	IAINSPLLE	239	1.4000	14.89
11	LAVIKVVGI	7	1.3000	13.83
12	ITDLITTPG	193	1.3000	13.83

13	INEAASLVQ	271	1.2000	12.77
14	MDAFRSADE	176	1.0000	10.64
15	VRVTVIAAG	302	1.0000	10.64
16	VLLNGVQGI	185	0.9000	9.57
17	FEINEAASL	269	0.9000	9.57
18	LKAAEIAIN	234	0.6000	6.38
19	LVQDAAHPD	277	0.6000	6.38
20	IIFGTVIDD	288	0.4800	5.11
21	VQGITDLIT	190	0.4000	4.26
22	VTVIAAGFD	304	0.4000	4.26
23	FEPVDAVSV	344	0.4000	4.26
24	LLQMGDAAV	165	0.3000	3.19
25	MGDAAVSLM	168	0.3000	3.19
26	VLMSIAGGS	256	0.2000	2.13
27	LHTNGATLS	354	0.2000	2.13
28	IKVVGIGGG	10	0.1000	1.06
29	VGRDSTRGL	57	0.1000	1.06
30	LNGVQGITD	187	0.0800	0.85
31	VNAVNRMIE	20	-0.1000	0
32	LQMGDAAVS	166	-0.1000	0
33	FRSADEVLL	179	-0.1000	0
34	LRGADMVFV	89	-0.2000	0
35	LGALTVGVV	120	-0.2000	0
36	VNRMIEQGL	23	-0.3000	0

ALLELE: DRB1_0408	Threshold for 3 % with score: 1.2	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	FIAINTDAQ	36	3.4000	38.64
2	VSLMDAFRS	173	2.1500	24.43
3	LGLFEINEA	266	2.1000	23.86
4	LMGIGSARG	221	1.4000	15.91
5	LAVIKVVGI	7	1.1000	12.50
6	LIVIPNDRL	157	0.8000	9.09
7	VLLNGVQGI	185	0.7000	7.95
8	MSGAGTALM	214	0.4000	4.55
9	INEAASLVQ	271	0.4000	4.55

10	MVFVTAGEG	94	0.2000	2.27
11	VKGIMSGAG	210	0.2000	2.27
12	VLMSIAGGS	256	0.2000	2.27
13	LHTNGATLS	354	0.2000	2.27
14	FEPVDAVSV	344	0.1000	1.14
15	VEFIAINTD	34	-0.1000	0
16	LQMGDAAVS	166	-0.1000	0
17	FEINEAASL	269	-0.1000	0
18	VRVTVIAAG	302	-0.3000	0
19	LRGADMVFV	89	-0.5000	0
20	LGALTVGVV	120	-0.5000	0
21	VQGITDLIT	190	-0.5000	0
22	LKGVEFIAI	31	-0.5200	0
23	LINVDFADV	202	-0.7000	0
24	LLMSDADVK	46	-0.8000	0
25	MGDAAVSLM	168	-0.8000	0
26	MTPPHNYLA	0	-0.9000	0
27	VGRDSTRGL	57	-0.9000	0
28	VVGIGGGGV	12	-1.0000	0
29	FRSADEVLL	179	-1.1000	0
30	IKVVGIGGG	10	-1.2000	0
31	VNRMIEQGL	23	-1.3000	0
32	IAINTDAQA	37	-1.3000	0
33	LKAAEIAIN	234	-1.4000	0
34	VVASIARKL	112	-1.5000	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	LMGIGSARG	221	3.7000	39.36
2	VEFIAINTD	34	3.6000	38.30
3	FIAINTDAQ	36	3.2000	34.04
4	VSLMDAFRS	173	3.1500	33.51
5	LGLFEINEA	266	3.1000	32.98
6	LIVIPNDRL	157	2.8000	29.79
7	MVFVTAGEG	94	2.5000	26.60
8	VKGIMSGAG	210	2.5000	26.60

9	MSGAGTALM	214	2.5000	26.60
10	IAINSPLLE	239	2.4000	25.53
11	LAVIKVVGI	7	2.3000	24.47
12	ITDLITTPG	193	2.3000	24.47
13	INEAASLVQ	271	2.2000	23.40
14	MDAFRSADE	176	2.0000	21.28
15	VRVTVIAAG	302	2.0000	21.28
16	VLLNGVQGI	185	1.9000	20.21
17	LKAAEIAIN	234	1.6000	17.02
18	LVQDAAHPD	277	1.6000	17.02
19	IIFGTVIDD	288	1.4800	15.74
20	VQGITDLIT	190	1.4000	14.89
21	VTVIAAGFD	304	1.4000	14.89
22	LLQMGDAAV	165	1.3000	13.83
23	MGDAAVSLM	168	1.3000	13.83
24	VLMSIAGGS	256	1.2000	12.77
25	LHTNGATLS	354	1.2000	12.77
26	IKVVGIGGG	10	1.1000	11.70
27	VGRDSTRGL	57	1.1000	11.70
28	LNGVQGITD	187	1.0800	11.49
29	VNAVNRMIE	20	0.9000	9.57
30	LQMGDAAVS	166	0.9000	9.57
31	LRGADMVFV	89	0.8000	8.51
32	LGALTVGVV	120	0.8000	8.51
33	VNRMIEQGL	23	0.7000	7.45
34	LMSIAGGSD	257	0.7000	7.45
35	LKGVEFIAI	31	0.6800	7.23
36	VTRPFSFEG	128	0.6500	6.91
37	LINVDFADV	202	0.6000	6.38

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	VLLNGVQGI	185	3.4000	37.78
2	FIAINTDAQ	36	3.3000	36.67
3	VRVTVIAAG	302	2.7000	30.00
4	LMGIGSARG	221	2.5000	27.78

5	FEINEAASL	269	2.4600	27.33
6	LIVIPNDRL	157	2.3600	26.22
7	VGRDSTRGL	57	2.2600	25.11
8	VLMSIAGGS	256	2.0000	22.22
9	MSGAGTALM	214	1.9000	21.11
10	LVQDAAHPD	277	1.9000	21.11
11	LAVIKVVGI	7	1.8800	20.89
12	IAINSPLLE	239	1.8000	20.00
13	LLMSDADVK	46	1.7000	18.89
14	LHTNGATLS	354	1.7000	18.89
15	IFGTVIDDS	289	1.4000	15.56
16	INVDFADVK	203	1.2000	13.33
17	VKGIMSGAG	210	1.2000	13.33
18	IPNDRLLQM	160	1.1000	12.22
19	LQMGDAAVS	166	1.1000	12.22
20	VKLDVGRDS	53	0.9000	10.00
21	VSLMDAFRS	173	0.7000	7.78
22	ITDLITTPG	193	0.7000	7.78
23	LRGADMVFV	89	0.6800	7.56
24	VVASIARKL	112	0.6600	7.33
25	LMSDADVKL	47	0.6400	7.11
26	VEFIAINTD	34	0.6000	6.67
27	IAINTDAQA	37	0.3000	3.33
28	VQGITDLIT	190	0.3000	3.33
29	LGALTVGVV	120	0.2000	2.22
30	LRESCDTLI	150	0.2000	2.22
31	MVFVTAGEG	94	0.1000	1.11
32	VFVTAGEGG	95	0.1000	1.11
33	LLQMGDAAV	165	0.1000	1.11
34	LGLFEINEA	266	0.1000	1.11
35	INEAASLVQ	271	0.1000	1.11
36	VPLHTNGAT	352	0.1000	1.11
37	FRSADEVLL	179	0.0400	0.44

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	VSLMDAFRS	173	3.1500	35.80
2	LGLFEINEA	266	3.1000	35.23
3	FIAINTDAQ	36	2.4000	27.27
4	LMGIGSARG	221	2.4000	27.27
5	LAVIKVVGI	7	2.1000	23.86
6	LIVIPNDRL	157	1.8000	20.45
7	VLLNGVQGI	185	1.7000	19.32
8	MSGAGTALM	214	1.4000	15.91
9	INEAASLVQ	271	1.4000	15.91
10	MVFVTAGEG	94	1.2000	13.64
11	VKGIMSGAG	210	1.2000	13.64
12	VLMSIAGGS	256	1.2000	13.64
13	LHTNGATLS	354	1.2000	13.64
14	LLQMGDAAV	165	1.0000	11.36
15	ITDLITTPG	193	1.0000	11.36
16	VEFIAINTD	34	0.9000	10.23
17	LQMGDAAVS	166	0.9000	10.23
18	VRVTVIAAG	302	0.7000	7.95
19	LRGADMVFV	89	0.5000	5.68
20	LGALTVGVV	120	0.5000	5.68
21	VQGITDLIT	190	0.5000	5.68
22	LKGVEFIAI	31	0.4800	5.45
23	LINVDFADV	202	0.3000	3.41
24	LLMSDADVK	46	0.2000	2.27
25	MGDAAVSLM	168	0.2000	2.27
26	MTPPHNYLA	0	0.1000	1.14
27	VGRDSTRGL	57	0.1000	1.14
28	IKVVGIGGG	10	-0.2000	0
29	VNRMIEQGL	23	-0.3000	0
30	IAINTDAQA	37	-0.3000	0
31	LKAAEIAIN	234	-0.4000	0
32	VVASIARKL	112	-0.5000	0
33	IFGTVIDDS	289	-0.5000	0
34	VIAAGFDVS	306	-0.5000	0
35	IAINSPLLE	239	-0.6000	0

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

	1.6	8.6

Rank	Sequence	At Position	Score	% of Highest Score
1	FIAINTDAQ	36	4.0000	46.51
2	VLLNGVQGI	185	2.5000	29.07
3	LLMSDADVK	46	1.6000	18.60
4	VLMSIAGGS	256	1.6000	18.60
5	FEINEAASL	269	1.5000	17.44
6	LIVIPNDRL	157	1.4000	16.28
7	VGRDSTRGL	57	1.3000	15.12
8	VRVTVIAAG	302	1.3000	15.12
9	LHTNGATLS	354	1.3000	15.12
10	INVDFADVK	203	1.1000	12.79
11	LMGIGSARG	221	1.1000	12.79
12	IFGTVIDDS	289	1.0000	11.63
13	LAVIKVVGI	7	0.9800	11.40
14	INEAASLVQ	271	0.8000	9.30
15	LVQDAAHPD	277	0.8000	9.30
16	LQMGDAAVS	166	0.7000	8.14
17	VKLDVGRDS	53	0.5000	5.81
18	MSGAGTALM	214	0.4000	4.65
19	IAINSPLLE	239	0.4000	4.65
20	IAINTDAQA	37	0.3000	3.49
21	VSLMDAFRS	173	0.3000	3.49
22	VIPNDRLLQ	159	0.1000	1.16
23	LGLFEINEA	266	0.1000	1.16
24	VKGIMSGAG	210	-0.2000	0
25	VVASIARKL	112	-0.3000	0
26	LMSDADVKL	47	-0.3200	0
27	LRGADMVFV	89	-0.3200	0
28	IPNDRLLQM	160	-0.4000	0
29	VQGITDLIT	190	-0.4000	0
30	VEFIAINTD	34	-0.5000	0
31	VIAAGFDVS	306	-0.6000	0
32	VPLHTNGAT	352	-0.6000	0
33	LRESCDTLI	150	-0.7000	0
34	ITDLITTPG	193	-0.7000	0
35	LGALTVGVV	120	-0.8000	0

36	FSFEGKRRS	132	-0.9000	0

ALLELE: DRB1_0701	Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VVASIARKL	112	6.7000	57.76
2	LKGVEFIAI	31	6.2000	53.45
3	LAVIKVVGI	7	5.7000	49.14
4	FRSADEVLL	179	4.9000	42.24
5	FEPVDAVSV	344	4.9000	42.24
6	VLLNGVQGI	185	4.5000	38.79
7	LRGADMVFV	89	4.2000	36.21
8	FEINEAASL	269	3.9000	33.62
9	VVGIGGGGV	12	3.8000	32.76
10	MSIAGGSDL	258	3.4000	29.31
11	LRESCDTLI	150	3.3000	28.45
12	LIVIPNDRL	157	3.2000	27.59
13	IVIPNDRLL	158	3.0000	25.86
14	IMSGAGTAL	213	2.9000	25.00
15	LINVDFADV	202	2.7000	23.28
16	IESAKAGKL	331	2.7000	23.28
17	LTSTLFEPV	339	2.7000	23.28
18	VGRDSTRGL	57	2.6200	22.59
19	LITTPGLIN	196	2.6000	22.41
20	VLMSIAGGS	256	2.6000	22.41
21	VDFADVKGI	205	2.5000	21.55
22	MEGAQGVLM	250	2.3000	19.83
23	VIKVVGIGG	9	2.2000	18.97
24	MVFVTAGEG	94	2.2000	18.97
25	IGGGGVNAV	15	2.1000	18.10
26	VNRMIEQGL	23	2.1000	18.10
27	VRVTVIAAG	302	2.0000	17.24
28	YLAVIKVVG	6	1.8000	15.52
29	VQGITDLIT	190	1.6000	13.79
30	LGLFEINEA	266	1.6000	13.79
31	LNGVQGITD	187	1.5000	12.93
32	VFVTAGEGG	95	1.4000	12.07

33	VKGIMSGAG	210	1.4000	12.07
34	LMGIGSARG	221	1.4000	12.07
35	ITTPGLINV	197	1.3000	11.21
36	LMSDADVKL	47	1.2000	10.34
37	IAGGSDLGL	260	1.2000	10.34

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVASIARKL	112	6.7000	57.76
2	LKGVEFIAI	31	6.2000	53.45
3	LAVIKVVGI	7	5.7000	49.14
4	FRSADEVLL	179	4.9000	42.24
5	FEPVDAVSV	344	4.9000	42.24
6	VLLNGVQGI	185	4.5000	38.79
7	LRGADMVFV	89	4.2000	36.21
8	FEINEAASL	269	3.9000	33.62
9	VVGIGGGGV	12	3.8000	32.76
10	MSIAGGSDL	258	3.4000	29.31
11	LRESCDTLI	150	3.3000	28.45
12	LIVIPNDRL	157	3.2000	27.59
13	IVIPNDRLL	158	3.0000	25.86
14	IMSGAGTAL	213	2.9000	25.00
15	LINVDFADV	202	2.7000	23.28
16	IESAKAGKL	331	2.7000	23.28
17	LTSTLFEPV	339	2.7000	23.28
18	VGRDSTRGL	57	2.6200	22.59
19	LITTPGLIN	196	2.6000	22.41
20	VLMSIAGGS	256	2.6000	22.41
21	VDFADVKGI	205	2.5000	21.55
22	MEGAQGVLM	250	2.3000	19.83
23	VIKVVGIGG	9	2.2000	18.97
24	MVFVTAGEG	94	2.2000	18.97
25	IGGGGVNAV	15	2.1000	18.10
26	VNRMIEQGL	23	2.1000	18.10
27	VRVTVIAAG	302	2.0000	17.24
28	YLAVIKVVG	6	1.8000	15.52

29	VQGITDLIT	190	1.6000	13.79
30	LGLFEINEA	266	1.6000	13.79
31	LNGVQGITD	187	1.5000	12.93
32	VFVTAGEGG	95	1.4000	12.07
33	VKGIMSGAG	210	1.4000	12.07
34	LMGIGSARG	221	1.4000	12.07
35	ITTPGLINV	197	1.3000	11.21
36	LMSDADVKL	47	1.2000	10.34
37	IAGGSDLGL	260	1.2000	10.34

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FEGKRRSNQ	134	3.6000	41.86
2	VIPNDRLLQ	159	2.4000	27.91
3	VNAVNRMIE	20	2.1000	24.42
4	MVFVTAGEG	94	2.0000	23.26
5	VVTRPFSFE	127	2.0000	23.26
6	IAINSPLLE	239	2.0000	23.26
7	YLAVIKVVG	6	1.8000	20.93
8	VRVTVIAAG	302	1.7000	19.77
9	FEINEAASL	269	1.6000	18.60
10	IKVVGIGGG	10	1.4000	16.28
11	LKAAEIAIN	234	1.4000	16.28
12	LQMGDAAVS	166	1.3000	15.12
13	IIFGTVIDD	288	1.3000	15.12
14	FIAINTDAQ	36	1.1000	12.79
15	IARKLGALT	116	1.0000	11.63
16	FSFEGKRRS	132	0.9000	10.47
17	VSLMDAFRS	173	0.9000	10.47
18	VLLNGVQGI	185	0.9000	10.47
19	VGVVTRPFS	125	0.8000	9.30
20	LMGIGSARG	221	0.8000	9.30
21	MGIGSARGE	222	0.7000	8.14
22	VEFIAINTD	34	0.6000	6.98
23	VLMSIAGGS	256	0.6000	6.98
24	FVTAGEGGG	96	0.5000	5.81

25	LGALTVGVV	120	0.5000	5.81
26	MSGAGTALM	214	0.4000	4.65
27	LMSIAGGSD	257	0.4000	4.65
28	LGLFEINEA	266	0.4000	4.65
29	VKGIMSGAG	210	0.3000	3.49
30	VTVIAAGFD	304	0.3000	3.49
31	IEQGLKGVE	27	0.2000	2.33
32	LVQDAAHPD	277	0.2000	2.33
33	VGRKAAEDA	73	0.1000	1.16
34	IEELLRGAD	85	0.1000	1.16

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	FEGKRRSNQ	134	2.8000	35.00
2	VIPNDRLLQ	159	1.6000	20.00
3	LQMGDAAVS	166	1.3000	16.25
4	FSFEGKRRS	132	0.9000	11.25
5	VSLMDAFRS	173	0.9000	11.25
6	VGVVTRPFS	125	0.8000	10.00
7	MVFVTAGEG	94	0.7000	8.75
8	VLLNGVQGI	185	0.7000	8.75
9	VLMSIAGGS	256	0.6000	7.50
10	FEINEAASL	269	0.6000	7.50
11	YLAVIKVVG	6	0.5000	6.25
12	LGLFEINEA	266	0.4000	5.00
13	VRVTVIAAG	302	0.4000	5.00
14	FIAINTDAQ	36	0.3000	3.75
15	LGALTVGVV	120	0.2000	2.50
16	IKVVGIGGG	10	0.1000	1.25
17	VGRKAAEDA	73	0.1000	1.25
18	IARKLGALT	116	0.1000	1.25
19	VVGIGGGGV	12	-0.3000	0
20	LAVIKVVGI	7	-0.4000	0
21	VKLDVGRDS	53	-0.5000	0
22	LMGIGSARG	221	-0.5000	0
23	LKAAEIAIN	234	-0.6000	0

24	MSGAGTALM	214	-0.7000	0
25	FVTAGEGGG	96	-0.8000	0
26	VNAVNRMIE	20	-0.9000	0
27	VVTRPFSFE	127	-1.0000	0
28	VKGIMSGAG	210	-1.0000	0
29	IAINSPLLE	239	-1.0000	0
30	FRSADEVLL	179	-1.1000	0
31	FEPVDAVSV	344	-1.1000	0
32	LINVDFADV	202	-1.2000	0
33	LRGADMVFV	89	-1.3000	0
34	VASIARKLG	113	-1.3000	0
35	INEAASLVQ	271	-1.3000	0
36	VDFADVKGI	205	-1.4000	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	VIPNDRLLQ	159	2.6000	32.50
2	LQMGDAAVS	166	2.3000	28.75
3	VSLMDAFRS	173	1.9000	23.75
4	VGVVTRPFS	125	1.8000	22.50
5	FEGKRRSNQ	134	1.8000	22.50
6	MVFVTAGEG	94	1.7000	21.25
7	VLLNGVQGI	185	1.7000	21.25
8	VLMSIAGGS	256	1.6000	20.00
9	LGLFEINEA	266	1.4000	17.50
10	VRVTVIAAG	302	1.4000	17.50
11	LGALTVGVV	120	1.2000	15.00
12	IKVVGIGGG	10	1.1000	13.75
13	VGRKAAEDA	73	1.1000	13.75
14	IARKLGALT	116	1.1000	13.75
15	VVGIGGGGV	12	0.7000	8.75
16	LAVIKVVGI	7	0.6000	7.50
17	VKLDVGRDS	53	0.5000	6.25
18	LMGIGSARG	221	0.5000	6.25
19	LKAAEIAIN	234	0.4000	5.00
20	MSGAGTALM	214	0.3000	3.75

21	VNAVNRMIE	20	0.1000	1.25
22	FSFEGKRRS	132	-0.1000	0
23	LINVDFADV	202	-0.2000	0
24	LRGADMVFV	89	-0.3000	0
25	VASIARKLG	113	-0.3000	0
26	INEAASLVQ	271	-0.3000	0
27	VDFADVKGI	205	-0.4000	0
28	FEINEAASL	269	-0.4000	0
29	IIFGTVIDD	288	-0.4000	0
30	YLAVIKVVG	6	-0.5000	0
31	VVASIARKL	112	-0.5000	0
32	VGRDSTRGL	57	-0.6000	0
33	VNRMIEQGL	23	-0.7000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VIPNDRLLQ	159	3.4000	39.53
2	VNAVNRMIE	20	3.1000	36.05
3	MVFVTAGEG	94	3.0000	34.88
4	VVTRPFSFE	127	3.0000	34.88
5	IAINSPLLE	239	3.0000	34.88
6	VRVTVIAAG	302	2.7000	31.40
7	FEGKRRSNQ	134	2.6000	30.23
8	IKVVGIGGG	10	2.4000	27.91
9	LKAAEIAIN	234	2.4000	27.91
10	LQMGDAAVS	166	2.3000	26.74
11	IIFGTVIDD	288	2.3000	26.74
12	IARKLGALT	116	2.0000	23.26
13	VSLMDAFRS	173	1.9000	22.09
14	VLLNGVQGI	185	1.9000	22.09
15	VGVVTRPFS	125	1.8000	20.93
16	LMGIGSARG	221	1.8000	20.93
17	MGIGSARGE	222	1.7000	19.77
18	VEFIAINTD	34	1.6000	18.60
19	VLMSIAGGS	256	1.6000	18.60
20	LGALTVGVV	120	1.5000	17.44

21	MSGAGTALM	214	1.4000	16.28
22	LMSIAGGSD	257	1.4000	16.28
23	LGLFEINEA	266	1.4000	16.28
24	VKGIMSGAG	210	1.3000	15.12
25	VTVIAAGFD	304	1.3000	15.12
26	IEQGLKGVE	27	1.2000	13.95
27	LVQDAAHPD	277	1.2000	13.95
28	VGRKAAEDA	73	1.1000	12.79
29	IEELLRGAD	85	1.1000	12.79
30	VVGIGGGGV	12	1.0000	11.63
31	VASIARKLG	113	1.0000	11.63
32	YLAVIKVVG	6	0.8000	9.30
33	LAVIKVVGI	7	0.8000	9.30
34	LNGVQGITD	187	0.8000	9.30
35	FEINEAASL	269	0.6000	6.98
36	VKLDVGRDS	53	0.5000	5.81
37	VVASIARKL	112	0.5000	5.81

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	FEGKRRSNQ	134	4.6000	52.87
2	LGLFEINEA	266	2.4000	27.59
3	VIPNDRLLQ	159	2.2000	25.29
4	VGRKAAEDA	73	1.8000	20.69
5	VSLMDAFRS	173	1.7500	20.11
6	VLLNGVQGI	185	1.7000	19.54
7	YLAVIKVVG	6	1.5000	17.24
8	FIAINTDAQ	36	1.5000	17.24
9	LQMGDAAVS	166	1.3000	14.94
10	VGVVTRPFS	125	1.0000	11.49
11	LHTNGATLS	354	0.9000	10.34
12	VVTRPFSFE	127	0.8000	9.20
13	LAVIKVVGI	7	0.6000	6.90
14	FSFEGKRRS	132	0.6000	6.90
15	FEINEAASL	269	0.6000	6.90
16	VRVTVIAAG	302	0.4000	4.60

17	VNAVNRMIE	20	0.1000	1.15
18	IARKLGALT	116	0.1000	1.15
19	IGGGGVNAV	15	-0.1000	0
20	VEFIAINTD	34	-0.1000	0
21	FRSADEVLL	179	-0.1000	0
22	VLMSIAGGS	256	-0.1000	0
23	FEPVDAVSV	344	-0.1000	0
24	LRGADMVFV	89	-0.3000	0
25	IAINSPLLE	239	-0.4000	0
26	LGALTVGVV	120	-0.5000	0
27	MGDAAVSLM	168	-0.5000	0
28	LMGIGSARG	221	-0.5000	0
29	IIFGTVIDD	288	-0.5200	0
30	IKVVGIGGG	10	-0.6000	0
31	LKAAEIAIN	234	-0.6000	0
32	VNRMIEQGL	23	-0.7000	0
33	MSGAGTALM	214	-0.7000	0
34	INEAASLVQ	271	-0.7000	0
35	VKLDVGRDS	53	-0.8000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VIPNDRLLQ	159	4.2000	41.58
2	IAINSPLLE	239	3.8000	37.62
3	VNAVNRMIE	20	3.7000	36.63
4	FEGKRRSNQ	134	3.6000	35.64
5	IIFGTVIDD	288	2.9000	28.71
6	YLAVIKVVG	6	2.3000	22.77
7	MVFVTAGEG	94	2.1000	20.79
8	VVTRPFSFE	127	2.0000	19.80
9	VGVVTRPFS	125	1.9500	19.31
10	VRVTVIAAG	302	1.7000	16.83
11	FEINEAASL	269	1.6000	15.84
12	IKVVGIGGG	10	1.5000	14.85
13	VSLMDAFRS	173	1.4000	13.86
14	LNGVQGITD	187	1.4000	13.86

15	LKAAEIAIN	234	1.4000	13.86
16	LQMGDAAVS	166	1.3000	12.87
17	INEAASLVQ	271	1.3000	12.87
18	VGRKAAEDA	73	1.2000	11.88
19	FSFEGKRRS	132	1.1000	10.89
20	IARKLGALT	116	1.0000	9.90
21	VLLNGVQGI	185	1.0000	9.90
22	VEFIAINTD	34	0.9000	8.91
23	MGIGSARGE	222	0.9000	8.91
24	LVQDAAHPD	277	0.9000	8.91
25	VIKVVGIGG	9	0.8000	7.92
26	FIAINTDAQ	36	0.8000	7.92
27	LMGIGSARG	221	0.8000	7.92
28	VLMSIAGGS	256	0.7000	6.93
29	LGLFEINEA	266	0.7000	6.93
30	FVTAGEGGG	96	0.6000	5.94
31	VASIARKLG	113	0.6000	5.94
32	LGALTVGVV	120	0.6000	5.94
33	LITTPGLIN	196	0.5000	4.95
34	LMSIAGGSD	257	0.5000	4.95
35	VDAVSVPLH	347	0.4500	4.46
36	IPNDRLLQM	160	0.4000	3.96
37	FRSADEVLL	179	0.4000	3.96

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VIPNDRLLQ	159	3.4000	40.96
2	VGVVTRPFS	125	2.0500	24.70
3	YLAVIKVVG	6	1.1000	13.25
4	VSLMDAFRS	173	1.0000	12.05
5	VLMSIAGGS	256	1.0000	12.05
6	MVFVTAGEG	94	0.9000	10.84
7	VNAVNRMIE	20	0.8000	9.64
8	VLLNGVQGI	185	0.8000	9.64
9	IAINSPLLE	239	0.8000	9.64
10	VRVTVIAAG	302	0.8000	9.64

11	LAVIKVVGI	7	0.7000	8.43
12	LGALTVGVV	120	0.7000	8.43
13	FIAINTDAQ	36	0.6000	7.23
14	LQMGDAAVS	166	0.6000	7.23
15	LGLFEINEA	266	0.6000	7.23
16	FEINEAASL	269	0.6000	7.23
17	INEAASLVQ	271	0.5000	6.02
18	VVGIGGGGV	12	0.4000	4.82
19	FSFEGKRRS	132	0.4000	4.82
20	IKVVGIGGG	10	0.3000	3.61
21	LMGIGSARG	221	0.1000	1.20
22	VASIARKLG	113	-0.1000	0
23	FADVKGIMS	207	-0.1000	0
24	LKGVEFIAI	31	-0.2000	0
25	VKGIMSGAG	210	-0.3000	0
26	VIKVVGIGG	9	-0.4000	0
27	IIFGTVIDD	288	-0.5000	0
28	FEPVDAVSV	344	-0.5000	0
29	FRSADEVLL	179	-0.6000	0
30	LKAAEIAIN	234	-0.6000	0
31	VDAVSVPLH	347	-0.6700	0
32	FVTAGEGGG	96	-0.7000	0
33	MSGAGTALM	214	-0.7000	0
34	LRGADMVFV	89	-0.8000	0
35	VQGITDLIT	190	-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	VIPNDRLLQ	159	3.4000	40.48
2	LGLFEINEA	266	3.1000	36.90
3	VSLMDAFRS	173	2.8000	33.33
4	VLLNGVQGI	185	2.6000	30.95
5	VKLDVGRDS	53	1.9000	22.62
6	LQMGDAAVS	166	1.8000	21.43
7	VVASIARKL	112	1.7000	20.24
8	FSFEGKRRS	132	1.6000	19.05

9	VGVVTRPFS	125	1.3000	15.48
10	VRVTVIAAG	302	1.3000	15.48
11	VGRKAAEDA	73	1.0000	11.90
12	VLMSIAGGS	256	1.0000	11.90
13	VGRDSTRGL	57	0.8000	9.52
14	IAINSPLLE	239	0.8000	9.52
15	LAVIKVVGI	7	0.7000	8.33
16	LRGADMVFV	89	0.7000	8.33
17	FEGKRRSNQ	134	0.7000	8.33
18	LHTNGATLS	354	0.7000	8.33
19	VDFADVKGI	205	0.4000	4.76
20	LKAAEIAIN	234	0.4000	4.76
21	INEAASLVQ	271	0.4000	4.76
22	MSGAGTALM	214	0.3000	3.57
23	LGALTVGVV	120	-0.1000	0
24	IVIPNDRLL	158	-0.1000	0
25	IGGGGVNAV	15	-0.2000	0
26	IFGTVIDDS	289	-0.2000	0
27	FEINEAASL	269	-0.3000	0
28	VASIARKLG	113	-0.4000	0
29	IARKLGALT	116	-0.4000	0
30	LMGIGSARG	221	-0.4000	0
31	VNRMIEQGL	23	-0.5000	0
32	MVFVTAGEG	94	-0.5000	0
33	VEFIAINTD	34	-0.6000	0

ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	VIPNDRLLQ	159	4.4000	53.01
2	VGVVTRPFS	125	3.0500	36.75
3	VSLMDAFRS	173	2.0000	24.10
4	VLMSIAGGS	256	2.0000	24.10
5	MVFVTAGEG	94	1.9000	22.89
6	VNAVNRMIE	20	1.8000	21.69
7	VLLNGVQGI	185	1.8000	21.69
8	IAINSPLLE	239	1.8000	21.69

9	VRVTVIAAG	302	1.8000	21.69
10	LAVIKVVGI	7	1.7000	20.48
11	LGALTVGVV	120	1.7000	20.48
12	LQMGDAAVS	166	1.6000	19.28
13	LGLFEINEA	266	1.6000	19.28
14	INEAASLVQ	271	1.5000	18.07
15	VVGIGGGGV	12	1.4000	16.87
16	IKVVGIGGG	10	1.3000	15.66
17	LMGIGSARG	221	1.1000	13.25
18	VASIARKLG	113	0.9000	10.84
19	LKGVEFIAI	31	0.8000	9.64
20	VKGIMSGAG	210	0.7000	8.43
21	VIKVVGIGG	9	0.6000	7.23
22	IIFGTVIDD	288	0.5000	6.02
23	LKAAEIAIN	234	0.4000	4.82
24	VDAVSVPLH	347	0.3300	3.98
25	MSGAGTALM	214	0.3000	3.61
26	LRGADMVFV	89	0.2000	2.41
27	VQGITDLIT	190	0.2000	2.41
28	VDFADVKGI	205	0.2000	2.41
29	LHTNGATLS	354	0.2000	2.41
30	YLAVIKVVG	6	0.1000	1.20
31	LITTPGLIN	196	-0.1000	0
32	LINVDFADV	202	-0.1000	0
33	VEFIAINTD	34	-0.2000	0
34	LNGVQGITD	187	-0.2000	0

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	VIPNDRLLQ	159	4.4000	53.01
2	VGVVTRPFS	125	3.0500	36.75
3	VSLMDAFRS	173	2.0000	24.10
4	VLMSIAGGS	256	2.0000	24.10
5	MVFVTAGEG	94	1.9000	22.89
6	VNAVNRMIE	20	1.8000	21.69
7	VLLNGVQGI	185	1.8000	21.69

8	IAINSPLLE	239	1.8000	21.69
9	VRVTVIAAG	302	1.8000	21.69
10	LAVIKVVGI	7	1.7000	20.48
11	LGALTVGVV	120	1.7000	20.48
12	LQMGDAAVS	166	1.6000	19.28
13	LGLFEINEA	266	1.6000	19.28
14	INEAASLVQ	271	1.5000	18.07
15	VVGIGGGGV	12	1.4000	16.87
16	IKVVGIGGG	10	1.3000	15.66
17	LMGIGSARG	221	1.1000	13.25
18	VASIARKLG	113	0.9000	10.84
19	LKGVEFIAI	31	0.8000	9.64
20	VKGIMSGAG	210	0.7000	8.43
21	VIKVVGIGG	9	0.6000	7.23
22	IIFGTVIDD	288	0.5000	6.02
23	LKAAEIAIN	234	0.4000	4.82
24	VDAVSVPLH	347	0.3300	3.98
25	MSGAGTALM	214	0.3000	3.61
26	LRGADMVFV	89	0.2000	2.41
27	VQGITDLIT	190	0.2000	2.41
28	VDFADVKGI	205	0.2000	2.41
29	LHTNGATLS	354	0.2000	2.41
30	YLAVIKVVG	6	0.1000	1.20
31	LITTPGLIN	196	-0.1000	0
32	LINVDFADV	202	-0.1000	0
33	VEFIAINTD	34	-0.2000	0
34	LNGVQGITD	187	-0.2000	0

ALLELE: DRB1_1107	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	VLMSIAGGS	256	3.9000	42.86
2	LQMGDAAVS	166	3.8000	41.76
3	VKLDVGRDS	53	3.5000	38.46
4	VGVVTRPFS	125	3.4000	37.36
5	VIPNDRLLQ	159	3.3000	36.26
6	VLLNGVQGI	185	3.0000	32.97

7	INVDFADVK	203	2.7000	29.67
8	VGRDSTRGL	57	2.4000	26.37
9	IPNDRLLQM	160	2.3000	25.27
10	IIFGTVIDD	288	2.3000	25.27
11	LLMSDADVK	46	2.2000	24.18
12	LAVIKVVGI	7	2.1000	23.08
13	MVFVTAGEG	94	2.0000	21.98
14	VSLMDAFRS	173	1.9000	20.88
15	LVQDAAHPD	277	1.9000	20.88
16	INTDAQALL	39	1.8000	19.78
17	IGGGGVNAV	15	1.6100	17.69
18	LHTNGATLS	354	1.6000	17.58
19	VVGIGGGGV	12	1.5000	16.48
20	IKVVGIGGG	10	1.4000	15.38
21	VRVTVIAAG	302	1.4000	15.38
22	FIAINTDAQ	36	1.3000	14.29
23	VNAVNRMIE	20	1.2000	13.19
24	LGLFEINEA	266	1.1100	12.20
25	LGALTVGVV	120	1.1000	12.09
26	LRGADMVFV	89	1.0000	10.99
27	VVASIARKL	112	0.9000	9.89
28	LTVGVVTRP	123	0.8000	8.79
29	VKGIMSGAG	210	0.8000	8.79
30	IFGTVIDDS	289	0.8000	8.79
31	LMGIGSARG	221	0.7000	7.69
32	IAINSPLLE	239	0.7000	7.69
33	INSPLLEAS	241	0.7000	7.69
34	VIDDSLGDE	293	0.7000	7.69
35	VDAVSVPLH	347	0.6800	7.47
36	LLNGVQGIT	186	0.6000	6.59
37	YLAVIKVVG	6	0.5000	5.49

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	FSFEGKRRS	132	2.6000	30.95
2	VIPNDRLLQ	159	2.4000	28.57

3	LGLFEINEA	266	2.1000	25.00
4	VSLMDAFRS	173	1.8000	21.43
5	FEGKRRSNQ	134	1.7000	20.24
6	VLLNGVQGI	185	1.6000	19.05
7	VKLDVGRDS	53	0.9000	10.71
8	LQMGDAAVS	166	0.8000	9.52
9	VVASIARKL	112	0.7000	8.33
10	FEINEAASL	269	0.7000	8.33
11	YLAVIKVVG	6	0.3000	3.57
12	FIAINTDAQ	36	0.3000	3.57
13	VGVVTRPFS	125	0.3000	3.57
14	VRVTVIAAG	302	0.3000	3.57
15	FRSADEVLL	179	-0.1000	0
16	VGRDSTRGL	57	-0.2000	0
17	IAINSPLLE	239	-0.2000	0
18	LAVIKVVGI	7	-0.3000	0
19	LRGADMVFV	89	-0.3000	0
20	LHTNGATLS	354	-0.3000	0
21	VDFADVKGI	205	-0.6000	0
22	LKAAEIAIN	234	-0.6000	0
23	INEAASLVQ	271	-0.6000	0
24	MSGAGTALM	214	-0.7000	0
25	MIEQGLKGV	26	-1.0000	0
26	LLMSDADVK	46	-1.0000	0
27	MGIGSARGE	222	-1.0000	0
28	LGALTVGVV	120	-1.1000	0
29	IVIPNDRLL	158	-1.1000	0
30	IGGGGVNAV	15	-1.2000	0
31	IFGTVIDDS	289	-1.2000	0
32	FEPVDAVSV	344	-1.3000	0
33	VASIARKLG	113	-1.4000	0
34	IARKLGALT	116	-1.4000	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	FSFEGKRRS	132	3.0000	34.09

2	VLLNGVQGI	185	2.5000	28.41
3	VSLMDAFRS	173	2.2000	25.00
4	LGLFEINEA	266	2.1000	23.86
5	YLAVIKVVG	6	1.7000	19.32
6	VIPNDRLLQ	159	1.7000	19.32
7	VRVTVIAAG	302	1.7000	19.32
8	VVASIARKL	112	1.6600	18.86
9	FEINEAASL	269	1.6600	18.86
10	VKLDVGRDS	53	1.3000	14.77
11	LQMGDAAVS	166	1.2000	13.64
12	IAINSPLLE	239	1.2000	13.64
13	FEGKRRSNQ	134	1.0000	11.36
14	FRSADEVLL	179	0.8600	9.77
15	MSGAGTALM	214	0.8000	9.09
16	VGRDSTRGL	57	0.7600	8.64
17	LRGADMVFV	89	0.7000	7.95
18	VGVVTRPFS	125	0.7000	7.95
19	LAVIKVVGI	7	0.6000	6.82
20	MGIGSARGE	222	0.4000	4.55
21	VLMSIAGGS	256	0.4000	4.55
22	VDFADVKGI	205	0.3000	3.41
23	LKAAEIAIN	234	0.2000	2.27
24	LHTNGATLS	354	0.1000	1.14
25	MVFVTAGEG	94	-0.1000	0
26	LGALTVGVV	120	-0.1000	0
27	IVIPNDRLL	158	-0.1400	0
28	IGGGGVNAV	15	-0.2000	0
29	FEPVDAVSV	344	-0.3000	0
30	VNAVNRMIE	20	-0.4000	0
31	FIAINTDAQ	36	-0.4000	0
32	FVTAGEGGG	96	-0.4000	0

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	VIPNDRLLQ	159	3.4000	40.48
2	LGLFEINEA	266	3.1000	36.90

3	VSLMDAFRS	173	2.8000	33.33
4	VLLNGVQGI	185	2.6000	30.95
5	VKLDVGRDS	53	1.9000	22.62
6	LQMGDAAVS	166	1.8000	21.43
7	VVASIARKL	112	1.7000	20.24
8	FSFEGKRRS	132	1.6000	19.05
9	VGVVTRPFS	125	1.3000	15.48
10	VRVTVIAAG	302	1.3000	15.48
11	VGRKAAEDA	73	1.0000	11.90
12	VLMSIAGGS	256	1.0000	11.90
13	VGRDSTRGL	57	0.8000	9.52
14	IAINSPLLE	239	0.8000	9.52
15	LAVIKVVGI	7	0.7000	8.33
16	LRGADMVFV	89	0.7000	8.33
17	FEGKRRSNQ	134	0.7000	8.33
18	LHTNGATLS	354	0.7000	8.33
19	VDFADVKGI	205	0.4000	4.76
20	LKAAEIAIN	234	0.4000	4.76
21	INEAASLVQ	271	0.4000	4.76
22	MSGAGTALM	214	0.3000	3.57
23	LGALTVGVV	120	-0.1000	0
24	IVIPNDRLL	158	-0.1000	0
25	IGGGGVNAV	15	-0.2000	0
26	IFGTVIDDS	289	-0.2000	0
27	FEINEAASL	269	-0.3000	0
28	VASIARKLG	113	-0.4000	0
29	IARKLGALT	116	-0.4000	0
30	LMGIGSARG	221	-0.4000	0
31	VNRMIEQGL	23	-0.5000	0
32	MVFVTAGEG	94	-0.5000	0
33	VEFIAINTD	34	-0.6000	0

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	VIPNDRLLQ	159	2.7000	31.03
2	YLAVIKVVG	6	2.5000	28.74

3	VGVVTRPFS	125	2.4500	28.16
4	MVFVTAGEG	94	2.3000	26.44
5	VNAVNRMIE	20	2.2000	25.29
6	IAINSPLLE	239	2.2000	25.29
7	VRVTVIAAG	302	2.2000	25.29
8	IKVVGIGGG	10	1.7000	19.54
9	LGALTVGVV	120	1.7000	19.54
10	VLLNGVQGI	185	1.7000	19.54
11	LAVIKVVGI	7	1.6000	18.39
12	FEINEAASL	269	1.5600	17.93
13	LMGIGSARG	221	1.5000	17.24
14	VVGIGGGGV	12	1.4000	16.09
15	VSLMDAFRS	173	1.4000	16.09
16	VLMSIAGGS	256	1.4000	16.09
17	VASIARKLG	113	1.3000	14.94
18	VKGIMSGAG	210	1.1000	12.64
19	VIKVVGIGG	9	1.0000	11.49
20	LQMGDAAVS	166	1.0000	11.49
21	FSFEGKRRS	132	0.8000	9.20
22	MSGAGTALM	214	0.8000	9.20
23	LKGVEFIAI	31	0.7000	8.05
24	FVTAGEGGG	96	0.7000	8.05
25	LGLFEINEA	266	0.6000	6.90
26	IIFGTVIDD	288	0.6000	6.90
27	FEPVDAVSV	344	0.5000	5.75
28	FRSADEVLL	179	0.3600	4.14
29	FADVKGIMS	207	0.3000	3.45
30	LRGADMVFV	89	0.2000	2.30
31	LKAAEIAIN	234	0.2000	2.30
32	IPNDRLLQM	160	0.1000	1.15
33	VDFADVKGI	205	0.1000	1.15
34	VVASIARKL	112	-0.0400	0
35	VEFIAINTD	34	-0.1000	0
36	FIAINTDAQ	36	-0.1000	0

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	VLLNGVQGI	185	3.5000	39.77
2	VSLMDAFRS	173	3.2000	36.36
3	LGLFEINEA	266	3.1000	35.23
4	VIPNDRLLQ	159	2.7000	30.68
5	VRVTVIAAG	302	2.7000	30.68
6	VVASIARKL	112	2.6600	30.23
7	VKLDVGRDS	53	2.3000	26.14
8	LQMGDAAVS	166	2.2000	25.00
9	IAINSPLLE	239	2.2000	25.00
10	FSFEGKRRS	132	2.0000	22.73
11	MSGAGTALM	214	1.8000	20.45
12	VGRDSTRGL	57	1.7600	20.00
13	LRGADMVFV	89	1.7000	19.32
14	VGVVTRPFS	125	1.7000	19.32
15	LAVIKVVGI	7	1.6000	18.18
16	MGIGSARGE	222	1.4000	15.91
17	VLMSIAGGS	256	1.4000	15.91
18	VDFADVKGI	205	1.3000	14.77
19	LKAAEIAIN	234	1.2000	13.64
20	LHTNGATLS	354	1.1000	12.50
21	MIEQGLKGV	26	1.0000	11.36
22	VGRKAAEDA	73	1.0000	11.36
23	VASIARKLG	113	1.0000	11.36
24	LMGIGSARG	221	1.0000	11.36
25	MVFVTAGEG	94	0.9000	10.23
26	LGALTVGVV	120	0.9000	10.23
27	IVIPNDRLL	158	0.8600	9.77
28	IGGGGVNAV	15	0.8000	9.09
29	YLAVIKVVG	6	0.7000	7.95
30	FEINEAASL	269	0.6600	7.50
31	VNAVNRMIE	20	0.6000	6.82
32	MGDAAVSLM	168	0.6000	6.82
33	MEGAQGVLM	250	0.6000	6.82
34	VEFIAINTD	34	0.5000	5.68
35	IIFGTVIDD	288	0.5000	5.68
36	VNRMIEQGL	23	0.4600	5.23
37	LVQDAAHPD	277	0.4000	4.55

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	FSFEGKRRS	132	3.0000	34.09
2	VLLNGVQGI	185	2.5000	28.41
3	VSLMDAFRS	173	2.2000	25.00
4	LGLFEINEA	266	2.1000	23.86
5	YLAVIKVVG	6	1.7000	19.32
6	VIPNDRLLQ	159	1.7000	19.32
7	VRVTVIAAG	302	1.7000	19.32
8	VVASIARKL	112	1.6600	18.86
9	FEINEAASL	269	1.6600	18.86
10	VKLDVGRDS	53	1.3000	14.77
11	LQMGDAAVS	166	1.2000	13.64
12	IAINSPLLE	239	1.2000	13.64
13	FEGKRRSNQ	134	1.0000	11.36
14	FRSADEVLL	179	0.8600	9.77
15	MSGAGTALM	214	0.8000	9.09
16	VGRDSTRGL	57	0.7600	8.64
17	LRGADMVFV	89	0.7000	7.95
18	VGVVTRPFS	125	0.7000	7.95
19	LAVIKVVGI	7	0.6000	6.82
20	MGIGSARGE	222	0.4000	4.55
21	VLMSIAGGS	256	0.4000	4.55
22	VDFADVKGI	205	0.3000	3.41
23	LKAAEIAIN	234	0.2000	2.27
24	LHTNGATLS	354	0.1000	1.14
25	MVFVTAGEG	94	-0.1000	0
26	LGALTVGVV	120	-0.1000	0
27	IVIPNDRLL	158	-0.1400	0
28	IGGGGVNAV	15	-0.2000	0
29	FEPVDAVSV	344	-0.3000	0
30	VNAVNRMIE	20	-0.4000	0
31	FIAINTDAQ	36	-0.4000	0
32	FVTAGEGGG	96	-0.4000	0

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	VIPNDRLLQ	159	4.2000	46.67
2	IAINSPLLE	239	3.8000	42.22
3	LGLFEINEA	266	3.1000	34.44
4	MGIGSARGE	222	3.0000	33.33
5	VSLMDAFRS	173	2.8000	31.11
6	VLLNGVQGI	185	2.8000	31.11
7	VVASIARKL	112	2.7000	30.00
8	VRVTVIAAG	302	2.6000	28.89
9	LKAAEIAIN	234	2.4000	26.67
10	VNAVNRMIE	20	2.2000	24.44
11	VEFIAINTD	34	2.1000	23.33
12	IIFGTVIDD	288	2.1000	23.33
13	LVQDAAHPD	277	2.0000	22.22
14	VKLDVGRDS	53	1.9000	21.11
15	VGRDSTRGL	57	1.8000	20.00
16	LQMGDAAVS	166	1.8000	20.00
17	FSFEGKRRS	132	1.6000	17.78
18	FEGKRRSNQ	134	1.5000	16.67
19	MSGAGTALM	214	1.4000	15.56
20	VGVVTRPFS	125	1.3000	14.44
21	VVTRPFSFE	127	1.3000	14.44
22	INEAASLVQ	271	1.2000	13.33
23	VGRKAAEDA	73	1.0000	11.11
24	LRGADMVFV	89	1.0000	11.11
25	VLMSIAGGS	256	1.0000	11.11
26	LAVIKVVGI	7	0.9000	10.00
27	VASIARKLG	113	0.9000	10.00
28	IVIPNDRLL	158	0.9000	10.00
29	LMDAFRSAD	175	0.9000	10.00
30	LMGIGSARG	221	0.9000	10.00
31	MVFVTAGEG	94	0.8000	8.89
32	MDAFRSADE	176	0.7000	7.78
33	FEINEAASL	269	0.7000	7.78
34	LHTNGATLS	354	0.7000	7.78

35	YLAVIKVVG	6	0.6000	6.67
36	MSDADVKLD	48	0.6000	6.67
37	VDFADVKGI	205	0.6000	6.67

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VIPNDRLLQ	159	2.7000	31.03
2	YLAVIKVVG	6	2.5000	28.74
3	VGVVTRPFS	125	2.4500	28.16
4	MVFVTAGEG	94	2.3000	26.44
5	VNAVNRMIE	20	2.2000	25.29
6	IAINSPLLE	239	2.2000	25.29
7	VRVTVIAAG	302	2.2000	25.29
8	IKVVGIGGG	10	1.7000	19.54
9	LGALTVGVV	120	1.7000	19.54
10	VLLNGVQGI	185	1.7000	19.54
11	LAVIKVVGI	7	1.6000	18.39
12	FEINEAASL	269	1.5600	17.93
13	LMGIGSARG	221	1.5000	17.24
14	VVGIGGGGV	12	1.4000	16.09
15	VSLMDAFRS	173	1.4000	16.09
16	VLMSIAGGS	256	1.4000	16.09
17	VASIARKLG	113	1.3000	14.94
18	VKGIMSGAG	210	1.1000	12.64
19	VIKVVGIGG	9	1.0000	11.49
20	LQMGDAAVS	166	1.0000	11.49
21	FSFEGKRRS	132	0.8000	9.20
22	MSGAGTALM	214	0.8000	9.20
23	LKGVEFIAI	31	0.7000	8.05
24	FVTAGEGGG	96	0.7000	8.05
25	LGLFEINEA	266	0.6000	6.90
26	IIFGTVIDD	288	0.6000	6.90
27	FEPVDAVSV	344	0.5000	5.75
28	FRSADEVLL	179	0.3600	4.14
29	FADVKGIMS	207	0.3000	3.45
30	LRGADMVFV	89	0.2000	2.30

31	LKAAEIAIN	234	0.2000	2.30
32	IPNDRLLQM	160	0.1000	1.15
33	VDFADVKGI	205	0.1000	1.15
34	VVASIARKL	112	-0.0400	0
35	VEFIAINTD	34	-0.1000	0
36	FIAINTDAQ	36	-0.1000	0

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	VIPNDRLLQ	159	1.6000	23.53
2	FIAINTDAQ	36	0.9000	13.24
3	VGVVTRPFS	125	0.9000	13.24
4	VLMSIAGGS	256	0.9000	13.24
5	MVFVTAGEG	94	0.8000	11.76
6	VRVTVIAAG	302	0.8000	11.76
7	VLLNGVQGI	185	0.7000	10.29
8	YLAVIKVVG	6	0.6000	8.82
9	LGALTVGVV	120	0.6000	8.82
10	LQMGDAAVS	166	0.6000	8.82
11	FEINEAASL	269	0.6000	8.82
12	VSLMDAFRS	173	0.5000	7.35
13	VVGIGGGGV	12	0.3000	4.41
14	LGLFEINEA	266	0.3000	4.41
15	LAVIKVVGI	7	0.2000	2.94
16	IKVVGIGGG	10	0.2000	2.94
17	FSFEGKRRS	132	0.2000	2.94
18	LMGIGSARG	221	0.1000	1.47
19	VKGIMSGAG	210	-0.4000	0
20	LKAAEIAIN	234	-0.6000	0
21	VASIARKLG	113	-0.7000	0
22	MSGAGTALM	214	-0.7000	0
23	VNAVNRMIE	20	-0.8000	0
24	FVTAGEGGG	96	-0.8000	0
25	IAINSPLLE	239	-1.0000	0
26	FEPVDAVSV	344	-1.0000	0
27	FRSADEVLL	179	-1.1000	0

28	LINVDFADV	202	-1.1000	0
29	VKLDVGRDS	53	-1.2000	0
30	VVASIARKL	112	-1.2000	0
31	LFEINEAAS	268	-1.2000	0
32	LRGADMVFV	89	-1.3000	0
33	INEAASLVQ	271	-1.3000	0
34	VDFADVKGI	205	-1.4000	0
35	VEFIAINTD	34	-1.5000	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	VIPNDRLLQ	159	4.4000	53.01
2	VGVVTRPFS	125	3.0500	36.75
3	VSLMDAFRS	173	2.0000	24.10
4	VLMSIAGGS	256	2.0000	24.10
5	MVFVTAGEG	94	1.9000	22.89
6	VNAVNRMIE	20	1.8000	21.69
7	VLLNGVQGI	185	1.8000	21.69
8	IAINSPLLE	239	1.8000	21.69
9	VRVTVIAAG	302	1.8000	21.69
10	LAVIKVVGI	7	1.7000	20.48
11	LGALTVGVV	120	1.7000	20.48
12	LQMGDAAVS	166	1.6000	19.28
13	LGLFEINEA	266	1.6000	19.28
14	INEAASLVQ	271	1.5000	18.07
15	VVGIGGGGV	12	1.4000	16.87
16	IKVVGIGGG	10	1.3000	15.66
17	LMGIGSARG	221	1.1000	13.25
18	VASIARKLG	113	0.9000	10.84
19	LKGVEFIAI	31	0.8000	9.64
20	VKGIMSGAG	210	0.7000	8.43
21	VIKVVGIGG	9	0.6000	7.23
22	IIFGTVIDD	288	0.5000	6.02
23	LKAAEIAIN	234	0.4000	4.82
24	VDAVSVPLH	347	0.3300	3.98
25	MSGAGTALM	214	0.3000	3.61

26	LRGADMVFV	89	0.2000	2.41
27	VQGITDLIT	190	0.2000	2.41
28	VDFADVKGI	205	0.2000	2.41
29	LHTNGATLS	354	0.2000	2.41
30	YLAVIKVVG	6	0.1000	1.20
31	LITTPGLIN	196	-0.1000	0
32	LINVDFADV	202	-0.1000	0
33	VEFIAINTD	34	-0.2000	0
34	LNGVQGITD	187	-0.2000	0

ALLELE: DRB1_1321	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.9

Rank	Sequence	At Position	Score	% of Highest Score
1	VIPNDRLLQ	159	4.2000	47.19
2	VNAVNRMIE	20	3.8000	42.70
3	IAINSPLLE	239	3.8000	42.70
4	YLAVIKVVG	6	2.4000	26.97
5	MVFVTAGEG	94	2.2000	24.72
6	IIFGTVIDD	288	2.2000	24.72
7	VRVTVIAAG	302	2.1000	23.60
8	VGVVTRPFS	125	2.0500	23.03
9	IKVVGIGGG	10	1.6000	17.98
10	FEINEAASL	269	1.6000	17.98
11	VEFIAINTD	34	1.5000	16.85
12	LNGVQGITD	187	1.5000	16.85
13	FIAINTDAQ	36	1.4000	15.73
14	LMGIGSARG	221	1.4000	15.73
15	LKAAEIAIN	234	1.4000	15.73
16	INEAASLVQ	271	1.3000	14.61
17	VASIARKLG	113	1.2000	13.48
18	LMSIAGGSD	257	1.1000	12.36
19	LGALTVGVV	120	1.0000	11.24
20	VSLMDAFRS	173	1.0000	11.24
21	VLLNGVQGI	185	1.0000	11.24
22	VKGIMSGAG	210	1.0000	11.24
23	VLMSIAGGS	256	1.0000	11.24
24	VTVIAAGFD	304	1.0000	11.24

25	LAVIKVVGI	7	0.9000	10.11
26	VIKVVGIGG	9	0.9000	10.11
27	LITTPGLIN	196	0.9000	10.11
28	FEGKRRSNQ	134	0.8000	8.99
29	VVGIGGGGV	12	0.7000	7.87
30	IEELLRGAD	85	0.6000	6.74
31	FVTAGEGGG	96	0.6000	6.74
32	LQMGDAAVS	166	0.6000	6.74
33	LGLFEINEA	266	0.6000	6.74
34	VDAVSVPLH	347	0.5500	6.18
35	FSFEGKRRS	132	0.4000	4.49
36	FRSADEVLL	179	0.4000	4.49
37	MSGAGTALM	214	0.4000	4.49

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	VIPNDRLLQ	159	3.4000	40.48
2	LGLFEINEA	266	3.1000	36.90
3	VSLMDAFRS	173	2.8000	33.33
4	VLLNGVQGI	185	2.6000	30.95
5	VKLDVGRDS	53	1.9000	22.62
6	LQMGDAAVS	166	1.8000	21.43
7	VVASIARKL	112	1.7000	20.24
8	FSFEGKRRS	132	1.6000	19.05
9	VGVVTRPFS	125	1.3000	15.48
10	VRVTVIAAG	302	1.3000	15.48
11	VGRKAAEDA	73	1.0000	11.90
12	VLMSIAGGS	256	1.0000	11.90
13	VGRDSTRGL	57	0.8000	9.52
14	IAINSPLLE	239	0.8000	9.52
15	LAVIKVVGI	7	0.7000	8.33
16	LRGADMVFV	89	0.7000	8.33
17	FEGKRRSNQ	134	0.7000	8.33
18	LHTNGATLS	354	0.7000	8.33
19	VDFADVKGI	205	0.4000	4.76
20	LKAAEIAIN	234	0.4000	4.76

21	INEAASLVQ	271	0.4000	4.76
22	MSGAGTALM	214	0.3000	3.57
23	LGALTVGVV	120	-0.1000	0
24	IVIPNDRLL	158	-0.1000	0
25	IGGGGVNAV	15	-0.2000	0
26	IFGTVIDDS	289	-0.2000	0
27	FEINEAASL	269	-0.3000	0
28	VASIARKLG	113	-0.4000	0
29	IARKLGALT	116	-0.4000	0
30	LMGIGSARG	221	-0.4000	0
31	VNRMIEQGL	23	-0.5000	0
32	MVFVTAGEG	94	-0.5000	0
33	VEFIAINTD	34	-0.6000	0

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4

Rank	Sequence	At Position	Score	% of Highest Score
1	FSFEGKRRS	132	2.6000	30.95
2	VIPNDRLLQ	159	2.4000	28.57
3	LGLFEINEA	266	2.1000	25.00
4	VSLMDAFRS	173	1.8000	21.43
5	FEGKRRSNQ	134	1.7000	20.24
6	VLLNGVQGI	185	1.6000	19.05
7	VKLDVGRDS	53	0.9000	10.71
8	LQMGDAAVS	166	0.8000	9.52
9	VVASIARKL	112	0.7000	8.33
10	FEINEAASL	269	0.7000	8.33
11	YLAVIKVVG	6	0.3000	3.57
12	FIAINTDAQ	36	0.3000	3.57
13	VGVVTRPFS	125	0.3000	3.57
14	VRVTVIAAG	302	0.3000	3.57
15	FRSADEVLL	179	-0.1000	0
16	VGRDSTRGL	57	-0.2000	0
17	IAINSPLLE	239	-0.2000	0
18	LAVIKVVGI	7	-0.3000	0
19	LRGADMVFV	89	-0.3000	0
20	LHTNGATLS	354	-0.3000	0

21	VDFADVKGI	205	-0.6000	0
22	LKAAEIAIN	234	-0.6000	0
23	INEAASLVQ	271	-0.6000	0
24	MSGAGTALM	214	-0.7000	0
25	MIEQGLKGV	26	-1.0000	0
26	LLMSDADVK	46	-1.0000	0
27	MGIGSARGE	222	-1.0000	0
28	LGALTVGVV	120	-1.1000	0
29	IVIPNDRLL	158	-1.1000	0
30	IGGGGVNAV	15	-1.2000	0
31	IFGTVIDDS	289	-1.2000	0
32	FEPVDAVSV	344	-1.3000	0
33	VASIARKLG	113	-1.4000	0
34	IARKLGALT	116	-1.4000	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	VLLNGVQGI	185	3.5000	39.77
2	VSLMDAFRS	173	3.2000	36.36
3	LGLFEINEA	266	3.1000	35.23
4	VIPNDRLLQ	159	2.7000	30.68
5	VRVTVIAAG	302	2.7000	30.68
6	VVASIARKL	112	2.6600	30.23
7	VKLDVGRDS	53	2.3000	26.14
8	LQMGDAAVS	166	2.2000	25.00
9	IAINSPLLE	239	2.2000	25.00
10	FSFEGKRRS	132	2.0000	22.73
11	MSGAGTALM	214	1.8000	20.45
12	VGRDSTRGL	57	1.7600	20.00
13	LRGADMVFV	89	1.7000	19.32
14	VGVVTRPFS	125	1.7000	19.32
15	LAVIKVVGI	7	1.6000	18.18
16	MGIGSARGE	222	1.4000	15.91
17	VLMSIAGGS	256	1.4000	15.91
18	VDFADVKGI	205	1.3000	14.77
19	LKAAEIAIN	234	1.2000	13.64

20	LHTNGATLS	354	1.1000	12.50
21	MIEQGLKGV	26	1.0000	11.36
22	VGRKAAEDA	73	1.0000	11.36
23	VASIARKLG	113	1.0000	11.36
24	LMGIGSARG	221	1.0000	11.36
25	MVFVTAGEG	94	0.9000	10.23
26	LGALTVGVV	120	0.9000	10.23
27	IVIPNDRLL	158	0.8600	9.77
28	IGGGGVNAV	15	0.8000	9.09
29	YLAVIKVVG	6	0.7000	7.95
30	FEINEAASL	269	0.6600	7.50
31	VNAVNRMIE	20	0.6000	6.82
32	MGDAAVSLM	168	0.6000	6.82
33	MEGAQGVLM	250	0.6000	6.82
34	VEFIAINTD	34	0.5000	5.68
35	IIFGTVIDD	288	0.5000	5.68
36	VNRMIEQGL	23	0.4600	5.23
37	LVQDAAHPD	277	0.4000	4.55

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	VLLNGVQGI	185	3.5000	39.77
2	VSLMDAFRS	173	3.2000	36.36
3	LGLFEINEA	266	3.1000	35.23
4	VIPNDRLLQ	159	2.7000	30.68
5	VRVTVIAAG	302	2.7000	30.68
6	VVASIARKL	112	2.6600	30.23
7	VKLDVGRDS	53	2.3000	26.14
8	LQMGDAAVS	166	2.2000	25.00
9	IAINSPLLE	239	2.2000	25.00
10	FSFEGKRRS	132	2.0000	22.73
11	MSGAGTALM	214	1.8000	20.45
12	VGRDSTRGL	57	1.7600	20.00
13	LRGADMVFV	89	1.7000	19.32
14	VGVVTRPFS	125	1.7000	19.32
15	LAVIKVVGI	7	1.6000	18.18

16	MGIGSARGE	222	1.4000	15.91
17	VLMSIAGGS	256	1.4000	15.91
18	VDFADVKGI	205	1.3000	14.77
19	LKAAEIAIN	234	1.2000	13.64
20	LHTNGATLS	354	1.1000	12.50
21	MIEQGLKGV	26	1.0000	11.36
22	VGRKAAEDA	73	1.0000	11.36
23	VASIARKLG	113	1.0000	11.36
24	LMGIGSARG	221	1.0000	11.36
25	MVFVTAGEG	94	0.9000	10.23
26	LGALTVGVV	120	0.9000	10.23
27	IVIPNDRLL	158	0.8600	9.77
28	IGGGGVNAV	15	0.8000	9.09
29	YLAVIKVVG	6	0.7000	7.95
30	FEINEAASL	269	0.6600	7.50
31	VNAVNRMIE	20	0.6000	6.82
32	MGDAAVSLM	168	0.6000	6.82
33	MEGAQGVLM	250	0.6000	6.82
34	VEFIAINTD	34	0.5000	5.68
35	IIFGTVIDD	288	0.5000	5.68
36	VNRMIEQGL	23	0.4600	5.23
37	LVQDAAHPD	277	0.4000	4.55

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	LGLFEINEA	266	4.6500	47.45
2	VVGIGGGGV	12	3.7000	37.76
3	LKGVEFIAI	31	3.4000	34.69
4	VQGITDLIT	190	3.3000	33.67
5	LRGADMVFV	89	3.1000	31.63
6	IVIPNDRLL	158	2.9000	29.59
7	VSLMDAFRS	173	2.8000	28.57
8	LIVIPNDRL	157	2.7000	27.55
9	LLRGADMVF	88	2.6000	26.53
10	VIKVVGIGG	9	2.5000	25.51
11	VIPNDRLLQ	159	2.5000	25.51

12	IMSGAGTAL	213	2.5000	25.51
13	MSIAGGSDL	258	2.5000	25.51
14	MVFVTAGEG	94	2.3000	23.47
15	LQMGDAAVS	166	2.3000	23.47
16	VGVVTRPFS	125	2.2000	22.45
17	IAGGSDLGL	260	2.2000	22.45
18	VPLHTNGAT	352	2.1000	21.43
19	LITTPGLIN	196	2.0000	20.41
20	LLQMGDAAV	165	1.9000	19.39
21	VLLNGVQGI	185	1.9000	19.39
22	LAVIKVVGI	7	1.8000	18.37
23	VNAVNRMIE	20	1.8000	18.37
24	VVASIARKL	112	1.8000	18.37
25	LINVDFADV	202	1.8000	18.37
26	VLMSIAGGS	256	1.8000	18.37
27	IPNDRLLQM	160	1.7800	18.16
28	VNRMIEQGL	23	1.7000	17.35
29	ITTPGLINV	197	1.7000	17.35
30	VKGIMSGAG	210	1.7000	17.35
31	LMGIGSARG	221	1.7000	17.35
32	VRVTVIAAG	302	1.6500	16.84
33	VTRPFSFEG	128	1.6000	16.33
34	MTPPHNYLA	0	1.4000	14.29
35	IGGGGVNAV	15	1.4000	14.29
36	VKLDVGRDS	53	1.4000	14.29
37	VGIGGGGVN	13	1.3000	13.27

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	LGLFEINEA	266	3.6500	37.24
2	VVGIGGGGV	12	2.7000	27.55
3	LKGVEFIAI	31	2.4000	24.49
4	VQGITDLIT	190	2.3000	23.47
5	FRSADEVLL	179	2.2000	22.45
6	LRGADMVFV	89	2.1000	21.43
7	IVIPNDRLL	158	1.9000	19.39

8	FEINEAASL	269	1.9000	19.39
9	VSLMDAFRS	173	1.8000	18.37
10	LIVIPNDRL	157	1.7000	17.35
11	LLRGADMVF	88	1.6000	16.33
12	VIKVVGIGG	9	1.5000	15.31
13	VIPNDRLLQ	159	1.5000	15.31
14	IMSGAGTAL	213	1.5000	15.31
15	MSIAGGSDL	258	1.5000	15.31
16	MVFVTAGEG	94	1.3000	13.27
17	LQMGDAAVS	166	1.3000	13.27
18	VGVVTRPFS	125	1.2000	12.24
19	IAGGSDLGL	260	1.2000	12.24
20	FEPVDAVSV	344	1.2000	12.24
21	VPLHTNGAT	352	1.1000	11.22
22	LITTPGLIN	196	1.0000	10.20
23	LLQMGDAAV	165	0.9000	9.18
24	VLLNGVQGI	185	0.9000	9.18
25	LAVIKVVGI	7	0.8000	8.16
26	VNAVNRMIE	20	0.8000	8.16
27	VVASIARKL	112	0.8000	8.16
28	LINVDFADV	202	0.8000	8.16
29	VLMSIAGGS	256	0.8000	8.16
30	IPNDRLLQM	160	0.7800	7.96
31	VNRMIEQGL	23	0.7000	7.14
32	ITTPGLINV	197	0.7000	7.14
33	VKGIMSGAG	210	0.7000	7.14
34	LMGIGSARG	221	0.7000	7.14
35	VRVTVIAAG	302	0.6500	6.63
36	VTRPFSFEG	128	0.6000	6.12
37	FADVKGIMS	207	0.6000	6.12

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	LGLFEINEA	266	4.6500	47.45
2	VVGIGGGGV	12	3.7000	37.76
3	LKGVEFIAI	31	3.4000	34.69

4	VQGITDLIT	190	3.3000	33.67
5	LRGADMVFV	89	3.1000	31.63
6	IVIPNDRLL	158	2.9000	29.59
7	VSLMDAFRS	173	2.8000	28.57
8	LIVIPNDRL	157	2.7000	27.55
9	LLRGADMVF	88	2.6000	26.53
10	VIKVVGIGG	9	2.5000	25.51
11	VIPNDRLLQ	159	2.5000	25.51
12	IMSGAGTAL	213	2.5000	25.51
13	MSIAGGSDL	258	2.5000	25.51
14	MVFVTAGEG	94	2.3000	23.47
15	LQMGDAAVS	166	2.3000	23.47
16	VGVVTRPFS	125	2.2000	22.45
17	IAGGSDLGL	260	2.2000	22.45
18	VPLHTNGAT	352	2.1000	21.43
19	LITTPGLIN	196	2.0000	20.41
20	LLQMGDAAV	165	1.9000	19.39
21	VLLNGVQGI	185	1.9000	19.39
22	LAVIKVVGI	7	1.8000	18.37
23	VNAVNRMIE	20	1.8000	18.37
24	VVASIARKL	112	1.8000	18.37
25	LINVDFADV	202	1.8000	18.37
26	VLMSIAGGS	256	1.8000	18.37
27	IPNDRLLQM	160	1.7800	18.16
28	VNRMIEQGL	23	1.7000	17.35
29	ITTPGLINV	197	1.7000	17.35
30	VKGIMSGAG	210	1.7000	17.35
31	LMGIGSARG	221	1.7000	17.35
32	VRVTVIAAG	302	1.6500	16.84
33	VTRPFSFEG	128	1.6000	16.33
34	MTPPHNYLA	0	1.4000	14.29
35	IGGGGVNAV	15	1.4000	14.29
36	VKLDVGRDS	53	1.4000	14.29
37	VGIGGGGVN	13	1.3000	13.27

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	MVFVTAGEG	94	4.0000	40.82
2	VSLMDAFRS	173	3.6000	36.73
3	VVASIARKL	112	3.2000	32.65
4	VVGIGGGGV	12	2.7000	27.55
5	VIKVVGIGG	9	2.5000	25.51
6	VNRMIEQGL	23	2.2000	22.45
7	VLMSIAGGS	256	2.2000	22.45
8	FDVSGPGRK	311	2.2000	22.45
9	LKGVEFIAI	31	2.1000	21.43
10	LLMSDADVK	46	2.1000	21.43
11	VKGIMSGAG	210	2.1000	21.43
12	IVIPNDRLL	158	1.7000	17.35
13	LMGIGSARG	221	1.5000	15.31
14	FRSADEVLL	179	1.4000	14.29
15	FADVKGIMS	207	1.4000	14.29
16	IKVVGIGGG	10	1.3000	13.27
17	FEINEAASL	269	1.2000	12.24
18	IESAKAGKL	331	1.2000	12.24
19	FVTAGEGGG	96	1.1000	11.22
20	IGSARGEGR	224	1.0000	10.20
21	MSIAGGSDL	258	1.0000	10.20
22	VRVTVIAAG	302	1.0000	10.20
23	FEPVDAVSV	344	1.0000	10.20
24	VKLDVGRDS	53	0.9000	9.18
25	FIAINTDAQ	36	0.8000	8.16
26	MGETGGAHR	322	0.8000	8.16
27	YLAVIKVVG	6	0.7000	7.14
28	LQMGDAAVS	166	0.7000	7.14
29	LITTPGLIN	196	0.7000	7.14
30	VASIARKLG	113	0.5000	5.10
31	LNGVQGITD	187	0.5000	5.10
32	LAVIKVVGI	7	0.4000	4.08
33	LIVIPNDRL	157	0.4000	4.08
34	LMSIAGGSD	257	0.4000	4.08
35	VMGETGGAH	321	0.3000	3.06
36	VGRDSTRGL	57	0.1000	1.02
37	VQGITDLIT	190	0.1000	1.02

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	MVFVTAGEG	94	4.0000	40.82
2	VSLMDAFRS	173	3.6000	36.73
3	VVASIARKL	112	3.2000	32.65
4	VVGIGGGGV	12	2.7000	27.55
5	VIKVVGIGG	9	2.5000	25.51
6	VNRMIEQGL	23	2.2000	22.45
7	VLMSIAGGS	256	2.2000	22.45
8	FDVSGPGRK	311	2.2000	22.45
9	LKGVEFIAI	31	2.1000	21.43
10	LLMSDADVK	46	2.1000	21.43
11	VKGIMSGAG	210	2.1000	21.43
12	IVIPNDRLL	158	1.7000	17.35
13	LMGIGSARG	221	1.5000	15.31
14	FRSADEVLL	179	1.4000	14.29
15	FADVKGIMS	207	1.4000	14.29
16	IKVVGIGGG	10	1.3000	13.27
17	FEINEAASL	269	1.2000	12.24
18	IESAKAGKL	331	1.2000	12.24
19	FVTAGEGGG	96	1.1000	11.22
20	IGSARGEGR	224	1.0000	10.20
21	MSIAGGSDL	258	1.0000	10.20
22	VRVTVIAAG	302	1.0000	10.20
23	FEPVDAVSV	344	1.0000	10.20
24	VKLDVGRDS	53	0.9000	9.18
25	FIAINTDAQ	36	0.8000	8.16
26	MGETGGAHR	322	0.8000	8.16
27	YLAVIKVVG	6	0.7000	7.14
28	LQMGDAAVS	166	0.7000	7.14
29	LITTPGLIN	196	0.7000	7.14
30	VASIARKLG	113	0.5000	5.10
31	LNGVQGITD	187	0.5000	5.10
32	LAVIKVVGI	7	0.4000	4.08
33	LIVIPNDRL	157	0.4000	4.08

34	LMSIAGGSD	257	0.4000	4.08
35	VMGETGGAH	321	0.3000	3.06
36	VGRDSTRGL	57	0.1000	1.02
37	VQGITDLIT	190	0.1000	1.02