MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Fri Feb 26 16:46:38 2010
Length of input sequence	345 amino acids
Number of nanomers from input sequence	337
Number of nanomers with obligatory P1 anchor residue	105
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	34

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	VVPLAGSLV	206	2.1000	35.00
2	LVSGTCVRV	241	1.6000	26.67
3	VRFFASARS	31	1.1800	19.67
4	YQAVSGSGL	155	1.1500	19.17
5	YVAPIAFNV	198	0.8000	13.33
6	LRKGAALNT	325	0.6000	10.00
7	LVRLVVSSY	147	0.5000	8.33
8	IVGATGQVG	6	0.4000	6.67

9	LRFESRKIL	227	0.1000	1.67
10	INAEFAQPL	259	0.1000	1.67
11	VRLVVSSYQ	148	-0.2500	0
12	FAAAGVTVI	83	-0.3100	0
13	VFTGHSLSI	251	-0.5000	0
14	IGIVGATGQ	4	-0.5600	0
15	LVVSSYQAV	150	-0.6000	0
16	VPVFTGHSL	249	-0.6200	0
17	MGLSIGIVG	0	-0.7000	0
18	MAAMPVLKV	132	-0.7000	0
19	LSPERAREL	267	-0.8100	0
20	LFSAGSAMS	68	-0.9000	0
21	VVSEVNFER	106	-0.9000	0
22	FVSGDNLRK	319	-0.9000	0
23	VQLVDVPTP	282	-0.9800	0
24	IALFSAGSA	66	-1.0200	0
25	FNVVPLAGS	204	-1.0500	0
26	LNTIQIAEL	331	-1.1000	0
27	IIANPNCTT	123	-1.1600	0
28	IAFNVVPLA	202	-1.1900	0
29	FASARSQGR	34	-1.2000	0
30	LDGATGVQL	276	-1.2000	0
31	VTVIDNSSA	88	-1.3000	0
32	LVDVPTPLA	284	-1.3800	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	VVPLAGSLV	206	3.1000	51.67
2	LVSGTCVRV	241	2.6000	43.33
3	VRFFASARS	31	2.1800	36.33
4	LRKGAALNT	325	1.6000	26.67
5	LVRLVVSSY	147	1.5000	25.00

6	IVGATGQVG	6	1.4000	23.33
7	LRFESRKIL	227	1.1000	18.33
8	INAEFAQPL	259	1.1000	18.33
9	IQIAELLTA	334	1.0000	16.67
10	VRLVVSSYQ	148	0.7500	12.50
11	VFTGHSLSI	251	0.5000	8.33
12	IGIVGATGQ	4	0.4400	7.33
13	LVVSSYQAV	150	0.4000	6.67
14	VPVFTGHSL	249	0.3800	6.33
15	MGLSIGIVG	0	0.3000	5.00
16	MAAMPVLKV	132	0.3000	5.00
17	LSPERAREL	267	0.1900	3.17
18	YQAVSGSGL	155	0.1500	2.50
19	LFSAGSAMS	68	0.1000	1.67
20	VVSEVNFER	106	0.1000	1.67
21	VQLVDVPTP	282	0.0200	0.33
22	IALFSAGSA	66	-0.0200	0
23	LNTIQIAEL	331	-0.1000	0
24	IIANPNCTT	123	-0.1600	0
25	IAFNVVPLA	202	-0.1900	0
26	YVAPIAFNV	198	-0.2000	0
27	LDGATGVQL	276	-0.2000	0
28	VTVIDNSSA	88	-0.3000	0
29	FAAAGVTVI	83	-0.3100	0
30	LVDVPTPLA	284	-0.3800	0
31	IEVEDAETA	51	-0.4000	0
32	ILGIPDLLV	234	-0.4000	0
33	VVSSYQAVS	151	-0.5000	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	LVRLVVSSY	147	4.3700	46.00

2	LVYDGGALE	183	4.2000	44.21
3	LVVSEVNFE	105	4.1100	43.26
4	IRRDPGVPD	304	4.1000	43.16
5	VVSSYQAVS	151	3.8000	40.00
6	VQLVDVPTP	282	3.8000	40.00
7	LLVSGTCVR	240	3.5000	36.84
8	LVSGTCVRV	241	3.3000	34.74
9	IQIAELLTA	334	3.1000	32.63
10	VRFFASARS	31	3.0000	31.58
11	VRLVVSSYQ	148	2.9700	31.26
12	VLHDEARLV	140	2.9000	30.53
13	IAFNVVPLA	202	2.9000	30.53
14	LVDDGSGET	213	2.6000	27.37
15	LSIGIVGAT	2	2.5000	26.32
16	LGIPDLLVS	235	2.5000	26.32
17	VGRIRRDPG	301	2.5000	26.32
18	LRKGAALNT	325	2.4000	25.26
19	MGLSIGIVG	0	2.3000	24.21
20	LVDVPTPLA	284	2.3000	24.21
21	LVVSSYQAV	150	2.1000	22.11
22	VVPLAGSLV	206	2.0700	21.79
23	LRFESRKIL	227	2.0600	21.68
24	LFSAGSAMS	68	2.0000	21.05
25	VFTGHSLSI	251	2.0000	21.05
26	FFASARSQG	33	1.9700	20.74
27	LNTIQIAEL	331	1.9600	20.63
28	IVGATGQVG	6	1.9000	20.00
29	LAGSLVDDG	209	1.9000	20.00
30	VSGDNLRKG	320	1.9000	20.00
31	IGIVGATGQ	4	1.7000	17.89
32	VVSEVNFER	106	1.7000	17.89
33	MAAMPVLKV	132	1.7000	17.89
34	LAAAGVDES	291	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	VRLVVSSYQ	148	2.6700	29.34
2	VVSSYQAVS	151	2.4000	26.37
3	FNVVPLAGS	204	2.2000	24.18
4	FVSGDNLRK	319	2.1000	23.08
5	IQIAELLTA	334	2.1000	23.08
6	LVRLVVSSY	147	2.0700	22.75
7	IRRDPGVPD	304	2.0000	21.98
8	IAFNVVPLA	202	1.9000	20.88
9	LVYDGGALE	183	1.8000	19.78
10	VQLVDVPTP	282	1.8000	19.78
11	LVVSEVNFE	105	1.7100	18.79
12	VRFFASARS	31	1.6000	17.58
13	FFASARSQG	33	1.5700	17.25
14	IGIVGATGQ	4	1.4000	15.38
15	WRKDPDVPL	97	1.3000	14.29
16	LVSGTCVRV	241	1.3000	14.29
17	LVDVPTPLA	284	1.3000	14.29
18	FRGQEIEVE	46	1.2000	13.19
19	LGIPDLLVS	235	1.1000	12.09
20	FSAGSAMSK	69	1.0000	10.99
21	LLVSGTCVR	240	1.0000	10.99
22	VLHDEARLV	140	0.9000	9.89
23	YVAPIAFNV	198	0.9000	9.89
24	LVDDGSGET	213	0.9000	9.89
25	LSIGIVGAT	2	0.8000	8.79
26	FAAAGVTVI	83	0.8000	8.79
27	FERDAHRRP	112	0.8000	8.79
28	LRKGAALNT	325	0.7000	7.69
29	LFSAGSAMS	68	0.6000	6.59
30	LLDGATGVQ	275	0.6000	6.59

31	LAAAGVDES	291	0.3000	3.30
32	LVVSSYQAV	150	0.1000	1.10
33	LRFESRKIL	227	0.1000	1.10
34	VFTGHSLSI	251	0.1000	1.10

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IQIAELLTA	334	3.6000	40.91
2	LVVSEVNFE	105	3.4000	38.64
3	VRLVVSSYQ	148	3.4000	38.64
4	VVSSYQAVS	151	3.4000	38.64
5	IRRDPGVPD	304	2.8800	32.73
6	LVRLVVSSY	147	2.8000	31.82
7	LVYDGGALE	183	2.8000	31.82
8	VRFFASARS	31	2.6000	29.55
9	LGIPDLLVS	235	2.6000	29.55
10	IGIVGATGQ	4	2.4000	27.27
11	LRKGAALNT	325	2.2000	25.00
12	LVSGTCVRV	241	2.1800	24.77
13	LLVSGTCVR	240	2.0000	22.73
14	LRFESRKIL	227	1.7000	19.32
15	LFSAGSAMS	68	1.6000	18.18
16	VLHDEARLV	140	1.6000	18.18
17	VFTGHSLSI	251	1.6000	18.18
18	LAAAGVDES	291	1.6000	18.18
19	FVSGDNLRK	319	1.6000	18.18
20	IAFNVVPLA	202	1.5000	17.05
21	VQLVDVPTP	282	1.4000	15.91
22	VGRIRRDPG	301	1.4000	15.91
23	MAAMPVLKV	132	1.2000	13.64
24	LVVSSYQAV	150	1.2000	13.64
25	FNVVPLAGS	204	1.2000	13.64

26	LNTIQIAEL	331	1.0000	11.36
27	LVDVPTPLA	284	0.9000	10.23
28	VVPLAGSLV	206	0.8000	9.09
29	LAGSLVDDG	209	0.8000	9.09
30	IVGATGQVG	6	0.6000	6.82
31	FRGQEIEVE	46	0.6000	6.82
32	VLKVLHDEA	137	0.6000	6.82
33	MGLSIGIVG	0	0.5800	6.59
34	LVDDGSGET	213	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IQIAELLTA	334	3.6000	40.91
2	LVVSEVNFE	105	3.4000	38.64
3	VRLVVSSYQ	148	3.4000	38.64
4	VVSSYQAVS	151	3.4000	38.64
5	IRRDPGVPD	304	2.8800	32.73
6	LVRLVVSSY	147	2.8000	31.82
7	LVYDGGALE	183	2.8000	31.82
8	VRFFASARS	31	2.6000	29.55
9	LGIPDLLVS	235	2.6000	29.55
10	IGIVGATGQ	4	2.4000	27.27
11	LRKGAALNT	325	2.2000	25.00
12	LVSGTCVRV	241	2.1800	24.77
13	LLVSGTCVR	240	2.0000	22.73
14	LRFESRKIL	227	1.7000	19.32
15	LFSAGSAMS	68	1.6000	18.18
16	VLHDEARLV	140	1.6000	18.18
17	VFTGHSLSI	251	1.6000	18.18
18	LAAAGVDES	291	1.6000	18.18
19	FVSGDNLRK	319	1.6000	18.18
20	IAFNVVPLA	202	1.5000	17.05

21	VQLVDVPTP	282	1.4000	15.91
22	VGRIRRDPG	301	1.4000	15.91
23	MAAMPVLKV	132	1.2000	13.64
24	LVVSSYQAV	150	1.2000	13.64
25	FNVVPLAGS	204	1.2000	13.64
26	LNTIQIAEL	331	1.0000	11.36
27	LVDVPTPLA	284	0.9000	10.23
28	VVPLAGSLV	206	0.8000	9.09
29	LAGSLVDDG	209	0.8000	9.09
30	IVGATGQVG	6	0.6000	6.82
31	FRGQEIEVE	46	0.6000	6.82
32	VLKVLHDEA	137	0.6000	6.82
33	MGLSIGIVG	0	0.5800	6.59
34	LVDDGSGET	213	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IQIAELLTA	334	3.6000	40.91
2	LVVSEVNFE	105	3.4000	38.64
3	VRLVVSSYQ	148	3.4000	38.64
4	VVSSYQAVS	151	3.4000	38.64
5	IRRDPGVPD	304	2.8800	32.73
6	LVRLVVSSY	147	2.8000	31.82
7	LVYDGGALE	183	2.8000	31.82
8	VRFFASARS	31	2.6000	29.55
9	LGIPDLLVS	235	2.6000	29.55
10	IGIVGATGQ	4	2.4000	27.27
11	LRKGAALNT	325	2.2000	25.00
12	LVSGTCVRV	241	2.1800	24.77
13	LLVSGTCVR	240	2.0000	22.73
14	LRFESRKIL	227	1.7000	19.32
15	LFSAGSAMS	68	1.6000	18.18

16	VLHDEARLV	140	1.6000	18.18
17	VFTGHSLSI	251	1.6000	18.18
18	LAAAGVDES	291	1.6000	18.18
19	FVSGDNLRK	319	1.6000	18.18
20	IAFNVVPLA	202	1.5000	17.05
21	VQLVDVPTP	282	1.4000	15.91
22	VGRIRRDPG	301	1.4000	15.91
23	MAAMPVLKV	132	1.2000	13.64
24	LVVSSYQAV	150	1.2000	13.64
25	FNVVPLAGS	204	1.2000	13.64
26	LNTIQIAEL	331	1.0000	11.36
27	LVDVPTPLA	284	0.9000	10.23
28	VVPLAGSLV	206	0.8000	9.09
29	LAGSLVDDG	209	0.8000	9.09
30	IVGATGQVG	6	0.6000	6.82
31	FRGQEIEVE	46	0.6000	6.82
32	VLKVLHDEA	137	0.6000	6.82
33	MGLSIGIVG	0	0.5800	6.59
34	LVDDGSGET	213	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLVVSSY	147	3.3700	35.47
2	LVYDGGALE	183	3.2000	33.68
3	LVVSEVNFE	105	3.1100	32.74
4	IRRDPGVPD	304	3.1000	32.63
5	FFASARSQG	33	2.9700	31.26
6	VVSSYQAVS	151	2.8000	29.47
7	VQLVDVPTP	282	2.8000	29.47
8	FRGQEIEVE	46	2.6000	27.37
9	FNVVPLAGS	204	2.6000	27.37
10	LLVSGTCVR	240	2.5000	26.32

11	LVSGTCVRV	241	2.3000	24.21
12	WRKDPDVPL	97	2.2600	23.79
13	FVSGDNLRK	319	2.2000	23.16
14	IQIAELLTA	334	2.1000	22.11
15	VRFFASARS	31	2.0000	21.05
16	VRLVVSSYQ	148	1.9700	20.74
17	VLHDEARLV	140	1.9000	20.00
18	YVAPIAFNV	198	1.9000	20.00
19	IAFNVVPLA	202	1.9000	20.00
20	FERDAHRRP	112	1.8000	18.95
21	FAAAGVTVI	83	1.7000	17.89
22	LVDDGSGET	213	1.6000	16.84
23	LSIGIVGAT	2	1.5000	15.79
24	LGIPDLLVS	235	1.5000	15.79
25	VGRIRRDPG	301	1.5000	15.79
26	FPASAVRFF	26	1.4000	14.74
27	LRKGAALNT	325	1.4000	14.74
28	MGLSIGIVG	0	1.3000	13.68
29	LVDVPTPLA	284	1.3000	13.68
30	FSAGSAMSK	69	1.1000	11.58
31	LVVSSYQAV	150	1.1000	11.58
32	VVPLAGSLV	206	1.0700	11.26
33	LRFESRKIL	227	1.0600	11.16
34	LFSAGSAMS	68	1.0000	10.53

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	IQIAELLTA	334	3.6000	40.91
2	LVVSEVNFE	105	3.4000	38.64
3	VRLVVSSYQ	148	3.4000	38.64
4	VVSSYQAVS	151	3.4000	38.64
5	IRRDPGVPD	304	2.8800	32.73

6	LVRLVVSSY	147	2.8000	31.82
7	LVYDGGALE	183	2.8000	31.82
8	VRFFASARS	31	2.6000	29.55
9	LGIPDLLVS	235	2.6000	29.55
10	IGIVGATGQ	4	2.4000	27.27
11	LRKGAALNT	325	2.2000	25.00
12	LVSGTCVRV	241	2.1800	24.77
13	LLVSGTCVR	240	2.0000	22.73
14	LRFESRKIL	227	1.7000	19.32
15	LFSAGSAMS	68	1.6000	18.18
16	VLHDEARLV	140	1.6000	18.18
17	VFTGHSLSI	251	1.6000	18.18
18	LAAAGVDES	291	1.6000	18.18
19	FVSGDNLRK	319	1.6000	18.18
20	IAFNVVPLA	202	1.5000	17.05
21	VQLVDVPTP	282	1.4000	15.91
22	VGRIRRDPG	301	1.4000	15.91
23	MAAMPVLKV	132	1.2000	13.64
24	LVVSSYQAV	150	1.2000	13.64
25	FNVVPLAGS	204	1.2000	13.64
26	LNTIQIAEL	331	1.0000	11.36
27	LVDVPTPLA	284	0.9000	10.23
28	VVPLAGSLV	206	0.8000	9.09
29	LAGSLVDDG	209	0.8000	9.09
30	IVGATGQVG	6	0.6000	6.82
31	FRGQEIEVE	46	0.6000	6.82
32	VLKVLHDEA	137	0.6000	6.82
33	MGLSIGIVG	0	0.5800	6.59
34	LVDDGSGET	213	0.5000	5.68

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

Rank	Sequence	At Position	Score	% of Highest Score

1	VRFFASARS	31	2.8000	32.56
2	VRLVVSSYQ	148	2.6000	30.23
3	FVSGDNLRK	319	2.4000	27.91
4	LVRLVVSSY	147	2.3000	26.74
5	LVVSEVNFE	105	2.2000	25.58
6	LLVSGTCVR	240	2.2000	25.58
7	VVSEVNFER	106	2.1000	24.42
8	LFSAGSAMS	68	1.7000	19.77
9	FRGQEIEVE	46	1.6000	18.60
10	WRKDPDVPL	97	1.5800	18.37
11	VTVIDNSSA	88	1.4000	16.28
12	IEVEDAETA	51	1.3000	15.12
13	VVSSYQAVS	151	1.3000	15.12
14	IQIAELLTA	334	1.3000	15.12
15	IIANPNCTT	123	1.1000	12.79
16	IAFNVVPLA	202	0.9000	10.47
17	MAAMPVLKV	132	0.8000	9.30
18	IGIVGATGQ	4	0.5000	5.81
19	FAAAGVTVI	83	0.5000	5.81
20	INAEFAQPL	259	0.3000	3.49
21	LAAAGVDES	291	0.3000	3.49
22	FASARSQGR	34	0.2000	2.33
23	LVVSSYQAV	150	0.2000	2.33
24	IRRDPGVPD	304	0.1800	2.09
25	LVYDGGALE	183	0.1000	1.16
26	LVDVPTPLA	284	0.1000	1.16
27	ILGIPDLLV	234	-0.1000	0
28	VVPLAGSLV	206	-0.2000	0
29	LRFESRKIL	227	-0.2000	0
30	VIDNSSAWR	90	-0.3000	0
31	MPVLKVLHD	135	-0.3000	0

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

	1.8	9.6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFFASARS	31	5.0000	52.08
2	VRLVVSSYQ	148	3.6000	37.50
3	LFSAGSAMS	68	2.7000	28.13
4	FVSGDNLRK	319	2.6000	27.08
5	IQIAELLTA	334	2.6000	27.08
6	IGIVGATGQ	4	1.9000	19.79
7	MAAMPVLKV	132	1.8000	18.75
8	VFTGHSLSI	251	1.8000	18.75
9	LVRLVVSSY	147	1.7000	17.71
10	VTVIDNSSA	88	1.4800	15.42
11	LVVSEVNFE	105	1.4000	14.58
12	LLVSGTCVR	240	1.4000	14.58
13	LGIPDLLVS	235	1.3000	13.54
14	LVGRIRRDP	300	1.3000	13.54
15	LRKGAALNT	325	1.3000	13.54
16	LVSGTCVRV	241	1.1000	11.46
17	LVDVPTPLA	284	1.0000	10.42
18	IVGATGQVG	6	0.9000	9.38
19	FESRKILGI	229	0.9000	9.38
20	VVSEVNFER	106	0.8000	8.33
21	IIANPNCTT	123	0.8000	8.33
22	VPLAGSLVD	207	0.8000	8.33
23	VSGTCVRVP	242	0.7000	7.29
24	LVVSSYQAV	150	0.5000	5.21
25	VVSSYQAVS	151	0.5000	5.21
26	ILGIPDLLV	234	0.4800	5.00
27	VRVPVFTGH	247	0.4800	5.00
28	FASARSQGR	34	0.3000	3.12
29	FPPPNTYVA	192	0.3000	3.12
30	IAFNVVPLA	202	0.3000	3.12
31	VQLVDVPTP	282	0.1000	1.04
32	VLHDEARLV	140	-0.1000	0

33	LNTIQIAEL	331	-0.2200	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	VRFFASARS	31	5.7000	64.77
2	VRLVVSSYQ	148	5.7000	64.77
3	LVRLVVSSY	147	4.2000	47.73
4	IGIVGATGQ	4	3.4000	38.64
5	VTVIDNSSA	88	3.4000	38.64
6	LFSAGSAMS	68	2.7000	30.68
7	MAAMPVLKV	132	2.3000	26.14
8	LVDVPTPLA	284	2.2000	25.00
9	IQIAELLTA	334	1.9000	21.59
10	LVVSEVNFE	105	1.8000	20.45
11	VVPLAGSLV	206	1.7000	19.32
12	LLVSGTCVR	240	1.7000	19.32
13	VVSEVNFER	106	1.4500	16.48
14	VQLVDVPTP	282	1.3000	14.77
15	IALFSAGSA	66	0.8000	9.09
16	VVSSYQAVS	151	0.8000	9.09
17	ILGIPDLLV	234	0.8000	9.09
18	LNTIQIAEL	331	0.8000	9.09
19	VRVPVFTGH	247	0.7800	8.86
20	IAELLTADL	336	0.7000	7.95
21	LGIPDLLVS	235	0.6000	6.82
22	IIANPNCTT	123	0.5000	5.68
23	MPVLKVLHD	135	0.5000	5.68
24	FNVVPLAGS	204	0.4000	4.55
25	LAAAGVDES	291	0.4000	4.55
26	LALFVSGDN	316	0.4000	4.55
27	VAPIAFNVV	199	0.3000	3.41
28	FVSGDNLRK	319	0.2000	2.27

29	VPLAGSLVD	207	0.1000	1.14
30	VPLVVSEVN	103	-0.1000	0
31	LKVLHDEAR	138	-0.2000	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	VRLVVSSYQ	148	5.5000	58.51
2	VRFFASARS	31	4.7000	50.00
3	LVRLVVSSY	147	4.3000	45.74
4	LVVSEVNFE	105	3.8000	40.43
5	IGIVGATGQ	4	3.2000	34.04
6	FRGQEIEVE	46	2.9000	30.85
7	VTVIDNSSA	88	2.4000	25.53
8	MPVLKVLHD	135	2.2000	23.40
9	VPLAGSLVD	207	1.8000	19.15
10	LFSAGSAMS	68	1.7000	18.09
11	MAAMPVLKV	132	1.6000	17.02
12	MRTLLDERD	17	1.4000	14.89
13	FNVVPLAGS	204	1.4000	14.89
14	LALFVSGDN	316	1.4000	14.89
15	FAAAGVTVI	83	1.2000	12.77
16	LVDVPTPLA	284	1.2000	12.77
17	VVPLAGSLV	206	1.0000	10.64
18	VRVPVFTGH	247	1.0000	10.64
19	VPLVVSEVN	103	0.9000	9.57
20	IQIAELLTA	334	0.9000	9.57
21	LNTIQIAEL	331	0.8000	8.51
22	YQAVSGSGL	155	0.7000	7.45
23	LLVSGTCVR	240	0.7000	7.45
24	VQLVDVPTP	282	0.7000	7.45
25	IAELLTADL	336	0.7000	7.45
26	LVYDGGALE	183	0.6000	6.38

27	FVSGDNLRK	319	0.5000	5.32
28	VVSEVNFER	106	0.4500	4.79
29	IIANPNCTT	123	0.4000	4.26
30	YVAPIAFNV	198	0.3500	3.72
31	FPPPNTYVA	192	0.2000	2.13
32	IRRDPGVPD	304	0.2000	2.13
33	ILGIPDLLV	234	0.1000	1.06

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	VRFFASARS	31	4.7000	53.41
2	VRLVVSSYQ	148	4.7000	53.41
3	LVRLVVSSY	147	3.2000	36.36
4	IGIVGATGQ	4	2.4000	27.27
5	VTVIDNSSA	88	2.4000	27.27
6	LFSAGSAMS	68	1.7000	19.32
7	FNVVPLAGS	204	1.4000	15.91
8	MAAMPVLKV	132	1.3000	14.77
9	LVDVPTPLA	284	1.2000	13.64
10	FVSGDNLRK	319	1.2000	13.64
11	FAAAGVTVI	83	1.0000	11.36
12	IQIAELLTA	334	0.9000	10.23
13	LVVSEVNFE	105	0.8000	9.09
14	VVPLAGSLV	206	0.7000	7.95
15	LLVSGTCVR	240	0.7000	7.95
16	VVSEVNFER	106	0.4500	5.11
17	VQLVDVPTP	282	0.3000	3.41
18	FPPPNTYVA	192	0.2000	2.27
19	YVAPIAFNV	198	0.0500	0.57
20	FRGQEIEVE	46	-0.1000	0
21	IALFSAGSA	66	-0.2000	0
22	VVSSYQAVS	151	-0.2000	0

23	ILGIPDLLV	234	-0.2000	0
24	LNTIQIAEL	331	-0.2000	0
25	VRVPVFTGH	247	-0.2200	0
26	YQAVSGSGL	155	-0.3000	0
27	IAELLTADL	336	-0.3000	0
28	LGIPDLLVS	235	-0.4000	0
29	IIANPNCTT	123	-0.5000	0
30	MPVLKVLHD	135	-0.5000	0
31	LAAAGVDES	291	-0.6000	0
32	LALFVSGDN	316	-0.6000	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	VRLVVSSYQ	148	6.5000	69.15
2	VRFFASARS	31	5.7000	60.64
3	LVRLVVSSY	147	5.3000	56.38
4	LVVSEVNFE	105	4.8000	51.06
5	IGIVGATGQ	4	4.2000	44.68
6	VTVIDNSSA	88	3.4000	36.17
7	MPVLKVLHD	135	3.2000	34.04
8	VPLAGSLVD	207	2.8000	29.79
9	LFSAGSAMS	68	2.7000	28.72
10	MAAMPVLKV	132	2.6000	27.66
11	MRTLLDERD	17	2.4000	25.53
12	LALFVSGDN	316	2.4000	25.53
13	LVDVPTPLA	284	2.2000	23.40
14	VVPLAGSLV	206	2.0000	21.28
15	VRVPVFTGH	247	2.0000	21.28
16	FRGQEIEVE	46	1.9000	20.21
17	VPLVVSEVN	103	1.9000	20.21
18	IQIAELLTA	334	1.9000	20.21
19	LNTIQIAEL	331	1.8000	19.15

20	LLVSGTCVR	240	1.7000	18.09
21	VQLVDVPTP	282	1.7000	18.09
22	IAELLTADL	336	1.7000	18.09
23	LVYDGGALE	183	1.6000	17.02
24	VVSEVNFER	106	1.4500	15.43
25	IIANPNCTT	123	1.4000	14.89
26	IRRDPGVPD	304	1.2000	12.77
27	ILGIPDLLV	234	1.1000	11.70
28	IVGATGQVG	6	0.9000	9.57
29	IALFSAGSA	66	0.8000	8.51
30	VVSSYQAVS	151	0.8000	8.51
31	VAPIAFNVV	199	0.6000	6.38
32	LGIPDLLVS	235	0.6000	6.38
33	LEFPPPNTY	190	0.4000	4.26
34	FNVVPLAGS	204	0.4000	4.26

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	LLVSGTCVR	240	3.7000	41.11
2	LVVSEVNFE	105	3.6000	40.00
3	VVSEVNFER	106	3.6000	40.00
4	LVRLVVSSY	147	3.6000	40.00
5	VRFFASARS	31	3.2000	35.56
6	FRGQEIEVE	46	3.0000	33.33
7	WRKDPDVPL	97	2.5400	28.22
8	FVSGDNLRK	319	2.5000	27.78
9	LFSAGSAMS	68	2.1000	23.33
10	VRLVVSSYQ	148	1.9000	21.11
11	IIANPNCTT	123	1.8000	20.00
12	MAAMPVLKV	132	1.8000	20.00
13	FASARSQGR	34	1.7000	18.89
14	VVSSYQAVS	151	1.7000	18.89

15	VNFERDAHR	110	1.5000	16.67
16	LVYDGGALE	183	1.5000	16.67
17	FAAAGVTVI	83	1.4000	15.56
18	VTVIDNSSA	88	1.4000	15.56
19	IEVEDAETA	51	1.3000	14.44
20	IQIAELLTA	334	1.3000	14.44
21	IRRDPGVPD	304	1.2800	14.22
22	INAEFAQPL	259	1.2600	14.00
23	VIDNSSAWR	90	1.2000	13.33
24	LVVSSYQAV	150	1.2000	13.33
25	LFVSGDNLR	318	1.1000	12.22
26	LKVLHDEAR	138	1.0000	11.11
27	LAGSLVDDG	209	1.0000	11.11
28	FPASAVRFF	26	0.9000	10.00
29	IAFNVVPLA	202	0.9000	10.00
30	ILGIPDLLV	234	0.9000	10.00
31	MPVLKVLHD	135	0.8000	8.89
32	VVPLAGSLV	206	0.8000	8.89
33	LRFESRKIL	227	0.7600	8.44
34	VLHDEARLV	140	0.7000	7.78

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	VRFFASARS	31	5.7000	64.77
2	VRLVVSSYQ	148	5.7000	64.77
3	LVRLVVSSY	147	4.2000	47.73
4	IGIVGATGQ	4	3.4000	38.64
5	VTVIDNSSA	88	3.4000	38.64
6	LFSAGSAMS	68	2.7000	30.68
7	MAAMPVLKV	132	2.3000	26.14
8	LVDVPTPLA	284	2.2000	25.00
9	IQIAELLTA	334	1.9000	21.59

10	LVVSEVNFE	105	1.8000	20.45
11	VVPLAGSLV	206	1.7000	19.32
12	LLVSGTCVR	240	1.7000	19.32
13	VVSEVNFER	106	1.4500	16.48
14	VQLVDVPTP	282	1.3000	14.77
15	IALFSAGSA	66	0.8000	9.09
16	VVSSYQAVS	151	0.8000	9.09
17	ILGIPDLLV	234	0.8000	9.09
18	LNTIQIAEL	331	0.8000	9.09
19	VRVPVFTGH	247	0.7800	8.86
20	IAELLTADL	336	0.7000	7.95
21	LGIPDLLVS	235	0.6000	6.82
22	IIANPNCTT	123	0.5000	5.68
23	MPVLKVLHD	135	0.5000	5.68
24	FNVVPLAGS	204	0.4000	4.55
25	LAAAGVDES	291	0.4000	4.55
26	LALFVSGDN	316	0.4000	4.55
27	VAPIAFNVV	199	0.3000	3.41
28	FVSGDNLRK	319	0.2000	2.27
29	VPLAGSLVD	207	0.1000	1.14
30	VPLVVSEVN	103	-0.1000	0
31	LKVLHDEAR	138	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFFASARS	31	2.8000	32.56
2	VRLVVSSYQ	148	2.6000	30.23
3	FVSGDNLRK	319	2.4000	27.91
4	LVRLVVSSY	147	2.3000	26.74
5	LVVSEVNFE	105	2.2000	25.58
6	LLVSGTCVR	240	2.2000	25.58
7	VVSEVNFER	106	2.1000	24.42

8	LFSAGSAMS	68	1.7000	19.77
9	FRGQEIEVE	46	1.6000	18.60
10	WRKDPDVPL	97	1.5800	18.37
11	VTVIDNSSA	88	1.4000	16.28
12	IEVEDAETA	51	1.3000	15.12
13	VVSSYQAVS	151	1.3000	15.12
14	IQIAELLTA	334	1.3000	15.12
15	IIANPNCTT	123	1.1000	12.79
16	IAFNVVPLA	202	0.9000	10.47
17	MAAMPVLKV	132	0.8000	9.30
18	IGIVGATGQ	4	0.5000	5.81
19	FAAAGVTVI	83	0.5000	5.81
20	INAEFAQPL	259	0.3000	3.49
21	LAAAGVDES	291	0.3000	3.49
22	FASARSQGR	34	0.2000	2.33
23	LVVSSYQAV	150	0.2000	2.33
24	IRRDPGVPD	304	0.1800	2.09
25	LVYDGGALE	183	0.1000	1.16
26	LVDVPTPLA	284	0.1000	1.16
27	ILGIPDLLV	234	-0.1000	0
28	VVPLAGSLV	206	-0.2000	0
29	LRFESRKIL	227	-0.2000	0
30	VIDNSSAWR	90	-0.3000	0
31	MPVLKVLHD	135	-0.3000	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	YQAVSGSGL	155	5.3000	45.69
2	LVVSSYQAV	150	5.2000	44.83
3	YVAPIAFNV	198	5.0000	43.10
4	VFTGHSLSI	251	4.9000	42.24
5	FAAAGVTVI	83	4.4000	37.93

6	LVVSEVNFE	105	4.3000	37.07
7	FESRKILGI	229	4.3000	37.07
8	FPASAVRFF	26	3.9000	33.62
9	LVSGTCVRV	241	3.8000	32.76
10	LNTIQIAEL	331	3.8000	32.76
11	VGQVMRTLL	13	3.6000	31.03
12	LRFESRKIL	227	3.4000	29.31
13	MGLSIGIVG	0	3.2000	27.59
14	VRLVVSSYQ	148	3.2000	27.59
15	WRKDPDVPL	97	3.1000	26.72
16	VAPIAFNVV	199	3.0000	25.86
17	ILGIPDLLV	234	3.0000	25.86
18	IQIAELLTA	334	3.0000	25.86
19	MAAMPVLKV	132	2.9000	25.00
20	VPVFTGHSL	249	2.9000	25.00
21	INAEFAQPL	259	2.9000	25.00
22	LRKGAALNT	325	2.7000	23.28
23	LVRLVVSSY	147	2.6000	22.41
24	VRFFASARS	31	2.5000	21.55
25	VVPLAGSLV	206	2.4000	20.69
26	LDGATGVQL	276	2.3000	19.83
27	IGIVGATGQ	4	1.9000	16.38
28	IGGAEQLVY	177	1.9000	16.38
29	VYDGGALEF	184	1.8000	15.52
30	LSPERAREL	267	1.7000	14.66
31	FVSGDNLRK	319	1.7000	14.66
32	MSKVQAPRF	75	1.5000	12.93
33	VSGSGLAGV	158	1.5000	12.93
34	VDESLVGRI	296	1.5000	12.93

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	YQAVSGSGL	155	5.3000	45.69
2	LVVSSYQAV	150	5.2000	44.83
3	YVAPIAFNV	198	5.0000	43.10
4	VFTGHSLSI	251	4.9000	42.24
5	FAAAGVTVI	83	4.4000	37.93
6	LVVSEVNFE	105	4.3000	37.07
7	FESRKILGI	229	4.3000	37.07
8	FPASAVRFF	26	3.9000	33.62
9	LVSGTCVRV	241	3.8000	32.76
10	LNTIQIAEL	331	3.8000	32.76
11	VGQVMRTLL	13	3.6000	31.03
12	LRFESRKIL	227	3.4000	29.31
13	MGLSIGIVG	0	3.2000	27.59
14	VRLVVSSYQ	148	3.2000	27.59
15	WRKDPDVPL	97	3.1000	26.72
16	VAPIAFNVV	199	3.0000	25.86
17	ILGIPDLLV	234	3.0000	25.86
18	IQIAELLTA	334	3.0000	25.86
19	MAAMPVLKV	132	2.9000	25.00
20	VPVFTGHSL	249	2.9000	25.00
21	INAEFAQPL	259	2.9000	25.00
22	LRKGAALNT	325	2.7000	23.28
23	LVRLVVSSY	147	2.6000	22.41
24	VRFFASARS	31	2.5000	21.55
25	VVPLAGSLV	206	2.4000	20.69
26	LDGATGVQL	276	2.3000	19.83
27	IGIVGATGQ	4	1.9000	16.38
28	IGGAEQLVY	177	1.9000	16.38
29	VYDGGALEF	184	1.8000	15.52
30	LSPERAREL	267	1.7000	14.66
31	FVSGDNLRK	319	1.7000	14.66
32	MSKVQAPRF	75	1.5000	12.93
33	VSGSGLAGV	158	1.5000	12.93
34	VDESLVGRI	296	1.5000	12.93

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	VRFFASARS	31	3.1000	36.05
2	LVGRIRRDP	300	3.1000	36.05
3	FESRKILGI	229	2.9000	33.72
4	LVRLVVSSY	147	2.5000	29.07
5	FNVVPLAGS	204	2.5000	29.07
6	VRLVVSSYQ	148	2.4000	27.91
7	LVVSEVNFE	105	1.8000	20.93
8	MPVLKVLHD	135	1.6000	18.60
9	IQIAELLTA	334	1.6000	18.60
10	LVYDGGALE	183	1.5000	17.44
11	LRFESRKIL	227	1.2000	13.95
12	FRGQEIEVE	46	1.0000	11.63
13	MAAMPVLKV	132	0.9000	10.47
14	LNTIQIAEL	331	0.8000	9.30
15	LAFRGQEIE	44	0.7000	8.14
16	VVSSYQAVS	151	0.7000	8.14
17	LFSAGSAMS	68	0.6000	6.98
18	LGIPDLLVS	235	0.6000	6.98
19	VQLVDVPTP	282	0.6000	6.98
20	LALFVSGDN	316	0.5000	5.81
21	VSSYQAVSG	152	0.3000	3.49
22	IGIVGATGQ	4	0.2000	2.33
23	VPLAGSLVD	207	0.1000	1.16
24	IRRDPGVPD	304	0.1000	1.16
25	FFASARSQG	33	-0.2000	0
26	YVAPIAFNV	198	-0.2000	0
27	IAFNVVPLA	202	-0.2000	0
28	IVGATGQVG	6	-0.3000	0
29	VVPLAGSLV	206	-0.3000	0
30	LVDVPTPLA	284	-0.3000	0

31	LSIGIVGAT	2	-0.4000	0
32	LRKGAALNT	325	-0.4000	0

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	VRFFASARS	31	3.1000	38.75
2	FESRKILGI	229	2.7000	33.75
3	LVGRIRRDP	300	2.7000	33.75
4	FNVVPLAGS	204	2.5000	31.25
5	VRLVVSSYQ	148	1.6000	20.00
6	IQIAELLTA	334	1.6000	20.00
7	LVRLVVSSY	147	1.4000	17.50
8	VVSSYQAVS	151	0.7000	8.75
9	LFSAGSAMS	68	0.6000	7.50
10	MAAMPVLKV	132	0.6000	7.50
11	LGIPDLLVS	235	0.6000	7.50
12	LRFESRKIL	227	0.2000	2.50
13	VQLVDVPTP	282	0.2000	2.50
14	FVSGDNLRK	319	0.1000	1.25
15	IAFNVVPLA	202	-0.2000	0
16	LNTIQIAEL	331	-0.2000	0
17	LVDVPTPLA	284	-0.3000	0
18	YVAPIAFNV	198	-0.5000	0
19	IGIVGATGQ	4	-0.6000	0
20	VVPLAGSLV	206	-0.6000	0
21	LLVSGTCVR	240	-0.7000	0
22	VSSYQAVSG	152	-1.0000	0
23	MPVLKVLHD	135	-1.1000	0
24	LVVSEVNFE	105	-1.2000	0
25	LSIGIVGAT	2	-1.3000	0
26	LRKGAALNT	325	-1.3000	0
27	FFASARSQG	33	-1.5000	0

28	FAAAGVTVI	83	-1.5000	0
29	YQAVSGSGL	155	-1.5000	0
30	LVYDGGALE	183	-1.5000	0
31	FPPPNTYVA	192	-1.5000	0
32	LVSGTCVRV	241	-1.5000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFFASARS	31	4.1000	51.25
2	LVGRIRRDP	300	3.7000	46.25
3	VRLVVSSYQ	148	2.6000	32.50
4	IQIAELLTA	334	2.6000	32.50
5	LVRLVVSSY	147	2.4000	30.00
6	VVSSYQAVS	151	1.7000	21.25
7	FESRKILGI	229	1.7000	21.25
8	LFSAGSAMS	68	1.6000	20.00
9	MAAMPVLKV	132	1.6000	20.00
10	LGIPDLLVS	235	1.6000	20.00
11	FNVVPLAGS	204	1.5000	18.75
12	LRFESRKIL	227	1.2000	15.00
13	VQLVDVPTP	282	1.2000	15.00
14	IALFSAGSA	66	1.0000	12.50
15	IAFNVVPLA	202	0.8000	10.00
16	LNTIQIAEL	331	0.8000	10.00
17	LVDVPTPLA	284	0.7000	8.75
18	IGIVGATGQ	4	0.4000	5.00
19	VVPLAGSLV	206	0.4000	5.00
20	LLVSGTCVR	240	0.3000	3.75
21	MPVLKVLHD	135	-0.1000	0
22	LVVSEVNFE	105	-0.2000	0
23	LSIGIVGAT	2	-0.3000	0
24	LRKGAALNT	325	-0.3000	0

25	LVYDGGALE	183	-0.5000	0
26	LVSGTCVRV	241	-0.5000	0
27	LLDGATGVQ	275	-0.5000	0
28	LAAAGVDES	291	-0.5000	0
29	LALFVSGDN	316	-0.5000	0
30	IVGATGQVG	6	-0.6000	0
31	LSINAEFAQ	257	-0.6000	0
32	IIANPNCTT	123	-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	VRFFASARS	31	4.1000	47.67
2	LVGRIRRDP	300	4.1000	47.67
3	LVRLVVSSY	147	3.5000	40.70
4	VRLVVSSYQ	148	3.4000	39.53
5	LVVSEVNFE	105	2.8000	32.56
6	MPVLKVLHD	135	2.6000	30.23
7	IQIAELLTA	334	2.6000	30.23
8	LVYDGGALE	183	2.5000	29.07
9	LRFESRKIL	227	2.2000	25.58
10	MAAMPVLKV	132	1.9000	22.09
11	FESRKILGI	229	1.9000	22.09
12	LNTIQIAEL	331	1.8000	20.93
13	LAFRGQEIE	44	1.7000	19.77
14	VVSSYQAVS	151	1.7000	19.77
15	LFSAGSAMS	68	1.6000	18.60
16	LGIPDLLVS	235	1.6000	18.60
17	VQLVDVPTP	282	1.6000	18.60
18	FNVVPLAGS	204	1.5000	17.44
19	LALFVSGDN	316	1.5000	17.44
20	VSSYQAVSG	152	1.3000	15.12
21	IGIVGATGQ	4	1.2000	13.95

22	VPLAGSLVD	207	1.1000	12.79
23	IRRDPGVPD	304	1.1000	12.79
24	IALFSAGSA	66	1.0000	11.63
25	IAFNVVPLA	202	0.8000	9.30
26	IVGATGQVG	6	0.7000	8.14
27	VVPLAGSLV	206	0.7000	8.14
28	LVDVPTPLA	284	0.7000	8.14
29	LSIGIVGAT	2	0.6000	6.98
30	LRKGAALNT	325	0.6000	6.98
31	VGRIRRDPG	301	0.4000	4.65
32	LLVSGTCVR	240	0.3000	3.49
33	LLDGATGVQ	275	0.3000	3.49
34	IAELLTADL	336	0.3000	3.49

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	VRLVVSSYQ	148	3.4000	39.08
2	FESRKILGI	229	3.3000	37.93
3	LVRLVVSSY	147	3.2000	36.78
4	VRFFASARS	31	3.1000	35.63
5	FNVVPLAGS	204	2.5000	28.74
6	LVGRIRRDP	300	2.4000	27.59
7	IGIVGATGQ	4	2.2000	25.29
8	IQIAELLTA	334	2.2000	25.29
9	FAAAGVTVI	83	1.3000	14.94
10	MAAMPVLKV	132	1.2000	13.79
11	VVPLAGSLV	206	1.2000	13.79
12	LGIPDLLVS	235	1.2000	13.79
13	LVVSEVNFE	105	0.8000	9.20
14	VVSSYQAVS	151	0.7000	8.05
15	FVSGDNLRK	319	0.7000	8.05
16	LFSAGSAMS	68	0.6000	6.90

17	VQLVDVPTP	282	0.4000	4.60
18	YVAPIAFNV	198	0.3500	4.02
19	FFASARSQG	33	0.3000	3.45
20	YQAVSGSGL	155	0.3000	3.45
21	VGQVMRTLL	13	0.2000	2.30
22	LVDVPTPLA	284	-0.1000	0
23	LNTIQIAEL	331	-0.2000	0
24	VRVPVFTGH	247	-0.2200	0
25	FRGQEIEVE	46	-0.3000	0
26	VTVIDNSSA	88	-0.3000	0
27	LRFESRKIL	227	-0.3000	0
28	LAAAGVDES	291	-0.3000	0
29	MPVLKVLHD	135	-0.5000	0
30	LVSGTCVRV	241	-0.5000	0
31	IVGATGQVG	6	-0.6000	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	FESRKILGI	229	4.7000	46.53
2	MPVLKVLHD	135	3.4000	33.66
3	IQIAELLTA	334	3.4000	33.66
4	LVGRIRRDP	300	3.3000	32.67
5	VRFFASARS	31	3.1000	30.69
6	MAAMPVLKV	132	2.7000	26.73
7	LVRLVVSSY	147	2.5000	24.75
8	FNVVPLAGS	204	2.5000	24.75
9	VRLVVSSYQ	148	2.4000	23.76
10	LGIPDLLVS	235	2.4000	23.76
11	FRGQEIEVE	46	2.1000	20.79
12	LVVSEVNFE	105	2.1000	20.79
13	VPLAGSLVD	207	1.9000	18.81
14	LAFRGQEIE	44	1.8000	17.82

15	LRFESRKIL	227	1.8000	17.82
16	VQLVDVPTP	282	1.7500	17.33
17	LVYDGGALE	183	1.5000	14.85
18	LRKGAALNT	325	1.4000	13.86
19	IGIVGATGQ	4	1.3000	12.87
20	FVSGDNLRK	319	1.2000	11.88
21	IGGAEQLVY	177	1.0000	9.90
22	IAFNVVPLA	202	0.9500	9.41
23	LAGVAELAE	163	0.9000	8.91
24	LVDVPTPLA	284	0.8500	8.42
25	VSSYQAVSG	152	0.8000	7.92
26	LNTIQIAEL	331	0.8000	7.92
27	VVSSYQAVS	151	0.7000	6.93
28	LFSAGSAMS	68	0.6000	5.94
29	IRRDPGVPD	304	0.6000	5.94
30	LALFVSGDN	316	0.6000	5.94
31	YVAPIAFNV	198	0.3000	2.97
32	IALFSAGSA	66	0.1000	0.99
33	VFTGHSLSI	251	0.1000	0.99

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	IQIAELLTA	334	3.4000	40.96
2	VRFFASARS	31	3.0000	36.14
3	FNVVPLAGS	204	2.6000	31.33
4	MAAMPVLKV	132	2.0000	24.10
5	LVRLVVSSY	147	1.8000	21.69
6	VRLVVSSYQ	148	1.7000	20.48
7	LGIPDLLVS	235	1.7000	20.48
8	FESRKILGI	229	1.5000	18.07
9	VQLVDVPTP	282	1.4500	17.47
10	FVSGDNLRK	319	1.2000	14.46

11	MPVLKVLHD	135	1.1000	13.25
12	VVSSYQAVS	151	1.0000	12.05
13	IAFNVVPLA	202	0.9500	11.45
14	LVDVPTPLA	284	0.9500	11.45
15	IGIVGATGQ	4	0.6000	7.23
16	LFSAGSAMS	68	0.6000	7.23
17	LNTIQIAEL	331	0.4000	4.82
18	LRFESRKIL	227	0.1000	1.20
19	IGGAEQLVY	177	-0.1000	0
20	LVGRIRRDP	300	-0.1000	0
21	VVPLAGSLV	206	-0.2000	0
22	LRKGAALNT	325	-0.2000	0
23	FRGQEIEVE	46	-0.3000	0
24	FAAAGVTVI	83	-0.4000	0
25	LLVSGTCVR	240	-0.4000	0
26	ILGIPDLLV	234	-0.5000	0
27	LVVSEVNFE	105	-0.6000	0
28	YVAPIAFNV	198	-0.7000	0
29	VPLAGSLVD	207	-0.8000	0
30	VFTGHSLSI	251	-0.8000	0
31	FSAGSAMSK	69	-1.0000	0
32	MGLSIGIVG	0	-1.1000	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	VRFFASARS	31	4.4000	52.38
2	LVGRIRRDP	300	3.4000	40.48
3	IQIAELLTA	334	3.3000	39.29
4	LVRLVVSSY	147	2.5000	29.76
5	VVSSYQAVS	151	2.1000	25.00
6	LRFESRKIL	227	1.9000	22.62
7	VRLVVSSYQ	148	1.8000	21.43

8	LGIPDLLVS	235	1.8000	21.43
9	MAAMPVLKV	132	1.7000	20.24
10	LFSAGSAMS	68	1.6000	19.05
11	LVVSEVNFE	105	1.6000	19.05
12	IAFNVVPLA	202	1.6000	19.05
13	LSINAEFAQ	257	1.0000	11.90
14	IGIVGATGQ	4	0.7000	8.33
15	LLVSGTCVR	240	0.7000	8.33
16	VQLVDVPTP	282	0.7000	8.33
17	VVPLAGSLV	206	0.5000	5.95
18	LAAAGVDES	291	0.4000	4.76
19	IALFSAGSA	66	0.3000	3.57
20	MPVLKVLHD	135	0.3000	3.57
21	VLHDEARLV	140	0.3000	3.57
22	FNVVPLAGS	204	0.3000	3.57
23	FESRKILGI	229	0.3000	3.57
24	IVGATGQVG	6	0.2000	2.38
25	VVSEVNFER	106	0.2000	2.38
26	LVDVPTPLA	284	0.2000	2.38
27	LAEQARAVI	169	0.1000	1.19
28	VSGTCVRVP	242	-0.1000	0
29	LRKGAALNT	325	-0.1000	0
30	LNTIQIAEL	331	-0.1000	0
31	IGGAEQLVY	177	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IQIAELLTA	334	4.4000	53.01
2	VRFFASARS	31	4.0000	48.19
3	MAAMPVLKV	132	3.0000	36.14
4	LVRLVVSSY	147	2.8000	33.73
5	VRLVVSSYQ	148	2.7000	32.53

6	LGIPDLLVS	235	2.7000	32.53
7	VQLVDVPTP	282	2.4500	29.52
8	MPVLKVLHD	135	2.1000	25.30
9	VVSSYQAVS	151	2.0000	24.10
10	IAFNVVPLA	202	1.9500	23.49
11	LVDVPTPLA	284	1.9500	23.49
12	IGIVGATGQ	4	1.6000	19.28
13	LFSAGSAMS	68	1.6000	19.28
14	FNVVPLAGS	204	1.6000	19.28
15	LNTIQIAEL	331	1.4000	16.87
16	LRFESRKIL	227	1.1000	13.25
17	IALFSAGSA	66	1.0000	12.05
18	IGGAEQLVY	177	0.9000	10.84
19	LVGRIRRDP	300	0.9000	10.84
20	VVPLAGSLV	206	0.8000	9.64
21	LRKGAALNT	325	0.8000	9.64
22	LLVSGTCVR	240	0.6000	7.23
23	FESRKILGI	229	0.5000	6.02
24	ILGIPDLLV	234	0.5000	6.02
25	LVVSEVNFE	105	0.4000	4.82
26	VPLAGSLVD	207	0.2000	2.41
27	VFTGHSLSI	251	0.2000	2.41
28	FVSGDNLRK	319	0.2000	2.41
29	MGLSIGIVG	0	-0.1000	0
30	LSINAEFAQ	257	-0.1000	0
31	IAELLTADL	336	-0.3000	0
32	VGQVMRTLL	13	-0.4000	0
33	IVGATGQVG	6	-0.5000	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	IQIAELLTA	334	4.4000	53.01

2	VRFFASARS	31	4.0000	48.19
3	MAAMPVLKV	132	3.0000	36.14
4	LVRLVVSSY	147	2.8000	33.73
5	VRLVVSSYQ	148	2.7000	32.53
6	LGIPDLLVS	235	2.7000	32.53
7	VQLVDVPTP	282	2.4500	29.52
8	MPVLKVLHD	135	2.1000	25.30
9	VVSSYQAVS	151	2.0000	24.10
10	IAFNVVPLA	202	1.9500	23.49
11	LVDVPTPLA	284	1.9500	23.49
12	IGIVGATGQ	4	1.6000	19.28
13	LFSAGSAMS	68	1.6000	19.28
14	FNVVPLAGS	204	1.6000	19.28
15	LNTIQIAEL	331	1.4000	16.87
16	LRFESRKIL	227	1.1000	13.25
17	IALFSAGSA	66	1.0000	12.05
18	IGGAEQLVY	177	0.9000	10.84
19	LVGRIRRDP	300	0.9000	10.84
20	VVPLAGSLV	206	0.8000	9.64
21	LRKGAALNT	325	0.8000	9.64
22	LLVSGTCVR	240	0.6000	7.23
23	FESRKILGI	229	0.5000	6.02
24	ILGIPDLLV	234	0.5000	6.02
25	LVVSEVNFE	105	0.4000	4.82
26	VPLAGSLVD	207	0.2000	2.41
27	VFTGHSLSI	251	0.2000	2.41
28	FVSGDNLRK	319	0.2000	2.41
29	MGLSIGIVG	0	-0.1000	0
30	LSINAEFAQ	257	-0.1000	0
31	IAELLTADL	336	-0.3000	0
32	VGQVMRTLL	13	-0.4000	0
33	IVGATGQVG	6	-0.5000	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	VRLVVSSYQ	148	3.6700	40.33
2	VVSSYQAVS	151	3.4000	37.36
3	IQIAELLTA	334	3.1000	34.07
4	LVRLVVSSY	147	3.0700	33.74
5	IRRDPGVPD	304	3.0000	32.97
6	IAFNVVPLA	202	2.9000	31.87
7	LVYDGGALE	183	2.8000	30.77
8	VQLVDVPTP	282	2.8000	30.77
9	LVVSEVNFE	105	2.7100	29.78
10	VRFFASARS	31	2.6000	28.57
11	IGIVGATGQ	4	2.4000	26.37
12	LVSGTCVRV	241	2.3000	25.27
13	LVDVPTPLA	284	2.3000	25.27
14	LGIPDLLVS	235	2.1000	23.08
15	LLVSGTCVR	240	2.0000	21.98
16	VLHDEARLV	140	1.9000	20.88
17	LVDDGSGET	213	1.9000	20.88
18	LSIGIVGAT	2	1.8000	19.78
19	LRKGAALNT	325	1.7000	18.68
20	LFSAGSAMS	68	1.6000	17.58
21	LLDGATGVQ	275	1.6000	17.58
22	LAAAGVDES	291	1.3000	14.29
23	FNVVPLAGS	204	1.2000	13.19
24	LVVSSYQAV	150	1.1000	12.09
25	LRFESRKIL	227	1.1000	12.09
26	VFTGHSLSI	251	1.1000	12.09
27	VGRIRRDPG	301	1.1000	12.09
28	FVSGDNLRK	319	1.1000	12.09
29	VVPLAGSLV	206	1.0700	11.76
30	LSINAEFAQ	257	1.0000	10.99
31	LNTIQIAEL	331	1.0000	10.99

32	MGLSIGIVG	0	0.9000	9.89
33	MAAMPVLKV	132	0.7000	7.69
34	FFASARSQG	33	0.5700	6.26

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	VRFFASARS	31	3.4000	40.48
2	LVGRIRRDP	300	2.4000	28.57
3	IQIAELLTA	334	2.3000	27.38
4	LVRLVVSSY	147	1.5000	17.86
5	FNVVPLAGS	204	1.3000	15.48
6	FESRKILGI	229	1.3000	15.48
7	VVSSYQAVS	151	1.1000	13.10
8	FRGQEIEVE	46	1.0000	11.90
9	LRFESRKIL	227	0.9000	10.71
10	VRLVVSSYQ	148	0.8000	9.52
11	LGIPDLLVS	235	0.8000	9.52
12	MAAMPVLKV	132	0.7000	8.33
13	LFSAGSAMS	68	0.6000	7.14
14	LVVSEVNFE	105	0.6000	7.14
15	IAFNVVPLA	202	0.6000	7.14
16	YVAPIAFNV	198	0.5000	5.95
17	FPASAVRFF	26	0.3000	3.57
18	FVSGDNLRK	319	0.3000	3.57
19	IGIVGATGQ	4	-0.3000	0
20	LLVSGTCVR	240	-0.3000	0
21	VQLVDVPTP	282	-0.3000	0
22	FTGHSLSIN	252	-0.4000	0
23	VVPLAGSLV	206	-0.5000	0
24	LAAAGVDES	291	-0.6000	0
25	FFASARSQG	33	-0.7000	0
26	IALFSAGSA	66	-0.7000	0

27	MPVLKVLHD	135	-0.7000	0
28	VLHDEARLV	140	-0.7000	0
29	IVGATGQVG	6	-0.8000	0
30	VVSEVNFER	106	-0.8000	0
31	FERDAHRRP	112	-0.8000	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	VRFFASARS	31	3.8000	43.18
2	LVGRIRRDP	300	3.4000	38.64
3	LVRLVVSSY	147	2.8000	31.82
4	FRGQEIEVE	46	2.4000	27.27
5	IQIAELLTA	334	2.3000	26.14
6	FPASAVRFF	26	2.2000	25.00
7	FESRKILGI	229	2.2000	25.00
8	LVVSEVNFE	105	2.0000	22.73
9	LRFESRKIL	227	1.8600	21.14
10	MAAMPVLKV	132	1.7000	19.32
11	FNVVPLAGS	204	1.7000	19.32
12	VVSSYQAVS	151	1.5000	17.05
13	YVAPIAFNV	198	1.5000	17.05
14	LGIPDLLVS	235	1.2000	13.64
15	LLVSGTCVR	240	1.2000	13.64
16	LFSAGSAMS	68	1.0000	11.36
17	FAAAGVTVI	83	0.9000	10.23
18	FFASARSQG	33	0.7000	7.95
19	VVSEVNFER	106	0.7000	7.95
20	VQLVDVPTP	282	0.7000	7.95
21	IVGATGQVG	6	0.6000	6.82
22	IAFNVVPLA	202	0.6000	6.82
23	VVPLAGSLV	206	0.5000	5.68
24	MPVLKVLHD	135	0.4000	4.55

25	FTGHSLSIN	252	0.4000	4.55
26	FVSGDNLRK	319	0.4000	4.55
27	VLHDEARLV	140	0.3000	3.41
28	FASARSQGR	34	0.2000	2.27
29	FERDAHRRP	112	0.2000	2.27
30	VRLVVSSYQ	148	0.1000	1.14
31	IGGAEQLVY	177	0.1000	1.14

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFFASARS	31	4.4000	52.38
2	LVGRIRRDP	300	3.4000	40.48
3	IQIAELLTA	334	3.3000	39.29
4	LVRLVVSSY	147	2.5000	29.76
5	VVSSYQAVS	151	2.1000	25.00
6	LRFESRKIL	227	1.9000	22.62
7	VRLVVSSYQ	148	1.8000	21.43
8	LGIPDLLVS	235	1.8000	21.43
9	MAAMPVLKV	132	1.7000	20.24
10	LFSAGSAMS	68	1.6000	19.05
11	LVVSEVNFE	105	1.6000	19.05
12	IAFNVVPLA	202	1.6000	19.05
13	LSINAEFAQ	257	1.0000	11.90
14	IGIVGATGQ	4	0.7000	8.33
15	LLVSGTCVR	240	0.7000	8.33
16	VQLVDVPTP	282	0.7000	8.33
17	VVPLAGSLV	206	0.5000	5.95
18	LAAAGVDES	291	0.4000	4.76
19	IALFSAGSA	66	0.3000	3.57
20	MPVLKVLHD	135	0.3000	3.57
21	VLHDEARLV	140	0.3000	3.57
22	FNVVPLAGS	204	0.3000	3.57

23	FESRKILGI	229	0.3000	3.57
24	IVGATGQVG	6	0.2000	2.38
25	VVSEVNFER	106	0.2000	2.38
26	LVDVPTPLA	284	0.2000	2.38
27	LAEQARAVI	169	0.1000	1.19
28	VSGTCVRVP	242	-0.1000	0
29	LRKGAALNT	325	-0.1000	0
30	LNTIQIAEL	331	-0.1000	0
31	IGGAEQLVY	177	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFFASARS	31	3.4000	39.08
2	IQIAELLTA	334	3.4000	39.08
3	LVRLVVSSY	147	3.1000	35.63
4	MAAMPVLKV	132	3.0000	34.48
5	FNVVPLAGS	204	3.0000	34.48
6	VQLVDVPTP	282	2.4500	28.16
7	FESRKILGI	229	2.4000	27.59
8	MPVLKVLHD	135	2.2000	25.29
9	LGIPDLLVS	235	2.1000	24.14
10	VVSSYQAVS	151	1.4000	16.09
11	LNTIQIAEL	331	1.3600	15.63
12	FVSGDNLRK	319	1.3000	14.94
13	IGGAEQLVY	177	1.2000	13.79
14	FRGQEIEVE	46	1.1000	12.64
15	LLVSGTCVR	240	1.1000	12.64
16	LRFESRKIL	227	1.0600	12.18
17	LFSAGSAMS	68	1.0000	11.49
18	VRLVVSSYQ	148	1.0000	11.49
19	IAFNVVPLA	202	0.9500	10.92
20	LVDVPTPLA	284	0.9500	10.92

21	LVGRIRRDP	300	0.9000	10.34
22	LVVSEVNFE	105	0.8000	9.20
23	VVPLAGSLV	206	0.8000	9.20
24	FPASAVRFF	26	0.5000	5.75
25	FAAAGVTVI	83	0.5000	5.75
26	ILGIPDLLV	234	0.5000	5.75
27	LRKGAALNT	325	0.5000	5.75
28	MGLSIGIVG	0	0.3000	3.45
29	YVAPIAFNV	198	0.3000	3.45
30	VPLAGSLVD	207	0.3000	3.45
31	FFASARSQG	33	0.2000	2.30
32	VFTGHSLSI	251	0.1000	1.15

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFFASARS	31	4.8000	54.55
2	LVGRIRRDP	300	4.4000	50.00
3	LVRLVVSSY	147	3.8000	43.18
4	IQIAELLTA	334	3.3000	37.50
5	LVVSEVNFE	105	3.0000	34.09
6	LRFESRKIL	227	2.8600	32.50
7	MAAMPVLKV	132	2.7000	30.68
8	VVSSYQAVS	151	2.5000	28.41
9	LGIPDLLVS	235	2.2000	25.00
10	LLVSGTCVR	240	2.2000	25.00
11	LFSAGSAMS	68	2.0000	22.73
12	VVSEVNFER	106	1.7000	19.32
13	VQLVDVPTP	282	1.7000	19.32
14	IVGATGQVG	6	1.6000	18.18
15	IAFNVVPLA	202	1.6000	18.18
16	VVPLAGSLV	206	1.5000	17.05
17	FRGQEIEVE	46	1.4000	15.91

18	MPVLKVLHD	135	1.4000	15.91
19	VLHDEARLV	140	1.3000	14.77
20	FPASAVRFF	26	1.2000	13.64
21	FESRKILGI	229	1.2000	13.64
22	VRLVVSSYQ	148	1.1000	12.50
23	IGGAEQLVY	177	1.1000	12.50
24	LAEQARAVI	169	1.0000	11.36
25	LVSGTCVRV	241	1.0000	11.36
26	VSGTCVRVP	242	0.9000	10.23
27	LNTIQIAEL	331	0.8600	9.77
28	LAAAGVDES	291	0.8000	9.09
29	FNVVPLAGS	204	0.7000	7.95
30	VSSYQAVSG	152	0.6000	6.82
31	LRKGAALNT	325	0.6000	6.82
32	LVVSSYQAV	150	0.5000	5.68
33	LVYDGGALE	183	0.5000	5.68
34	YVAPIAFNV	198	0.5000	5.68

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	VRFFASARS	31	3.8000	43.18
2	LVGRIRRDP	300	3.4000	38.64
3	LVRLVVSSY	147	2.8000	31.82
4	FRGQEIEVE	46	2.4000	27.27
5	IQIAELLTA	334	2.3000	26.14
6	FPASAVRFF	26	2.2000	25.00
7	FESRKILGI	229	2.2000	25.00
8	LVVSEVNFE	105	2.0000	22.73
9	LRFESRKIL	227	1.8600	21.14
10	MAAMPVLKV	132	1.7000	19.32
11	FNVVPLAGS	204	1.7000	19.32
12	VVSSYQAVS	151	1.5000	17.05

13	YVAPIAFNV	198	1.5000	17.05
14	LGIPDLLVS	235	1.2000	13.64
15	LLVSGTCVR	240	1.2000	13.64
16	LFSAGSAMS	68	1.0000	11.36
17	FAAAGVTVI	83	0.9000	10.23
18	FFASARSQG	33	0.7000	7.95
19	VVSEVNFER	106	0.7000	7.95
20	VQLVDVPTP	282	0.7000	7.95
21	IVGATGQVG	6	0.6000	6.82
22	IAFNVVPLA	202	0.6000	6.82
23	VVPLAGSLV	206	0.5000	5.68
24	MPVLKVLHD	135	0.4000	4.55
25	FTGHSLSIN	252	0.4000	4.55
26	FVSGDNLRK	319	0.4000	4.55
27	VLHDEARLV	140	0.3000	3.41
28	FASARSQGR	34	0.2000	2.27
29	FERDAHRRP	112	0.2000	2.27
30	VRLVVSSYQ	148	0.1000	1.14
31	IGGAEQLVY	177	0.1000	1.14

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVVSEVNFE	105	4.6000	51.11
2	VRFFASARS	31	4.4000	48.89
3	LVGRIRRDP	300	3.8000	42.22
4	LVRLVVSSY	147	3.6000	40.00
5	IQIAELLTA	334	3.3000	36.67
6	FRGQEIEVE	46	3.0000	33.33
7	MPVLKVLHD	135	3.0000	33.33
8	LRFESRKIL	227	2.9000	32.22
9	VRLVVSSYQ	148	2.6000	28.89
10	VVSSYQAVS	151	2.1000	23.33

11	LVYDGGALE	183	2.1000	23.33
12	MAAMPVLKV	132	2.0000	22.22
13	VPLAGSLVD	207	1.8000	20.00
14	LGIPDLLVS	235	1.8000	20.00
15	LSINAEFAQ	257	1.8000	20.00
16	IRRDPGVPD	304	1.7000	18.89
17	LFSAGSAMS	68	1.6000	17.78
18	IAFNVVPLA	202	1.6000	17.78
19	IGIVGATGQ	4	1.5000	16.67
20	IVGATGQVG	6	1.5000	16.67
21	VQLVDVPTP	282	1.1000	12.22
22	LAFRGQEIE	44	1.0000	11.11
23	IGGAEQLVY	177	0.9000	10.00
24	LNTIQIAEL	331	0.9000	10.00
25	VVPLAGSLV	206	0.8000	8.89
26	LALFVSGDN	316	0.8000	8.89
27	LRKGAALNT	325	0.8000	8.89
28	LLVSGTCVR	240	0.7000	7.78
29	VLHDEARLV	140	0.6000	6.67
30	FTGHSLSIN	252	0.6000	6.67
31	VSSYQAVSG	152	0.5000	5.56
32	FESRKILGI	229	0.5000	5.56
33	VPVFTGHSL	249	0.4000	4.44
34	LAAAGVDES	291	0.4000	4.44

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	VRFFASARS	31	3.4000	39.08
2	IQIAELLTA	334	3.4000	39.08
3	LVRLVVSSY	147	3.1000	35.63
4	MAAMPVLKV	132	3.0000	34.48
5	FNVVPLAGS	204	3.0000	34.48

6	VQLVDVPTP	282	2.4500	28.16
7	FESRKILGI	229	2.4000	27.59
8	MPVLKVLHD	135	2.2000	25.29
9	LGIPDLLVS	235	2.1000	24.14
10	VVSSYQAVS	151	1.4000	16.09
11	LNTIQIAEL	331	1.3600	15.63
12	FVSGDNLRK	319	1.3000	14.94
13	IGGAEQLVY	177	1.2000	13.79
14	FRGQEIEVE	46	1.1000	12.64
15	LLVSGTCVR	240	1.1000	12.64
16	LRFESRKIL	227	1.0600	12.18
17	LFSAGSAMS	68	1.0000	11.49
18	VRLVVSSYQ	148	1.0000	11.49
19	IAFNVVPLA	202	0.9500	10.92
20	LVDVPTPLA	284	0.9500	10.92
21	LVGRIRRDP	300	0.9000	10.34
22	LVVSEVNFE	105	0.8000	9.20
23	VVPLAGSLV	206	0.8000	9.20
24	FPASAVRFF	26	0.5000	5.75
25	FAAAGVTVI	83	0.5000	5.75
26	ILGIPDLLV	234	0.5000	5.75
27	LRKGAALNT	325	0.5000	5.75
28	MGLSIGIVG	0	0.3000	3.45
29	YVAPIAFNV	198	0.3000	3.45
30	VPLAGSLVD	207	0.3000	3.45
31	FFASARSQG	33	0.2000	2.30
32	VFTGHSLSI	251	0.1000	1.15

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFFASARS	31	3.0000	44.12
2	FNVVPLAGS	204	2.6000	38.24

3	LVRLVVSSY	147	1.8000	26.47
4	VRLVVSSYQ	148	1.7000	25.00
5	IQIAELLTA	334	1.6000	23.53
6	VVSSYQAVS	151	1.0000	14.71
7	LFSAGSAMS	68	0.6000	8.82
8	LNTIQIAEL	331	0.4000	5.88
9	VQLVDVPTP	282	0.3000	4.41
10	MAAMPVLKV	132	0.2000	2.94
11	IALFSAGSA	66	-0.1000	0
12	LGIPDLLVS	235	-0.1000	0
13	IAFNVVPLA	202	-0.2000	0
14	VVPLAGSLV	206	-0.2000	0
15	LVDVPTPLA	284	-0.2000	0
16	FESRKILGI	229	-0.3000	0
17	LVGRIRRDP	300	-0.3000	0
18	LLVSGTCVR	240	-0.4000	0
19	IGIVGATGQ	4	-0.5000	0
20	LRFESRKIL	227	-0.5000	0
21	FVSGDNLRK	319	-0.6000	0
22	MPVLKVLHD	135	-0.7000	0
23	LVVSEVNFE	105	-0.9000	0
24	FFASARSQG	33	-1.2000	0
25	YVAPIAFNV	198	-1.2000	0
26	VGRIRRDPG	301	-1.3000	0
27	IAELLTADL	336	-1.3000	0
28	FRGQEIEVE	46	-1.4000	0
29	YQAVSGSGL	155	-1.4000	0
30	FAAAGVTVI	83	-1.5000	0
31	VTVIDNSSA	88	-1.5000	0
32	LAAAGVDES	291	-1.5000	0
33	IVGATGQVG	6	-1.6000	0

ALLELE: DRB1_1311	Threshold for 3 % with score:	Highest Score achievable by any peptide: 8.3

	2.0	

Rank	Sequence	At Position	Score	% of Highest Score
1	IQIAELLTA	334	4.4000	53.01
2	VRFFASARS	31	4.0000	48.19
3	MAAMPVLKV	132	3.0000	36.14
4	LVRLVVSSY	147	2.8000	33.73
5	VRLVVSSYQ	148	2.7000	32.53
6	LGIPDLLVS	235	2.7000	32.53
7	VQLVDVPTP	282	2.4500	29.52
8	MPVLKVLHD	135	2.1000	25.30
9	VVSSYQAVS	151	2.0000	24.10
10	IAFNVVPLA	202	1.9500	23.49
11	LVDVPTPLA	284	1.9500	23.49
12	IGIVGATGQ	4	1.6000	19.28
13	LFSAGSAMS	68	1.6000	19.28
14	FNVVPLAGS	204	1.6000	19.28
15	LNTIQIAEL	331	1.4000	16.87
16	LRFESRKIL	227	1.1000	13.25
17	IALFSAGSA	66	1.0000	12.05
18	IGGAEQLVY	177	0.9000	10.84
19	LVGRIRRDP	300	0.9000	10.84
20	VVPLAGSLV	206	0.8000	9.64
21	LRKGAALNT	325	0.8000	9.64
22	LLVSGTCVR	240	0.6000	7.23
23	FESRKILGI	229	0.5000	6.02
24	ILGIPDLLV	234	0.5000	6.02
25	LVVSEVNFE	105	0.4000	4.82
26	VPLAGSLVD	207	0.2000	2.41
27	VFTGHSLSI	251	0.2000	2.41
28	FVSGDNLRK	319	0.2000	2.41
29	MGLSIGIVG	0	-0.1000	0
30	LSINAEFAQ	257	-0.1000	0
31	IAELLTADL	336	-0.3000	0
32	VGQVMRTLL	13	-0.4000	0

33	IVGATGQVG	6	-0.5000	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	MPVLKVLHD	135	3.8000	42.70
2	IQIAELLTA	334	3.4000	38.20
3	VRFFASARS	31	3.0000	33.71
4	LVRLVVSSY	147	2.9000	32.58
5	FRGQEIEVE	46	2.7000	30.34
6	FNVVPLAGS	204	2.6000	29.21
7	VRLVVSSYQ	148	2.5000	28.09
8	LVVSEVNFE	105	2.4000	26.97
9	MAAMPVLKV	132	2.3000	25.84
10	VPLAGSLVD	207	1.9000	21.35
11	VQLVDVPTP	282	1.8500	20.79
12	FESRKILGI	229	1.7000	19.10
13	LGIPDLLVS	235	1.7000	19.10
14	IGIVGATGQ	4	1.4000	15.73
15	LNTIQIAEL	331	1.4000	15.73
16	LRFESRKIL	227	1.1000	12.36
17	VVSSYQAVS	151	1.0000	11.24
18	LAGVAELAE	163	1.0000	11.24
19	IGGAEQLVY	177	1.0000	11.24
20	IAFNVVPLA	202	0.9500	10.67
21	LVDVPTPLA	284	0.9500	10.67
22	LVYDGGALE	183	0.8000	8.99
23	LRKGAALNT	325	0.7000	7.87
24	LFSAGSAMS	68	0.6000	6.74
25	LALFVSGDN	316	0.5000	5.62
26	FVSGDNLRK	319	0.5000	5.62
27	LVGRIRRDP	300	0.3000	3.37
28	MGLSIGIVG	0	0.2000	2.25

29	FFASARSQG	33	0.1000	1.12
30	VVPLAGSLV	206	0.1000	1.12
31	IRRDPGVPD	304	-0.1000	0
32	IVGATGQVG	6	-0.2000	0

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	VRFFASARS	31	4.4000	52.38
2	LVGRIRRDP	300	3.4000	40.48
3	IQIAELLTA	334	3.3000	39.29
4	LVRLVVSSY	147	2.5000	29.76
5	VVSSYQAVS	151	2.1000	25.00
6	LRFESRKIL	227	1.9000	22.62
7	VRLVVSSYQ	148	1.8000	21.43
8	LGIPDLLVS	235	1.8000	21.43
9	MAAMPVLKV	132	1.7000	20.24
10	LFSAGSAMS	68	1.6000	19.05
11	LVVSEVNFE	105	1.6000	19.05
12	IAFNVVPLA	202	1.6000	19.05
13	LSINAEFAQ	257	1.0000	11.90
14	IGIVGATGQ	4	0.7000	8.33
15	LLVSGTCVR	240	0.7000	8.33
16	VQLVDVPTP	282	0.7000	8.33
17	VVPLAGSLV	206	0.5000	5.95
18	LAAAGVDES	291	0.4000	4.76
19	IALFSAGSA	66	0.3000	3.57
20	MPVLKVLHD	135	0.3000	3.57
21	VLHDEARLV	140	0.3000	3.57
22	FNVVPLAGS	204	0.3000	3.57
23	FESRKILGI	229	0.3000	3.57
24	IVGATGQVG	6	0.2000	2.38
25	VVSEVNFER	106	0.2000	2.38

26	LVDVPTPLA	284	0.2000	2.38
27	LAEQARAVI	169	0.1000	1.19
28	VSGTCVRVP	242	-0.1000	0
29	LRKGAALNT	325	-0.1000	0
30	LNTIQIAEL	331	-0.1000	0
31	IGGAEQLVY	177	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRFFASARS	31	3.4000	40.48
2	LVGRIRRDP	300	2.4000	28.57
3	IQIAELLTA	334	2.3000	27.38
4	LVRLVVSSY	147	1.5000	17.86
5	FNVVPLAGS	204	1.3000	15.48
6	FESRKILGI	229	1.3000	15.48
7	VVSSYQAVS	151	1.1000	13.10
8	FRGQEIEVE	46	1.0000	11.90
9	LRFESRKIL	227	0.9000	10.71
10	VRLVVSSYQ	148	0.8000	9.52
11	LGIPDLLVS	235	0.8000	9.52
12	MAAMPVLKV	132	0.7000	8.33
13	LFSAGSAMS	68	0.6000	7.14
14	LVVSEVNFE	105	0.6000	7.14
15	IAFNVVPLA	202	0.6000	7.14
16	YVAPIAFNV	198	0.5000	5.95
17	FPASAVRFF	26	0.3000	3.57
18	FVSGDNLRK	319	0.3000	3.57
19	IGIVGATGQ	4	-0.3000	0
20	LLVSGTCVR	240	-0.3000	0
21	VQLVDVPTP	282	-0.3000	0
22	FTGHSLSIN	252	-0.4000	0
23	VVPLAGSLV	206	-0.5000	0

24	LAAAGVDES	291	-0.6000	0
25	FFASARSQG	33	-0.7000	0
26	IALFSAGSA	66	-0.7000	0
27	MPVLKVLHD	135	-0.7000	0
28	VLHDEARLV	140	-0.7000	0
29	IVGATGQVG	6	-0.8000	0
30	VVSEVNFER	106	-0.8000	0
31	FERDAHRRP	112	-0.8000	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	VRFFASARS	31	4.8000	54.55
2	LVGRIRRDP	300	4.4000	50.00
3	LVRLVVSSY	147	3.8000	43.18
4	IQIAELLTA	334	3.3000	37.50
5	LVVSEVNFE	105	3.0000	34.09
6	LRFESRKIL	227	2.8600	32.50
7	MAAMPVLKV	132	2.7000	30.68
8	VVSSYQAVS	151	2.5000	28.41
9	LGIPDLLVS	235	2.2000	25.00
10	LLVSGTCVR	240	2.2000	25.00
11	LFSAGSAMS	68	2.0000	22.73
12	VVSEVNFER	106	1.7000	19.32
13	VQLVDVPTP	282	1.7000	19.32
14	IVGATGQVG	6	1.6000	18.18
15	IAFNVVPLA	202	1.6000	18.18
16	VVPLAGSLV	206	1.5000	17.05
17	FRGQEIEVE	46	1.4000	15.91
18	MPVLKVLHD	135	1.4000	15.91
19	VLHDEARLV	140	1.3000	14.77
20	FPASAVRFF	26	1.2000	13.64
21	FESRKILGI	229	1.2000	13.64

22	VRLVVSSYQ	148	1.1000	12.50
23	IGGAEQLVY	177	1.1000	12.50
24	LAEQARAVI	169	1.0000	11.36
25	LVSGTCVRV	241	1.0000	11.36
26	VSGTCVRVP	242	0.9000	10.23
27	LNTIQIAEL	331	0.8600	9.77
28	LAAAGVDES	291	0.8000	9.09
29	FNVVPLAGS	204	0.7000	7.95
30	VSSYQAVSG	152	0.6000	6.82
31	LRKGAALNT	325	0.6000	6.82
32	LVVSSYQAV	150	0.5000	5.68
33	LVYDGGALE	183	0.5000	5.68
34	YVAPIAFNV	198	0.5000	5.68

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	VRFFASARS	31	4.8000	54.55
2	LVGRIRRDP	300	4.4000	50.00
3	LVRLVVSSY	147	3.8000	43.18
4	IQIAELLTA	334	3.3000	37.50
5	LVVSEVNFE	105	3.0000	34.09
6	LRFESRKIL	227	2.8600	32.50
7	MAAMPVLKV	132	2.7000	30.68
8	VVSSYQAVS	151	2.5000	28.41
9	LGIPDLLVS	235	2.2000	25.00
10	LLVSGTCVR	240	2.2000	25.00
11	LFSAGSAMS	68	2.0000	22.73
12	VVSEVNFER	106	1.7000	19.32
13	VQLVDVPTP	282	1.7000	19.32
14	IVGATGQVG	6	1.6000	18.18
15	IAFNVVPLA	202	1.6000	18.18
16	VVPLAGSLV	206	1.5000	17.05

17	FRGQEIEVE	46	1.4000	15.91
18	MPVLKVLHD	135	1.4000	15.91
19	VLHDEARLV	140	1.3000	14.77
20	FPASAVRFF	26	1.2000	13.64
21	FESRKILGI	229	1.2000	13.64
22	VRLVVSSYQ	148	1.1000	12.50
23	IGGAEQLVY	177	1.1000	12.50
24	LAEQARAVI	169	1.0000	11.36
25	LVSGTCVRV	241	1.0000	11.36
26	VSGTCVRVP	242	0.9000	10.23
27	LNTIQIAEL	331	0.8600	9.77
28	LAAAGVDES	291	0.8000	9.09
29	FNVVPLAGS	204	0.7000	7.95
30	VSSYQAVSG	152	0.6000	6.82
31	LRKGAALNT	325	0.6000	6.82
32	LVVSSYQAV	150	0.5000	5.68
33	LVYDGGALE	183	0.5000	5.68
34	YVAPIAFNV	198	0.5000	5.68

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	VRFFASARS	31	5.7000	58.16
2	IQIAELLTA	334	4.8000	48.98
3	VVPLAGSLV	206	4.0000	40.82
4	VPVFTGHSL	249	4.0000	40.82
5	VFTGHSLSI	251	4.0000	40.82
6	LRKGAALNT	325	3.9000	39.80
7	LRFESRKIL	227	3.6000	36.73
8	ILGIPDLLV	234	3.6000	36.73
9	LGIPDLLVS	235	3.5000	35.71
10	IALFSAGSA	66	3.4000	34.69
11	MAAMPVLKV	132	2.9000	29.59

12	LVSGTCVRV	241	2.9000	29.59
13	VVSEVNFER	106	2.8000	28.57
14	LALFVSGDN	316	2.8000	28.57
15	VRLVVSSYQ	148	2.7000	27.55
16	LVVSSYQAV	150	2.7000	27.55
17	YVAPIAFNV	198	2.5000	25.51
18	MGLSIGIVG	0	2.4000	24.49
19	VGQVMRTLL	13	2.4000	24.49
20	LVRLVVSSY	147	2.4000	24.49
21	FVSGDNLRK	319	2.2000	22.45
22	FESRKILGI	229	2.1500	21.94
23	VTVIDNSSA	88	2.1000	21.43
24	LNTIQIAEL	331	1.9500	19.90
25	VSSYQAVSG	152	1.9000	19.39
26	LVGRIRRDP	300	1.9000	19.39
27	IVGATGQVG	6	1.7000	17.35
28	YQAVSGSGL	155	1.7000	17.35
29	VAPIAFNVV	199	1.6000	16.33
30	IIANPNCTT	123	1.4000	14.29
31	IRRDPGVPD	304	1.4000	14.29
32	LFSAGSAMS	68	1.3000	13.27
33	VQLVDVPTP	282	1.3000	13.27
34	VGRIRRDPG	301	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	VRFFASARS	31	4.7000	47.96
2	IQIAELLTA	334	3.8000	38.78
3	YVAPIAFNV	198	3.5000	35.71
4	FVSGDNLRK	319	3.2000	32.65
5	FESRKILGI	229	3.1500	32.14
6	VVPLAGSLV	206	3.0000	30.61

7	VPVFTGHSL	249	3.0000	30.61
8	VFTGHSLSI	251	3.0000	30.61
9	LRKGAALNT	325	2.9000	29.59
10	YQAVSGSGL	155	2.7000	27.55
11	LRFESRKIL	227	2.6000	26.53
12	ILGIPDLLV	234	2.6000	26.53
13	LGIPDLLVS	235	2.5000	25.51
14	IALFSAGSA	66	2.4000	24.49
15	WRKDPDVPL	97	2.2000	22.45
16	MAAMPVLKV	132	1.9000	19.39
17	LVSGTCVRV	241	1.9000	19.39
18	VVSEVNFER	106	1.8000	18.37
19	LALFVSGDN	316	1.8000	18.37
20	VRLVVSSYQ	148	1.7000	17.35
21	LVVSSYQAV	150	1.7000	17.35
22	MGLSIGIVG	0	1.4000	14.29
23	VGQVMRTLL	13	1.4000	14.29
24	LVRLVVSSY	147	1.4000	14.29
25	FNVVPLAGS	204	1.4000	14.29
26	VTVIDNSSA	88	1.1000	11.22
27	FFASARSQG	33	1.0000	10.20
28	LNTIQIAEL	331	0.9500	9.69
29	VSSYQAVSG	152	0.9000	9.18
30	LVGRIRRDP	300	0.9000	9.18
31	IVGATGQVG	6	0.7000	7.14
32	FAAAGVTVI	83	0.6000	6.12
33	VAPIAFNVV	199	0.6000	6.12
34	FTGHSLSIN	252	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	VRFFASARS	31	5.7000	58.16

2	IQIAELLTA	334	4.8000	48.98
3	VVPLAGSLV	206	4.0000	40.82
4	VPVFTGHSL	249	4.0000	40.82
5	VFTGHSLSI	251	4.0000	40.82
6	LRKGAALNT	325	3.9000	39.80
7	LRFESRKIL	227	3.6000	36.73
8	ILGIPDLLV	234	3.6000	36.73
9	LGIPDLLVS	235	3.5000	35.71
10	IALFSAGSA	66	3.4000	34.69
11	MAAMPVLKV	132	2.9000	29.59
12	LVSGTCVRV	241	2.9000	29.59
13	VVSEVNFER	106	2.8000	28.57
14	LALFVSGDN	316	2.8000	28.57
15	VRLVVSSYQ	148	2.7000	27.55
16	LVVSSYQAV	150	2.7000	27.55
17	YVAPIAFNV	198	2.5000	25.51
18	MGLSIGIVG	0	2.4000	24.49
19	VGQVMRTLL	13	2.4000	24.49
20	LVRLVVSSY	147	2.4000	24.49
21	FVSGDNLRK	319	2.2000	22.45
22	FESRKILGI	229	2.1500	21.94
23	VTVIDNSSA	88	2.1000	21.43
24	LNTIQIAEL	331	1.9500	19.90
25	VSSYQAVSG	152	1.9000	19.39
26	LVGRIRRDP	300	1.9000	19.39
27	IVGATGQVG	6	1.7000	17.35
28	YQAVSGSGL	155	1.7000	17.35
29	VAPIAFNVV	199	1.6000	16.33
30	IIANPNCTT	123	1.4000	14.29
31	IRRDPGVPD	304	1.4000	14.29
32	LFSAGSAMS	68	1.3000	13.27
33	VQLVDVPTP	282	1.3000	13.27
34	VGRIRRDPG	301	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	VRLVVSSYQ	148	3.3000	33.67
2	IGIVGATGQ	4	3.1000	31.63
3	YQAVSGSGL	155	3.1000	31.63
4	FASARSQGR	34	2.9000	29.59
5	VVSEVNFER	106	2.7000	27.55
6	FVSGDNLRK	319	2.7000	27.55
7	LVRLVVSSY	147	2.2000	22.45
8	IVGATGQVG	6	2.1000	21.43
9	FNVVPLAGS	204	2.1000	21.43
10	YVAPIAFNV	198	1.9000	19.39
11	LLVSGTCVR	240	1.7000	17.35
12	VRFFASARS	31	1.6000	16.33
13	LRFESRKIL	227	1.6000	16.33
14	MGLSIGIVG	0	1.3000	13.27
15	VVPLAGSLV	206	1.3000	13.27
16	IQIAELLTA	334	1.3000	13.27
17	FSAGSAMSK	69	1.2000	12.24
18	VMRTLLDER	16	1.1000	11.22
19	LNTIQIAEL	331	1.0000	10.20
20	VGQVMRTLL	13	0.9000	9.18
21	IDNSSAWRK	91	0.8000	8.16
22	LKVLHDEAR	138	0.8000	8.16
23	LFVSGDNLR	318	0.8000	8.16
24	LVVSSYQAV	150	0.6000	6.12
25	VPVFTGHSL	249	0.6000	6.12
26	INAEFAQPL	259	0.5000	5.10
27	MSKVQAPRF	75	0.4000	4.08
28	LEFPPPNTY	190	0.4000	4.08
29	LSPERAREL	267	0.3000	3.06
30	FPASAVRFF	26	0.2000	2.04

31	LFSAGSAMS	68	0.2000	2.04
32	FAAAGVTVI	83	0.2000	2.04
33	IGGAEQLVY	177	0.2000	2.04
34	VVSSYQAVS	151	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	VRLVVSSYQ	148	3.3000	33.67
2	IGIVGATGQ	4	3.1000	31.63
3	YQAVSGSGL	155	3.1000	31.63
4	FASARSQGR	34	2.9000	29.59
5	VVSEVNFER	106	2.7000	27.55
6	FVSGDNLRK	319	2.7000	27.55
7	LVRLVVSSY	147	2.2000	22.45
8	IVGATGQVG	6	2.1000	21.43
9	FNVVPLAGS	204	2.1000	21.43
10	YVAPIAFNV	198	1.9000	19.39
11	LLVSGTCVR	240	1.7000	17.35
12	VRFFASARS	31	1.6000	16.33
13	LRFESRKIL	227	1.6000	16.33
14	MGLSIGIVG	0	1.3000	13.27
15	VVPLAGSLV	206	1.3000	13.27
16	IQIAELLTA	334	1.3000	13.27
17	FSAGSAMSK	69	1.2000	12.24
18	VMRTLLDER	16	1.1000	11.22
19	LNTIQIAEL	331	1.0000	10.20
20	VGQVMRTLL	13	0.9000	9.18
21	IDNSSAWRK	91	0.8000	8.16
22	LKVLHDEAR	138	0.8000	8.16
23	LFVSGDNLR	318	0.8000	8.16
24	LVVSSYQAV	150	0.6000	6.12
25	VPVFTGHSL	249	0.6000	6.12

26	INAEFAQPL	259	0.5000	5.10
27	MSKVQAPRF	75	0.4000	4.08
28	LEFPPPNTY	190	0.4000	4.08
29	LSPERAREL	267	0.3000	3.06
30	FPASAVRFF	26	0.2000	2.04
31	LFSAGSAMS	68	0.2000	2.04
32	FAAAGVTVI	83	0.2000	2.04
33	IGGAEQLVY	177	0.2000	2.04
34	VVSSYQAVS	151	0.1000	1.02