MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Jan 27 00:24:44 2010
Length of input sequence	250 amino acids
Number of nanomers from input sequence	242
Number of nanomers with obligatory P1 anchor residue	71
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	25

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	WRHFIAMRA	191	2.5700	42.83
2	LRQLAAVAP	215	1.7000	28.33
3	IRRLAIECL	207	0.8000	13.33
4	FIAMRASEH	194	0.6000	10.00
5	LRHILTEAA	127	0.1000	1.67
6	YITGISRSC	80	-0.1100	0
7	LRRKQARQA	161	-0.1100	0
8	LVEFAGRAC	34	-0.2300	0
9	LRVQLIAKT	6	-0.3000	0
10	LAKLEAKFA	146	-0.3000	0
11	YVPEKDSRV	107	-0.6000	0
12	VQLIAKTDF	8	-0.6100	0
13	FSVLEHASV	69	-0.8000	0
14	YSQLSQRYV	100	-0.8100	0
15	FYITGISRS	79	-1.0000	0
16	LRHIIDVGH	60	-1.2000	0
17	LAIECLRQL	210	-1.3100	0

18	MRASEHADV	197	-1.4000	0
19	YRAWRHFIA	188	-1.5000	0
20	IECLRQLAA	212	-1.5000	0
21	LAAVAPAVF	218	-1.6500	0
22	FAGRACYQS	37	-1.7000	0
23	FADFEVTTL	226	-1.7300	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	LRQLAAVAP	215	2.7000	45.00
2	IRRLAIECL	207	1.8000	30.00
3	WRHFIAMRA	191	1.5700	26.17
4	LRHILTEAA	127	1.1000	18.33
5	IVVTGNYRA	182	1.0000	16.67
6	LRRKQARQA	161	0.8900	14.83
7	LVEFAGRAC	34	0.7700	12.83
8	LRVQLIAKT	6	0.7000	11.67
9	LAKLEAKFA	146	0.7000	11.67
10	FIAMRASEH	194	0.6000	10.00
11	VQLIAKTDF	8	0.3900	6.50
12	LRHIIDVGH	60	-0.2000	0
13	LAIECLRQL	210	-0.3100	0
14	MRASEHADV	197	-0.4000	0
15	IECLRQLAA	212	-0.5000	0
16	LAAVAPAVF	218	-0.6500	0
17	FSVLEHASV	69	-0.8000	0
18	ISRSCTHEL	84	-0.9000	0
19	FYITGISRS	79	-1.0000	0
20	YITGISRSC	80	-1.1100	0
21	VGHFSVLEH	66	-1.1200	0
22	VLEHASVSF	71	-1.2000	0
23	ILTEAADAA	130	-1.4000	0
24	VVVPPGMED	115	-1.4100	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	VQLIAKTDF	8	4.8000	50.53
2	LRHILTEAA	127	3.5000	36.84
3	IRRLAIECL	207	3.3600	35.37
4	MRASEHADV	197	3.1000	32.63
5	LRVQLIAKT	6	2.9000	30.53
6	VLPNATETR	173	2.6000	27.37
7	LIRHRHFSY	92	2.5000	26.32
8	FYITGISRS	79	2.2700	23.89
9	VEFAGRACY	35	2.2000	23.16
10	LRQLAAVAP	215	2.1000	22.11
11	VTGNYRAWR	184	1.9000	20.00
12	LEHASVSFY	72	1.8700	19.68
13	VSFYITGIS	77	1.5000	15.79
14	WRHFIAMRA	191	1.5000	15.79
15	VVVPPGMED	115	1.4000	14.74
16	LAAVAPAVF	218	1.4000	14.74
17	VFADFEVTT	225	1.4000	14.74
18	ITGISRSCT	81	1.2700	13.37
19	YLRHIIDVG	59	1.2000	12.63
20	IRHRHFSYS	93	1.1700	12.32
21	YQSWSKPNP	43	1.1000	11.58
22	ISRSCTHEL	84	1.0600	11.16
23	LRRKQARQA	161	1.0000	10.53
24	FSYSQLSQR	98	0.9700	10.21
25	IVVTGNYRA	182	0.9500	10.00

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	FYITGISRS	79	2.8700	31.54
2	LRHILTEAA	127	2.5000	27.47
3	WRHFIAMRA	191	2.5000	27.47
4	VQLIAKTDF	8	1.9000	20.88
5	YRAWRHFIA	188	1.6000	17.58
6	IRRLAIECL	207	1.4000	15.38
7	FIAMRASEH	194	1.2500	13.74
8	LRVQLIAKT	6	1.2000	13.19
9	YQSWSKPNP	43	1.1000	12.09
10	MRASEHADV	197	1.1000	12.09

11	YLRHIIDVG	59	0.8000	8.79
12	YITGISRSC	80	0.6000	6.59
13	FSYSQLSQR	98	0.4700	5.16
14	LIRHRHFSY	92	0.2000	2.20
15	VGHFSVLEH	66	0.1800	1.98
16	VSFYITGIS	77	0.1000	1.10
17	VLPNATETR	173	0.1000	1.10
18	LRQLAAVAP	215	0.1000	1.10
19	IVVTGNYRA	182	-0.0500	0
20	VEFAGRACY	35	-0.1000	0
21	ILRRKQARQ	160	-0.1000	0
22	FAGRACYQS	37	-0.1500	0
23	LRHIIDVGH	60	-0.2200	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	LRHILTEAA	127	3.9000	44.32
2	VQLIAKTDF	8	2.9000	32.95
3	IRRLAIECL	207	2.8000	31.82
4	LRVQLIAKT	6	2.2000	25.00
5	MRASEHADV	197	2.1000	23.86
6	VGHFSVLEH	66	1.6800	19.09
7	FYITGISRS	79	1.6000	18.18
8	VLPNATETR	173	1.5000	17.05
9	WRHFIAMRA	191	1.2000	13.64
10	LRQLAAVAP	215	0.9800	11.14
11	VEFAGRACY	35	0.9000	10.23
12	ISRSCTHEL	84	0.9000	10.23
13	ILRRKQARQ	160	0.9000	10.23
14	LRRKQARQA	161	0.7000	7.95
15	LRHIIDVGH	60	0.6600	7.50
16	VFADFEVTT	225	0.5800	6.59
17	IRHRHFSYS	93	0.5000	5.68
18	IAMRASEHA	195	0.5000	5.68
19	IECLRQLAA	212	0.5000	5.68
20	VTGNYRAWR	184	0.4000	4.55
21	LEHASVSFY	72	0.3000	3.41
22	ITGISRSCT	81	0.3000	3.41
23	YLRHIIDVG	59	0.1000	1.14

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	LRHILTEAA	127	3.9000	44.32
2	VQLIAKTDF	8	2.9000	32.95
3	IRRLAIECL	207	2.8000	31.82
4	LRVQLIAKT	6	2.2000	25.00
5	MRASEHADV	197	2.1000	23.86
6	VGHFSVLEH	66	1.6800	19.09
7	FYITGISRS	79	1.6000	18.18
8	VLPNATETR	173	1.5000	17.05
9	WRHFIAMRA	191	1.2000	13.64
10	LRQLAAVAP	215	0.9800	11.14
11	VEFAGRACY	35	0.9000	10.23
12	ISRSCTHEL	84	0.9000	10.23
13	ILRRKQARQ	160	0.9000	10.23
14	LRRKQARQA	161	0.7000	7.95
15	LRHIIDVGH	60	0.6600	7.50
16	VFADFEVTT	225	0.5800	6.59
17	IRHRHFSYS	93	0.5000	5.68
18	IAMRASEHA	195	0.5000	5.68
19	IECLRQLAA	212	0.5000	5.68
20	VTGNYRAWR	184	0.4000	4.55
21	LEHASVSFY	72	0.3000	3.41
22	ITGISRSCT	81	0.3000	3.41
23	YLRHIIDVG	59	0.1000	1.14

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	LRHILTEAA	127	3.9000	44.32
2	VQLIAKTDF	8	2.9000	32.95
3	IRRLAIECL	207	2.8000	31.82
4	LRVQLIAKT	6	2.2000	25.00
5	MRASEHADV	197	2.1000	23.86
6	VGHFSVLEH	66	1.6800	19.09
7	FYITGISRS	79	1.6000	18.18

8	VLPNATETR	173	1.5000	17.05
9	WRHFIAMRA	191	1.2000	13.64
10	LRQLAAVAP	215	0.9800	11.14
11	VEFAGRACY	35	0.9000	10.23
12	ISRSCTHEL	84	0.9000	10.23
13	ILRRKQARQ	160	0.9000	10.23
14	LRRKQARQA	161	0.7000	7.95
15	LRHIIDVGH	60	0.6600	7.50
16	VFADFEVTT	225	0.5800	6.59
17	IRHRHFSYS	93	0.5000	5.68
18	IAMRASEHA	195	0.5000	5.68
19	IECLRQLAA	212	0.5000	5.68
20	VTGNYRAWR	184	0.4000	4.55
21	LEHASVSFY	72	0.3000	3.41
22	ITGISRSCT	81	0.3000	3.41
23	YLRHIIDVG	59	0.1000	1.14

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	VQLIAKTDF	8	3.8000	40.00
2	FYITGISRS	79	3.2700	34.42
3	LRHILTEAA	127	2.5000	26.32
4	WRHFIAMRA	191	2.5000	26.32
5	IRRLAIECL	207	2.3600	24.84
6	YLRHIIDVG	59	2.2000	23.16
7	YQSWSKPNP	43	2.1000	22.11
8	MRASEHADV	197	2.1000	22.11
9	FSYSQLSQR	98	1.9700	20.74
10	LRVQLIAKT	6	1.9000	20.00
11	VLPNATETR	173	1.6000	16.84
12	YRAWRHFIA	188	1.6000	16.84
13	LIRHRHFSY	92	1.5000	15.79
14	VEFAGRACY	35	1.2000	12.63
15	LRQLAAVAP	215	1.1000	11.58
16	VTGNYRAWR	184	0.9000	9.47
17	LEHASVSFY	72	0.8700	9.16
18	FIAMRASEH	194	0.6700	7.05
19	YITGISRSC	80	0.6000	6.32
20	VSFYITGIS	77	0.5000	5.26

21	FSVLEHASV	69	0.4000	4.21
22	VVVPPGMED	115	0.4000	4.21
23	LAAVAPAVF	218	0.4000	4.21
24	VFADFEVTT	225	0.4000	4.21
25	ITGISRSCT	81	0.2700	2.84

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	LRHILTEAA	127	3.9000	44.32
2	VQLIAKTDF	8	2.9000	32.95
3	IRRLAIECL	207	2.8000	31.82
4	LRVQLIAKT	6	2.2000	25.00
5	MRASEHADV	197	2.1000	23.86
6	VGHFSVLEH	66	1.6800	19.09
7	FYITGISRS	79	1.6000	18.18
8	VLPNATETR	173	1.5000	17.05
9	WRHFIAMRA	191	1.2000	13.64
10	LRQLAAVAP	215	0.9800	11.14
11	VEFAGRACY	35	0.9000	10.23
12	ISRSCTHEL	84	0.9000	10.23
13	ILRRKQARQ	160	0.9000	10.23
14	LRRKQARQA	161	0.7000	7.95
15	LRHIIDVGH	60	0.6600	7.50
16	VFADFEVTT	225	0.5800	6.59
17	IRHRHFSYS	93	0.5000	5.68
18	IAMRASEHA	195	0.5000	5.68
19	IECLRQLAA	212	0.5000	5.68
20	VTGNYRAWR	184	0.4000	4.55
21	LEHASVSFY	72	0.3000	3.41
22	ITGISRSCT	81	0.3000	3.41
23	YLRHIIDVG	59	0.1000	1.14

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	LRHILTEAA	127	4.3000	50.00

2	FYITGISRS	79	3.5000	40.70
3	IVVTGNYRA	182	2.4000	27.91
4	VLPNATETR	173	2.3000	26.74
5	WRHFIAMRA	191	2.3000	26.74
6	YVPEKDSRV	107	1.9000	22.09
7	FIAMRASEH	194	1.8800	21.86
8	IRRLAIECL	207	1.8000	20.93
9	YLRHIIDVG	59	1.4000	16.28
10	LRHIIDVGH	60	1.2600	14.65
11	LRVQLIAKT	6	1.2000	13.95
12	ILTEAADAA	130	1.2000	13.95
13	ISRSCTHEL	84	1.1000	12.79
14	LRQLAAVAP	215	0.7800	9.07
15	VGHFSVLEH	66	0.4800	5.58
16	VLEHASVSF	71	-0.0200	0
17	MRASEHADV	197	-0.1000	0
18	FADQPNAIL	153	-0.2000	0
19	IAMRASEHA	195	-0.3000	0
20	LAKLEAKFA	146	-0.5000	0
21	YITGISRSC	80	-0.7000	0
22	VSFYITGIS	77	-0.8000	0
23	FEVTTLADG	229	-0.8000	0
24	IECLRQLAA	212	-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	LRRKQARQA	161	4.7000	48.96
2	IVVTGNYRA	182	4.3000	44.79
3	LRHILTEAA	127	3.1800	33.13
4	VGHFSVLEH	66	2.9800	31.04
5	IRHRHFSYS	93	2.6000	27.08
6	WRHFIAMRA	191	2.5000	26.04
7	IAMRASEHA	195	2.2000	22.92
8	YITGISRSC	80	2.1000	21.88
9	YRAWRHFIA	188	1.9000	19.79
10	FAGRACYQS	37	1.8000	18.75
11	ILRRKQARQ	160	1.7000	17.71
12	LRHIIDVGH	60	1.6600	17.29
13	LVEFAGRAC	34	1.4000	14.58

14	VLEHASVSF	71	1.2000	12.50
15	FYITGISRS	79	1.1000	11.46
16	LIRHRHFSY	92	1.1000	11.46
17	LRVQLIAKT	6	1.0000	10.42
18	ISRSCTHEL	84	0.8000	8.33
19	LIAKTDFLA	10	0.6000	6.25
20	VSFYITGIS	77	0.6000	6.25
21	VLPNATETR	173	0.6000	6.25
22	VVTGNYRAW	183	0.6000	6.25
23	LRQLAAVAP	215	0.5000	5.21
24	VPEKDSRVV	108	0.4000	4.17
25	FIAMRASEH	194	0.3800	3.96

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	LRHILTEAA	127	4.7000	53.41
2	WRHFIAMRA	191	3.1000	35.23
3	VGHFSVLEH	66	2.9800	33.86
4	IVVTGNYRA	182	2.8000	31.82
5	FIAMRASEH	194	2.4800	28.18
6	LRHIIDVGH	60	2.3800	27.05
7	IRRLAIECL	207	2.1000	23.86
8	LRQLAAVAP	215	1.8000	20.45
9	FYITGISRS	79	1.6000	18.18
10	VSFYITGIS	77	1.5000	17.05
11	LRVQLIAKT	6	1.4000	15.91
12	VLPNATETR	173	0.8000	9.09
13	LEHASVSFY	72	0.7000	7.95
14	LRRKQARQA	161	0.5000	5.68
15	VQLIAKTDF	8	0.3000	3.41
16	ISRSCTHEL	84	0.2000	2.27
17	IRHRHFSYS	93	0.1000	1.14
18	IECLRQLAA	212	-0.1000	0
19	LAKLEAKFA	146	-0.3000	0
20	YRAWRHFIA	188	-0.3000	0
21	LVEFAGRAC	34	-0.5000	0
22	LAAVAPAVF	218	-0.5000	0
23	MRASEHADV	197	-0.6000	0
24	IAMRASEHA	195	-0.7000	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	FIAMRASEH	194	4.7000	50.00
2	WRHFIAMRA	191	4.1000	43.62
3	LRHILTEAA	127	3.7000	39.36
4	VGHFSVLEH	66	3.2000	34.04
5	LRHIIDVGH	60	2.6000	27.66
6	FYITGISRS	79	2.6000	27.66
7	IRRLAIECL	207	2.1000	22.34
8	IVVTGNYRA	182	1.8000	19.15
9	LRVQLIAKT	6	1.3000	13.83
10	LRQLAAVAP	215	1.2000	12.77
11	FADFEVTTL	226	1.0000	10.64
12	LEHASVSFY	72	0.8000	8.51
13	YRAWRHFIA	188	0.7000	7.45
14	VSFYITGIS	77	0.5000	5.32
15	VVVPPGMED	115	0.5000	5.32
16	YVPEKDSRV	107	0.3000	3.19
17	VQLIAKTDF	8	0.2000	2.13
18	ISRSCTHEL	84	0.2000	2.13
19	VLPNATETR	173	-0.2000	0
20	YLRHIIDVG	59	-0.3000	0
21	YSELLAKLE	142	-0.5000	0
22	LRRKQARQA	161	-0.5000	0
23	FSVLEHASV	69	-0.6000	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	WRHFIAMRA	191	4.1000	46.59
2	LRHILTEAA	127	3.7000	42.05
3	FIAMRASEH	194	3.4800	39.55
4	FYITGISRS	79	2.6000	29.55
5	VGHFSVLEH	66	1.9800	22.50
6	IVVTGNYRA	182	1.8000	20.45
7	LRHIIDVGH	60	1.3800	15.68

8	IRRLAIECL	207	1.1000	12.50
9	LRQLAAVAP	215	0.8000	9.09
10	YRAWRHFIA	188	0.7000	7.95
11	VSFYITGIS	77	0.5000	5.68
12	LRVQLIAKT	6	0.4000	4.55
13	VLPNATETR	173	-0.2000	0
14	LEHASVSFY	72	-0.3000	0
15	LRRKQARQA	161	-0.5000	0
16	VQLIAKTDF	8	-0.7000	0
17	ISRSCTHEL	84	-0.8000	0
18	FSVLEHASV	69	-0.9000	0
19	IRHRHFSYS	93	-0.9000	0
20	FADQPNAIL	153	-1.0000	0
21	IECLRQLAA	212	-1.1000	0
22	YITGISRSC	80	-1.2000	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	LRHILTEAA	127	4.7000	50.00
2	VGHFSVLEH	66	4.2000	44.68
3	FIAMRASEH	194	3.7000	39.36
4	LRHIIDVGH	60	3.6000	38.30
5	WRHFIAMRA	191	3.1000	32.98
6	IRRLAIECL	207	3.1000	32.98
7	IVVTGNYRA	182	2.8000	29.79
8	LRVQLIAKT	6	2.3000	24.47
9	LRQLAAVAP	215	2.2000	23.40
10	LEHASVSFY	72	1.8000	19.15
11	FYITGISRS	79	1.6000	17.02
12	VSFYITGIS	77	1.5000	15.96
13	VVVPPGMED	115	1.5000	15.96
14	VQLIAKTDF	8	1.2000	12.77
15	ISRSCTHEL	84	1.2000	12.77
16	VLPNATETR	173	0.8000	8.51
17	LRRKQARQA	161	0.5000	5.32
18	LAAVAPAVF	218	0.4000	4.26
19	VVPPGMEDD	116	0.3000	3.19
20	IRHRHFSYS	93	0.1000	1.06
21	IECLRQLAA	212	-0.1000	0

22	LAKLEAKFA	146	-0.3000	0

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	LRHILTEAA	127	4.3000	47.78
2	FYITGISRS	79	3.9000	43.33
3	VLPNATETR	173	3.8000	42.22
4	YVPEKDSRV	107	2.9000	32.22
5	YLRHIIDVG	59	2.8000	31.11
6	IRRLAIECL	207	2.7600	30.67
7	IVVTGNYRA	182	2.4000	26.67
8	WRHFIAMRA	191	2.3000	25.56
9	ISRSCTHEL	84	2.0600	22.89
10	LRVQLIAKT	6	1.9000	21.11
11	VLEHASVSF	71	1.8800	20.89
12	LRQLAAVAP	215	1.7800	19.78
13	FIAMRASEH	194	1.3000	14.44
14	ILTEAADAA	130	1.2000	13.33
15	MRASEHADV	197	0.9000	10.00
16	FADQPNAIL	153	0.7600	8.44
17	LRHIIDVGH	60	0.6800	7.56
18	FEVTTLADG	229	0.6000	6.67
19	FSYSQLSQR	98	0.5000	5.56
20	VQLIAKTDF	8	0.4000	4.44
21	LEHASVSFY	72	0.3000	3.33
22	VGHFSVLEH	66	-0.1000	0
23	FSVLEHASV	69	-0.1000	0
24	LIRHRHFSY	92	-0.2000	0

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	LRHILTEAA	127	4.7000	53.41
2	WRHFIAMRA	191	3.1000	35.23
3	VGHFSVLEH	66	2.9800	33.86
4	IVVTGNYRA	182	2.8000	31.82

5	FIAMRASEH	194	2.4800	28.18
6	LRHIIDVGH	60	2.3800	27.05
7	IRRLAIECL	207	2.1000	23.86
8	LRQLAAVAP	215	1.8000	20.45
9	FYITGISRS	79	1.6000	18.18
10	VSFYITGIS	77	1.5000	17.05
11	LRVQLIAKT	6	1.4000	15.91
12	VLPNATETR	173	0.8000	9.09
13	LEHASVSFY	72	0.7000	7.95
14	LRRKQARQA	161	0.5000	5.68
15	VQLIAKTDF	8	0.3000	3.41
16	ISRSCTHEL	84	0.2000	2.27
17	IRHRHFSYS	93	0.1000	1.14
18	IECLRQLAA	212	-0.1000	0
19	LAKLEAKFA	146	-0.3000	0
20	YRAWRHFIA	188	-0.3000	0
21	LVEFAGRAC	34	-0.5000	0
22	LAAVAPAVF	218	-0.5000	0
23	MRASEHADV	197	-0.6000	0
24	IAMRASEHA	195	-0.7000	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	LRHILTEAA	127	4.3000	50.00
2	FYITGISRS	79	3.5000	40.70
3	IVVTGNYRA	182	2.4000	27.91
4	VLPNATETR	173	2.3000	26.74
5	WRHFIAMRA	191	2.3000	26.74
6	YVPEKDSRV	107	1.9000	22.09
7	FIAMRASEH	194	1.8800	21.86
8	IRRLAIECL	207	1.8000	20.93
9	YLRHIIDVG	59	1.4000	16.28
10	LRHIIDVGH	60	1.2600	14.65
11	LRVQLIAKT	6	1.2000	13.95
12	ILTEAADAA	130	1.2000	13.95
13	ISRSCTHEL	84	1.1000	12.79
14	LRQLAAVAP	215	0.7800	9.07
15	VGHFSVLEH	66	0.4800	5.58
16	VLEHASVSF	71	-0.0200	0

17	MRASEHADV	197	-0.1000	0
18	FADQPNAIL	153	-0.2000	0
19	IAMRASEHA	195	-0.3000	0
20	LAKLEAKFA	146	-0.5000	0
21	YITGISRSC	80	-0.7000	0
22	VSFYITGIS	77	-0.8000	0
23	FEVTTLADG	229	-0.8000	0
24	IECLRQLAA	212	-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	ISRSCTHEL	84	5.1200	44.14
2	IRRLAIECL	207	4.9000	42.24
3	WRHFIAMRA	191	4.4000	37.93
4	VQLIAKTDF	8	4.2000	36.21
5	IVVTGNYRA	182	4.1000	35.34
6	MRASEHADV	197	3.9000	33.62
7	FYITGISRS	79	3.4000	29.31
8	LRHILTEAA	127	3.3200	28.62
9	LIRHRHFSY	92	3.3000	28.45
10	FADFEVTTL	226	3.3000	28.45
11	VLEHASVSF	71	3.2000	27.59
12	IIDVGHFSV	63	3.0000	25.86
13	VAETAPLRV	0	2.9000	25.00
14	YRAWRHFIA	188	2.4000	20.69
15	LAIECLRQL	210	2.3000	19.83
16	VGHFSVLEH	66	2.0000	17.24
17	LAAVAPAVF	218	1.5000	12.93
18	LRHIIDVGH	60	1.4000	12.07
19	LRQLAAVAP	215	1.4000	12.07
20	YITGISRSC	80	1.3000	11.21
21	LRRKQARQA	161	1.3000	11.21
22	IAKTDFLAP	11	1.2000	10.34
23	LEHASVSFY	72	0.9000	7.76
24	YVPEKDSRV	107	0.9000	7.76
25	FIAMRASEH	194	0.9000	7.76

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	ISRSCTHEL	84	5.1200	44.14
2	IRRLAIECL	207	4.9000	42.24
3	WRHFIAMRA	191	4.4000	37.93
4	VQLIAKTDF	8	4.2000	36.21
5	IVVTGNYRA	182	4.1000	35.34
6	MRASEHADV	197	3.9000	33.62
7	FYITGISRS	79	3.4000	29.31
8	LRHILTEAA	127	3.3200	28.62
9	LIRHRHFSY	92	3.3000	28.45
10	FADFEVTTL	226	3.3000	28.45
11	VLEHASVSF	71	3.2000	27.59
12	IIDVGHFSV	63	3.0000	25.86
13	VAETAPLRV	0	2.9000	25.00
14	YRAWRHFIA	188	2.4000	20.69
15	LAIECLRQL	210	2.3000	19.83
16	VGHFSVLEH	66	2.0000	17.24
17	LAAVAPAVF	218	1.5000	12.93
18	LRHIIDVGH	60	1.4000	12.07
19	LRQLAAVAP	215	1.4000	12.07
20	YITGISRSC	80	1.3000	11.21
21	LRRKQARQA	161	1.3000	11.21
22	IAKTDFLAP	11	1.2000	10.34
23	LEHASVSFY	72	0.9000	7.76
24	YVPEKDSRV	107	0.9000	7.76
25	FIAMRASEH	194	0.9000	7.76

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	VEIRRLAIE	205	4.4000	51.16
2	ILRRKQARQ	160	4.0000	46.51
3	LRRKQARQA	161	3.6000	41.86
4	VSFYITGIS	77	2.7000	31.40
5	WRHFIAMRA	191	2.6000	30.23
6	FIAMRASEH	194	2.5000	29.07
7	VGHFSVLEH	66	2.4000	27.91

8	FAGRACYQS	37	2.1000	24.42
9	IRHRHFSYS	93	1.7000	19.77
10	FYITGISRS	79	1.5000	17.44
11	YRAWRHFIA	188	1.2000	13.95
12	LRVQLIAKT	6	1.1000	12.79
13	VEFAGRACY	35	1.0000	11.63
14	IRRLAIECL	207	0.9000	10.47
15	LLAKLEAKF	145	0.8000	9.30
16	YQSWSKPNP	43	0.6000	6.98
17	VVVPPGMED	115	0.6000	6.98
18	FSVLEHASV	69	0.4000	4.65
19	VQLIAKTDF	8	0.3000	3.49
20	IAMRASEHA	195	0.2000	2.33
21	LRHILTEAA	127	0.1000	1.16
22	FEVTTLADG	229	0.1000	1.16
23	LRQLAAVAP	215	-0.1000	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	LRRKQARQA	161	3.6000	45.00
2	ILRRKQARQ	160	3.2000	40.00
3	VSFYITGIS	77	2.7000	33.75
4	WRHFIAMRA	191	2.6000	32.50
5	FAGRACYQS	37	2.1000	26.25
6	IRHRHFSYS	93	1.7000	21.25
7	FYITGISRS	79	1.5000	18.75
8	VEIRRLAIE	205	1.4000	17.50
9	FIAMRASEH	194	1.2800	16.00
10	YRAWRHFIA	188	1.2000	15.00
11	VGHFSVLEH	66	1.1800	14.75
12	LSQRYVPEK	103	0.7000	8.75
13	LRVQLIAKT	6	0.2000	2.50
14	YQSWSKPNP	43	0.2000	2.50
15	IAMRASEHA	195	0.2000	2.50
16	FSVLEHASV	69	0.1000	1.25
17	LRHILTEAA	127	0.1000	1.25
18	VEFAGRACY	35	-0.1000	0
19	LLAKLEAKF	145	-0.1000	0
20	IRRLAIECL	207	-0.1000	0

21	LRQLAAVAP	215	-0.5000	0
22	VQLIAKTDF	8	-0.6000	0
23	YITGISRSC	80	-0.6000	0
24	MRASEHADV	197	-0.6000	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	LRRKQARQA	161	4.6000	57.50
2	ILRRKQARQ	160	4.2000	52.50
3	VSFYITGIS	77	3.7000	46.25
4	IRHRHFSYS	93	2.7000	33.75
5	VEIRRLAIE	205	2.4000	30.00
6	VGHFSVLEH	66	2.1800	27.25
7	LSQRYVPEK	103	1.7000	21.25
8	WRHFIAMRA	191	1.6000	20.00
9	LRVQLIAKT	6	1.2000	15.00
10	IAMRASEHA	195	1.2000	15.00
11	FAGRACYQS	37	1.1000	13.75
12	LRHILTEAA	127	1.1000	13.75
13	VEFAGRACY	35	0.9000	11.25
14	LLAKLEAKF	145	0.9000	11.25
15	IRRLAIECL	207	0.9000	11.25
16	FYITGISRS	79	0.5000	6.25
17	LRQLAAVAP	215	0.5000	6.25
18	VQLIAKTDF	8	0.4000	5.00
19	MRASEHADV	197	0.4000	5.00
20	FIAMRASEH	194	0.2800	3.50
21	VTGNYRAWR	184	0.2000	2.50
22	YRAWRHFIA	188	0.2000	2.50
23	IECLRQLAA	212	0.2000	2.50
24	LIAKTDFLA	10	0.1000	1.25
25	LVEFAGRAC	34	0.1000	1.25

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	VEIRRLAIE	205	5.4000	62.79
2	ILRRKQARQ	160	5.0000	58.14
3	LRRKQARQA	161	4.6000	53.49
4	VSFYITGIS	77	3.7000	43.02
5	VGHFSVLEH	66	3.4000	39.53
6	IRHRHFSYS	93	2.7000	31.40
7	LRVQLIAKT	6	2.1000	24.42
8	VEFAGRACY	35	2.0000	23.26
9	IRRLAIECL	207	1.9000	22.09
10	LLAKLEAKF	145	1.8000	20.93
11	VVVPPGMED	115	1.6000	18.60
12	WRHFIAMRA	191	1.6000	18.60
13	FIAMRASEH	194	1.5000	17.44
14	VQLIAKTDF	8	1.3000	15.12
15	IAMRASEHA	195	1.2000	13.95
16	FAGRACYQS	37	1.1000	12.79
17	LRHILTEAA	127	1.1000	12.79
18	LSQRYVPEK	103	1.0000	11.63
19	LRQLAAVAP	215	0.9000	10.47
20	MRASEHADV	197	0.7000	8.14
21	LAAVAPAVF	218	0.7000	8.14
22	LRHIIDVGH	60	0.5000	5.81
23	FYITGISRS	79	0.5000	5.81
24	VATSPLATE	240	0.5000	5.81
25	LEHASVSFY	72	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	WRHFIAMRA	191	3.6000	41.38
2	IRHRHFSYS	93	3.5000	40.23
3	FYITGISRS	79	3.3000	37.93
4	LRRKQARQA	161	3.3000	37.93
5	ILRRKQARQ	160	3.2000	36.78
6	FIAMRASEH	194	3.0800	35.40
7	FAGRACYQS	37	3.0000	34.48
8	VQLIAKTDF	8	2.2000	25.29
9	YRAWRHFIA	188	2.0500	23.56
10	VSFYITGIS	77	2.0000	22.99
11	IAMRASEHA	195	1.9000	21.84

12	LRHILTEAA	127	1.8000	20.69
13	VGHFSVLEH	66	1.7800	20.46
14	IRRLAIECL	207	1.6000	18.39
15	VEIRRLAIE	205	1.4000	16.09
16	LSQRYVPEK	103	0.9000	10.34
17	LRQLAAVAP	215	0.5000	5.75
18	YQSWSKPNP	43	0.4000	4.60
19	LRVQLIAKT	6	0.2000	2.30
20	FSVLEHASV	69	0.1000	1.15
21	LIAKTDFLA	10	-0.0500	0
22	VEFAGRACY	35	-0.1000	0
23	LLAKLEAKF	145	-0.1000	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	VEIRRLAIE	205	4.4000	43.56
2	VGHFSVLEH	66	4.2000	41.58
3	WRHFIAMRA	191	4.2000	41.58
4	ILRRKQARQ	160	4.0000	39.60
5	LRRKQARQA	161	3.8000	37.62
6	FAGRACYQS	37	2.8000	27.72
7	VSFYITGIS	77	2.8000	27.72
8	FIAMRASEH	194	2.5000	24.75
9	VVVPPGMED	115	2.2000	21.78
10	IRRLAIECL	207	2.0000	19.80
11	YQSWSKPNP	43	1.7500	17.33
12	IRHRHFSYS	93	1.7000	16.83
13	YRAWRHFIA	188	1.7000	16.83
14	FYITGISRS	79	1.5000	14.85
15	VQLIAKTDF	8	1.4000	13.86
16	IAMRASEHA	195	1.3000	12.87
17	LRHILTEAA	127	1.2000	11.88
18	LSQRYVPEK	103	1.1500	11.39
19	LRVQLIAKT	6	1.1000	10.89
20	VEFAGRACY	35	1.0000	9.90
21	IECLRQLAA	212	1.0000	9.90
22	LLAKLEAKF	145	0.8000	7.92
23	FSVLEHASV	69	0.4000	3.96
24	LRQLAAVAP	215	0.4000	3.96

25	YSELLAKLE	142	0.3000	2.97

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	WRHFIAMRA	191	4.1000	49.40
2	VGHFSVLEH	66	2.8800	34.70
3	FYITGISRS	79	1.9000	22.89
4	LRHILTEAA	127	1.8000	21.69
5	YRAWRHFIA	188	1.6000	19.28
6	IRRLAIECL	207	1.4000	16.87
7	IECLRQLAA	212	1.4000	16.87
8	YQSWSKPNP	43	1.2500	15.06
9	VQLIAKTDF	8	1.1000	13.25
10	LRRKQARQA	161	1.0000	12.05
11	FIAMRASEH	194	0.8800	10.60
12	LRVQLIAKT	6	0.8000	9.64
13	FSVLEHASV	69	0.5000	6.02
14	LRQLAAVAP	215	0.4000	4.82
15	ILRRKQARQ	160	0.2000	2.41
16	VEFAGRACY	35	-0.1000	0
17	VSFYITGIS	77	-0.1000	0
18	LAKLEAKFA	146	-0.1000	0
19	FAGRACYQS	37	-0.2000	0
20	MRASEHADV	197	-0.3000	0
21	YSQLSQRYV	100	-0.6000	0
22	LRHIIDVGH	60	-0.6200	0
23	LVEFAGRAC	34	-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	LRRKQARQA	161	4.9000	58.33
2	VGHFSVLEH	66	3.1800	37.86
3	LRVQLIAKT	6	2.8000	33.33
4	LIRHRHFSY	92	2.8000	33.33
5	YRAWRHFIA	188	2.4000	28.57

6	LVEFAGRAC	34	2.2000	26.19
7	WRHFIAMRA	191	2.2000	26.19
8	ILRRKQARQ	160	2.1000	25.00
9	IRRLAIECL	207	2.0000	23.81
10	LRHILTEAA	127	1.6000	19.05
11	LRQLAAVAP	215	1.2000	14.29
12	VQLIAKTDF	8	1.0000	11.90
13	IRHRHFSYS	93	1.0000	11.90
14	VEFAGRACY	35	0.9000	10.71
15	VSFYITGIS	77	0.9000	10.71
16	FYITGISRS	79	0.8000	9.52
17	MRASEHADV	197	0.8000	9.52
18	LAIECLRQL	210	0.8000	9.52
19	IVVTGNYRA	182	0.7000	8.33
20	YQSWSKPNP	43	0.6000	7.14
21	IECLRQLAA	212	0.6000	7.14
22	IAMRASEHA	195	0.5000	5.95
23	YLRHIIDVG	59	0.4000	4.76
24	LAKLEAKFA	146	0.4000	4.76
25	LSQRYVPEK	103	0.3000	3.57

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	VGHFSVLEH	66	3.8800	46.75
2	WRHFIAMRA	191	3.1000	37.35
3	LRHILTEAA	127	2.8000	33.73
4	IRRLAIECL	207	2.4000	28.92
5	IECLRQLAA	212	2.4000	28.92
6	VQLIAKTDF	8	2.1000	25.30
7	LRRKQARQA	161	2.0000	24.10
8	LRVQLIAKT	6	1.8000	21.69
9	LRQLAAVAP	215	1.4000	16.87
10	ILRRKQARQ	160	1.2000	14.46
11	IVVTGNYRA	182	1.0000	12.05
12	VEFAGRACY	35	0.9000	10.84
13	VSFYITGIS	77	0.9000	10.84
14	FYITGISRS	79	0.9000	10.84
15	LAKLEAKFA	146	0.9000	10.84
16	MRASEHADV	197	0.7000	8.43

17	YRAWRHFIA	188	0.6000	7.23
18	LRHIIDVGH	60	0.3800	4.58
19	YQSWSKPNP	43	0.2500	3.01
20	LVEFAGRAC	34	0.2000	2.41
21	VTGNYRAWR	184	0.2000	2.41
22	LAAVAPAVF	218	-0.1000	0
23	FIAMRASEH	194	-0.1200	0
24	LSQRYVPEK	103	-0.1500	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	VGHFSVLEH	66	3.8800	46.75
2	WRHFIAMRA	191	3.1000	37.35
3	LRHILTEAA	127	2.8000	33.73
4	IRRLAIECL	207	2.4000	28.92
5	IECLRQLAA	212	2.4000	28.92
6	VQLIAKTDF	8	2.1000	25.30
7	LRRKQARQA	161	2.0000	24.10
8	LRVQLIAKT	6	1.8000	21.69
9	LRQLAAVAP	215	1.4000	16.87
10	ILRRKQARQ	160	1.2000	14.46
11	IVVTGNYRA	182	1.0000	12.05
12	VEFAGRACY	35	0.9000	10.84
13	VSFYITGIS	77	0.9000	10.84
14	FYITGISRS	79	0.9000	10.84
15	LAKLEAKFA	146	0.9000	10.84
16	MRASEHADV	197	0.7000	8.43
17	YRAWRHFIA	188	0.6000	7.23
18	LRHIIDVGH	60	0.3800	4.58
19	YQSWSKPNP	43	0.2500	3.01
20	LVEFAGRAC	34	0.2000	2.41
21	VTGNYRAWR	184	0.2000	2.41
22	LAAVAPAVF	218	-0.1000	0
23	FIAMRASEH	194	-0.1200	0
24	LSQRYVPEK	103	-0.1500	0

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

DRB1_1107	score: 2.1	peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	LRHILTEAA	127	3.5000	38.46
2	VQLIAKTDF	8	2.9000	31.87
3	IRRLAIECL	207	2.4000	26.37
4	LRVQLIAKT	6	2.2000	24.18
5	MRASEHADV	197	2.1000	23.08
6	FYITGISRS	79	1.8700	20.55
7	WRHFIAMRA	191	1.5000	16.48
8	LIRHRHFSY	92	1.2000	13.19
9	VGHFSVLEH	66	1.1800	12.97
10	VSFYITGIS	77	1.1000	12.09
11	VLPNATETR	173	1.1000	12.09
12	LRQLAAVAP	215	1.1000	12.09
13	LRRKQARQA	161	1.0000	10.99
14	IVVTGNYRA	182	0.9500	10.44
15	VEFAGRACY	35	0.9000	9.89
16	ILRRKQARQ	160	0.9000	9.89
17	LRHIIDVGH	60	0.7800	8.57
18	IRHRHFSYS	93	0.7700	8.46
19	VFADFEVTT	225	0.7000	7.69
20	YRAWRHFIA	188	0.6000	6.59
21	LEHASVSFY	72	0.5700	6.26
22	ITGISRSCT	81	0.5700	6.26
23	VTGNYRAWR	184	0.4000	4.40
24	LSQRYVPEK	103	0.3000	3.30
25	VVVPPGMED	115	0.3000	3.30

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	LRRKQARQA	161	3.9000	46.43
2	YRAWRHFIA	188	3.4000	40.48
3	WRHFIAMRA	191	3.2000	38.10
4	VGHFSVLEH	66	2.1800	25.95
5	LRVQLIAKT	6	1.8000	21.43
6	FYITGISRS	79	1.8000	21.43
7	LIRHRHFSY	92	1.8000	21.43
8	YQSWSKPNP	43	1.6000	19.05

9	YLRHIIDVG	59	1.4000	16.67
10	LVEFAGRAC	34	1.2000	14.29
11	ILRRKQARQ	160	1.1000	13.10
12	FIAMRASEH	194	1.0800	12.86
13	IRRLAIECL	207	1.0000	11.90
14	FAGRACYQS	37	0.9000	10.71
15	YITGISRSC	80	0.7000	8.33
16	LRHILTEAA	127	0.6000	7.14
17	YSQLSQRYV	100	0.3000	3.57
18	LRQLAAVAP	215	0.2000	2.38
19	VEFAGRACY	35	-0.1000	0
20	VSFYITGIS	77	-0.1000	0
21	FSVLEHASV	69	-0.2000	0
22	MRASEHADV	197	-0.2000	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	LRRKQARQA	161	3.9000	44.32
2	YRAWRHFIA	188	3.4000	38.64
3	WRHFIAMRA	191	3.2000	36.36
4	LIRHRHFSY	92	3.1000	35.23
5	YLRHIIDVG	59	2.8000	31.82
6	YQSWSKPNP	43	2.6000	29.55
7	LRVQLIAKT	6	2.5000	28.41
8	FYITGISRS	79	2.2000	25.00
9	IRRLAIECL	207	1.9600	22.27
10	VQLIAKTDF	8	1.9000	21.59
11	VGHFSVLEH	66	1.6000	18.18
12	FAGRACYQS	37	1.3000	14.77
13	YSQLSQRYV	100	1.3000	14.77
14	LVEFAGRAC	34	1.2000	13.64
15	VEFAGRACY	35	1.2000	13.64
16	LRQLAAVAP	215	1.2000	13.64
17	VLEHASVSF	71	1.0000	11.36
18	FSVLEHASV	69	0.8000	9.09
19	VTGNYRAWR	184	0.8000	9.09
20	MRASEHADV	197	0.8000	9.09
21	LAIECLRQL	210	0.7600	8.64
22	YITGISRSC	80	0.7000	7.95

23	VLPNATETR	173	0.7000	7.95
24	VEIRRLAIE	205	0.7000	7.95
25	LRHILTEAA	127	0.6000	6.82

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	LRRKQARQA	161	4.9000	58.33
2	VGHFSVLEH	66	3.1800	37.86
3	LRVQLIAKT	6	2.8000	33.33
4	LIRHRHFSY	92	2.8000	33.33
5	YRAWRHFIA	188	2.4000	28.57
6	LVEFAGRAC	34	2.2000	26.19
7	WRHFIAMRA	191	2.2000	26.19
8	ILRRKQARQ	160	2.1000	25.00
9	IRRLAIECL	207	2.0000	23.81
10	LRHILTEAA	127	1.6000	19.05
11	LRQLAAVAP	215	1.2000	14.29
12	VQLIAKTDF	8	1.0000	11.90
13	IRHRHFSYS	93	1.0000	11.90
14	VEFAGRACY	35	0.9000	10.71
15	VSFYITGIS	77	0.9000	10.71
16	FYITGISRS	79	0.8000	9.52
17	MRASEHADV	197	0.8000	9.52
18	LAIECLRQL	210	0.8000	9.52
19	IVVTGNYRA	182	0.7000	8.33
20	YQSWSKPNP	43	0.6000	7.14
21	IECLRQLAA	212	0.6000	7.14
22	IAMRASEHA	195	0.5000	5.95
23	YLRHIIDVG	59	0.4000	4.76
24	LAKLEAKFA	146	0.4000	4.76
25	LSQRYVPEK	103	0.3000	3.57

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	WRHFIAMRA	191	4.1000	47.13

2	VQLIAKTDF	8	3.0000	34.48
3	IRRLAIECL	207	2.3600	27.13
4	VGHFSVLEH	66	2.3000	26.44
5	FYITGISRS	79	2.3000	26.44
6	YQSWSKPNP	43	2.2500	25.86
7	LRHILTEAA	127	1.8000	20.69
8	YRAWRHFIA	188	1.6000	18.39
9	LRVQLIAKT	6	1.5000	17.24
10	FSVLEHASV	69	1.5000	17.24
11	IECLRQLAA	212	1.4000	16.09
12	LRQLAAVAP	215	1.4000	16.09
13	VEFAGRACY	35	1.2000	13.79
14	LRRKQARQA	161	1.0000	11.49
15	LAAVAPAVF	218	0.8000	9.20
16	VTGNYRAWR	184	0.7000	8.05
17	MRASEHADV	197	0.7000	8.05
18	FEVTTLADG	229	0.6000	6.90
19	YSQLSQRYV	100	0.4000	4.60
20	VSFYITGIS	77	0.3000	3.45
21	VLPNATETR	173	0.3000	3.45
22	FIAMRASEH	194	0.3000	3.45
23	FAGRACYQS	37	0.2000	2.30

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	LRRKQARQA	161	4.9000	55.68
2	LIRHRHFSY	92	4.1000	46.59
3	LRVQLIAKT	6	3.5000	39.77
4	IRRLAIECL	207	2.9600	33.64
5	VQLIAKTDF	8	2.9000	32.95
6	VGHFSVLEH	66	2.6000	29.55
7	YRAWRHFIA	188	2.4000	27.27
8	LVEFAGRAC	34	2.2000	25.00
9	VEFAGRACY	35	2.2000	25.00
10	WRHFIAMRA	191	2.2000	25.00
11	LRQLAAVAP	215	2.2000	25.00
12	VLEHASVSF	71	2.0000	22.73
13	YLRHIIDVG	59	1.8000	20.45
14	VTGNYRAWR	184	1.8000	20.45

15	MRASEHADV	197	1.8000	20.45
16	LAIECLRQL	210	1.7600	20.00
17	VLPNATETR	173	1.7000	19.32
18	VEIRRLAIE	205	1.7000	19.32
19	YQSWSKPNP	43	1.6000	18.18
20	LRHILTEAA	127	1.6000	18.18
21	IRHRHFSYS	93	1.4000	15.91
22	ILRRKQARQ	160	1.4000	15.91
23	VSFYITGIS	77	1.3000	14.77
24	LLAKLEAKF	145	1.3000	14.77
25	FYITGISRS	79	1.2000	13.64

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	LRRKQARQA	161	3.9000	44.32
2	YRAWRHFIA	188	3.4000	38.64
3	WRHFIAMRA	191	3.2000	36.36
4	LIRHRHFSY	92	3.1000	35.23
5	YLRHIIDVG	59	2.8000	31.82
6	YQSWSKPNP	43	2.6000	29.55
7	LRVQLIAKT	6	2.5000	28.41
8	FYITGISRS	79	2.2000	25.00
9	IRRLAIECL	207	1.9600	22.27
10	VQLIAKTDF	8	1.9000	21.59
11	VGHFSVLEH	66	1.6000	18.18
12	FAGRACYQS	37	1.3000	14.77
13	YSQLSQRYV	100	1.3000	14.77
14	LVEFAGRAC	34	1.2000	13.64
15	VEFAGRACY	35	1.2000	13.64
16	LRQLAAVAP	215	1.2000	13.64
17	VLEHASVSF	71	1.0000	11.36
18	FSVLEHASV	69	0.8000	9.09
19	VTGNYRAWR	184	0.8000	9.09
20	MRASEHADV	197	0.8000	9.09
21	LAIECLRQL	210	0.7600	8.64
22	YITGISRSC	80	0.7000	7.95
23	VLPNATETR	173	0.7000	7.95
24	VEIRRLAIE	205	0.7000	7.95
25	LRHILTEAA	127	0.6000	6.82

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	LRRKQARQA	161	4.9000	54.44
2	VGHFSVLEH	66	4.4000	48.89
3	LIRHRHFSY	92	3.9000	43.33
4	LRVQLIAKT	6	3.7000	41.11
5	VEIRRLAIE	205	3.3000	36.67
6	IRRLAIECL	207	3.0000	33.33
7	ILRRKQARQ	160	2.9000	32.22
8	YRAWRHFIA	188	2.4000	26.67
9	LVEFAGRAC	34	2.2000	24.44
10	WRHFIAMRA	191	2.2000	24.44
11	VEFAGRACY	35	2.0000	22.22
12	VQLIAKTDF	8	1.9000	21.11
13	LAIECLRQL	210	1.8000	20.00
14	YLRHIIDVG	59	1.7000	18.89
15	LRHILTEAA	127	1.6000	17.78
16	LRQLAAVAP	215	1.6000	17.78
17	VVVPPGMED	115	1.4000	15.56
18	FIAMRASEH	194	1.3000	14.44
19	MRASEHADV	197	1.1000	12.22
20	YQSWSKPNP	43	1.0000	11.11
21	VLEHASVSF	71	1.0000	11.11
22	IRHRHFSYS	93	1.0000	11.11
23	VSFYITGIS	77	0.9000	10.00
24	ISRSCTHEL	84	0.9000	10.00
25	VATSPLATE	240	0.9000	10.00

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

Rank	Sequence	At Position	Score	% of Highest Score
1	WRHFIAMRA	191	4.1000	47.13
2	VQLIAKTDF	8	3.0000	34.48
3	IRRLAIECL	207	2.3600	27.13
4	VGHFSVLEH	66	2.3000	26.44
5	FYITGISRS	79	2.3000	26.44

6	YQSWSKPNP	43	2.2500	25.86
7	LRHILTEAA	127	1.8000	20.69
8	YRAWRHFIA	188	1.6000	18.39
9	LRVQLIAKT	6	1.5000	17.24
10	FSVLEHASV	69	1.5000	17.24
11	IECLRQLAA	212	1.4000	16.09
12	LRQLAAVAP	215	1.4000	16.09
13	VEFAGRACY	35	1.2000	13.79
14	LRRKQARQA	161	1.0000	11.49
15	LAAVAPAVF	218	0.8000	9.20
16	VTGNYRAWR	184	0.7000	8.05
17	MRASEHADV	197	0.7000	8.05
18	FEVTTLADG	229	0.6000	6.90
19	YSQLSQRYV	100	0.4000	4.60
20	VSFYITGIS	77	0.3000	3.45
21	VLPNATETR	173	0.3000	3.45
22	FIAMRASEH	194	0.3000	3.45
23	FAGRACYQS	37	0.2000	2.30

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	WRHFIAMRA	191	2.5000	36.76
2	FYITGISRS	79	1.9000	27.94
3	YRAWRHFIA	188	1.1000	16.18
4	VGHFSVLEH	66	1.0800	15.88
5	FIAMRASEH	194	0.8800	12.94
6	LRVQLIAKT	6	0.8000	11.76
7	LRRKQARQA	161	0.8000	11.76
8	LRHILTEAA	127	0.7000	10.29
9	FSVLEHASV	69	0.5000	7.35
10	IRRLAIECL	207	0.3000	4.41
11	ILRRKQARQ	160	0.2000	2.94
12	YQSWSKPNP	43	0.1000	1.47
13	VEFAGRACY	35	-0.1000	0
14	LRQLAAVAP	215	-0.1000	0
15	VSFYITGIS	77	-0.2000	0
16	MRASEHADV	197	-0.3000	0
17	IECLRQLAA	212	-0.4000	0
18	LAKLEAKFA	146	-0.7000	0

19	IVVTGNYRA	182	-0.7000	0
20	YSQLSQRYV	100	-0.8000	0
21	VTGNYRAWR	184	-0.8000	0
22	FEVTTLADG	229	-0.8000	0
23	FAGRACYQS	37	-0.9000	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	VGHFSVLEH	66	3.8800	46.75
2	WRHFIAMRA	191	3.1000	37.35
3	LRHILTEAA	127	2.8000	33.73
4	IRRLAIECL	207	2.4000	28.92
5	IECLRQLAA	212	2.4000	28.92
6	VQLIAKTDF	8	2.1000	25.30
7	LRRKQARQA	161	2.0000	24.10
8	LRVQLIAKT	6	1.8000	21.69
9	LRQLAAVAP	215	1.4000	16.87
10	ILRRKQARQ	160	1.2000	14.46
11	IVVTGNYRA	182	1.0000	12.05
12	VEFAGRACY	35	0.9000	10.84
13	VSFYITGIS	77	0.9000	10.84
14	FYITGISRS	79	0.9000	10.84
15	LAKLEAKFA	146	0.9000	10.84
16	MRASEHADV	197	0.7000	8.43
17	YRAWRHFIA	188	0.6000	7.23
18	LRHIIDVGH	60	0.3800	4.58
19	YQSWSKPNP	43	0.2500	3.01
20	LVEFAGRAC	34	0.2000	2.41
21	VTGNYRAWR	184	0.2000	2.41
22	LAAVAPAVF	218	-0.1000	0
23	FIAMRASEH	194	-0.1200	0
24	LSQRYVPEK	103	-0.1500	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	VGHFSVLEH	66	4.1000	46.07
2	WRHFIAMRA	191	4.1000	46.07
3	IRRLAIECL	207	2.4000	26.97
4	FIAMRASEH	194	2.1000	23.60
5	VQLIAKTDF	8	2.0000	22.47
6	FYITGISRS	79	1.9000	21.35
7	LRHILTEAA	127	1.8000	20.22
8	LRVQLIAKT	6	1.7000	19.10
9	YQSWSKPNP	43	1.6500	18.54
10	YRAWRHFIA	188	1.6000	17.98
11	VVVPPGMED	115	1.5000	16.85
12	VEIRRLAIE	205	1.4000	15.73
13	IECLRQLAA	212	1.4000	15.73
14	VEFAGRACY	35	1.0000	11.24
15	ILRRKQARQ	160	1.0000	11.24
16	LRRKQARQA	161	1.0000	11.24
17	FSVLEHASV	69	0.8000	8.99
18	LRQLAAVAP	215	0.8000	8.99
19	YSELLAKLE	142	0.7000	7.87
20	LRHIIDVGH	60	0.6000	6.74
21	FEVTTLADG	229	0.5000	5.62
22	VSFYITGIS	77	-0.1000	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	LRRKQARQA	161	4.9000	58.33
2	VGHFSVLEH	66	3.1800	37.86
3	LRVQLIAKT	6	2.8000	33.33
4	LIRHRHFSY	92	2.8000	33.33
5	YRAWRHFIA	188	2.4000	28.57
6	LVEFAGRAC	34	2.2000	26.19
7	WRHFIAMRA	191	2.2000	26.19
8	ILRRKQARQ	160	2.1000	25.00
9	IRRLAIECL	207	2.0000	23.81
10	LRHILTEAA	127	1.6000	19.05
11	LRQLAAVAP	215	1.2000	14.29
12	VQLIAKTDF	8	1.0000	11.90
13	IRHRHFSYS	93	1.0000	11.90
14	VEFAGRACY	35	0.9000	10.71

15	VSFYITGIS	77	0.9000	10.71
16	FYITGISRS	79	0.8000	9.52
17	MRASEHADV	197	0.8000	9.52
18	LAIECLRQL	210	0.8000	9.52
19	IVVTGNYRA	182	0.7000	8.33
20	YQSWSKPNP	43	0.6000	7.14
21	IECLRQLAA	212	0.6000	7.14
22	IAMRASEHA	195	0.5000	5.95
23	YLRHIIDVG	59	0.4000	4.76
24	LAKLEAKFA	146	0.4000	4.76
25	LSQRYVPEK	103	0.3000	3.57

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	LRRKQARQA	161	3.9000	46.43
2	YRAWRHFIA	188	3.4000	40.48
3	WRHFIAMRA	191	3.2000	38.10
4	VGHFSVLEH	66	2.1800	25.95
5	LRVQLIAKT	6	1.8000	21.43
6	FYITGISRS	79	1.8000	21.43
7	LIRHRHFSY	92	1.8000	21.43
8	YQSWSKPNP	43	1.6000	19.05
9	YLRHIIDVG	59	1.4000	16.67
10	LVEFAGRAC	34	1.2000	14.29
11	ILRRKQARQ	160	1.1000	13.10
12	FIAMRASEH	194	1.0800	12.86
13	IRRLAIECL	207	1.0000	11.90
14	FAGRACYQS	37	0.9000	10.71
15	YITGISRSC	80	0.7000	8.33
16	LRHILTEAA	127	0.6000	7.14
17	YSQLSQRYV	100	0.3000	3.57
18	LRQLAAVAP	215	0.2000	2.38
19	VEFAGRACY	35	-0.1000	0
20	VSFYITGIS	77	-0.1000	0
21	FSVLEHASV	69	-0.2000	0
22	MRASEHADV	197	-0.2000	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	LRRKQARQA	161	4.9000	55.68
2	LIRHRHFSY	92	4.1000	46.59
3	LRVQLIAKT	6	3.5000	39.77
4	IRRLAIECL	207	2.9600	33.64
5	VQLIAKTDF	8	2.9000	32.95
6	VGHFSVLEH	66	2.6000	29.55
7	YRAWRHFIA	188	2.4000	27.27
8	LVEFAGRAC	34	2.2000	25.00
9	VEFAGRACY	35	2.2000	25.00
10	WRHFIAMRA	191	2.2000	25.00
11	LRQLAAVAP	215	2.2000	25.00
12	VLEHASVSF	71	2.0000	22.73
13	YLRHIIDVG	59	1.8000	20.45
14	VTGNYRAWR	184	1.8000	20.45
15	MRASEHADV	197	1.8000	20.45
16	LAIECLRQL	210	1.7600	20.00
17	VLPNATETR	173	1.7000	19.32
18	VEIRRLAIE	205	1.7000	19.32
19	YQSWSKPNP	43	1.6000	18.18
20	LRHILTEAA	127	1.6000	18.18
21	IRHRHFSYS	93	1.4000	15.91
22	ILRRKQARQ	160	1.4000	15.91
23	VSFYITGIS	77	1.3000	14.77
24	LLAKLEAKF	145	1.3000	14.77
25	FYITGISRS	79	1.2000	13.64

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	LRRKQARQA	161	4.9000	55.68
2	LIRHRHFSY	92	4.1000	46.59
3	LRVQLIAKT	6	3.5000	39.77
4	IRRLAIECL	207	2.9600	33.64
5	VQLIAKTDF	8	2.9000	32.95
6	VGHFSVLEH	66	2.6000	29.55
7	YRAWRHFIA	188	2.4000	27.27

8	LVEFAGRAC	34	2.2000	25.00
9	VEFAGRACY	35	2.2000	25.00
10	WRHFIAMRA	191	2.2000	25.00
11	LRQLAAVAP	215	2.2000	25.00
12	VLEHASVSF	71	2.0000	22.73
13	YLRHIIDVG	59	1.8000	20.45
14	VTGNYRAWR	184	1.8000	20.45
15	MRASEHADV	197	1.8000	20.45
16	LAIECLRQL	210	1.7600	20.00
17	VLPNATETR	173	1.7000	19.32
18	VEIRRLAIE	205	1.7000	19.32
19	YQSWSKPNP	43	1.6000	18.18
20	LRHILTEAA	127	1.6000	18.18
21	IRHRHFSYS	93	1.4000	15.91
22	ILRRKQARQ	160	1.4000	15.91
23	VSFYITGIS	77	1.3000	14.77
24	LLAKLEAKF	145	1.3000	14.77
25	FYITGISRS	79	1.2000	13.64

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	WRHFIAMRA	191	5.5000	56.12
2	IVVTGNYRA	182	3.7000	37.76
3	VGHFSVLEH	66	3.6000	36.73
4	LVEFAGRAC	34	3.3000	33.67
5	IRRLAIECL	207	3.2500	33.16
6	LIRHRHFSY	92	2.9000	29.59
7	VSFYITGIS	77	2.6600	27.14
8	VVVPPGMED	115	2.6000	26.53
9	YRAWRHFIA	188	2.5000	25.51
10	VQLIAKTDF	8	2.3000	23.47
11	IRHRHFSYS	93	2.3000	23.47
12	LRHILTEAA	127	2.2600	23.06
13	ITGISRSCT	81	1.9000	19.39
14	LRQLAAVAP	215	1.9000	19.39
15	LRHIIDVGH	60	1.8000	18.37
16	LRVQLIAKT	6	1.7500	17.86
17	LRRKQARQA	161	1.7000	17.35
18	MRASEHADV	197	1.7000	17.35

19	IECLRQLAA	212	1.7000	17.35
20	IAMRASEHA	195	1.5000	15.31
21	LIAKTDFLA	10	1.4000	14.29
22	VLEHASVSF	71	1.4000	14.29
23	IIDVGHFSV	63	1.2000	12.24
24	ISRSCTHEL	84	1.1600	11.84
25	FYITGISRS	79	1.1500	11.73

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	WRHFIAMRA	191	6.5000	66.33
2	YRAWRHFIA	188	3.5000	35.71
3	IVVTGNYRA	182	2.7000	27.55
4	VGHFSVLEH	66	2.6000	26.53
5	LVEFAGRAC	34	2.3000	23.47
6	IRRLAIECL	207	2.2500	22.96
7	FYITGISRS	79	2.1500	21.94
8	YVPEKDSRV	107	2.0000	20.41
9	LIRHRHFSY	92	1.9000	19.39
10	VSFYITGIS	77	1.6600	16.94
11	VVVPPGMED	115	1.6000	16.33
12	FADFEVTTL	226	1.5000	15.31
13	YLRHIIDVG	59	1.3500	13.78
14	VQLIAKTDF	8	1.3000	13.27
15	IRHRHFSYS	93	1.3000	13.27
16	FIAMRASEH	194	1.3000	13.27
17	LRHILTEAA	127	1.2600	12.86
18	YITGISRSC	80	1.2000	12.24
19	ITGISRSCT	81	0.9000	9.18
20	LRQLAAVAP	215	0.9000	9.18
21	FAGRACYQS	37	0.8000	8.16
22	LRHIIDVGH	60	0.8000	8.16
23	LRVQLIAKT	6	0.7500	7.65
24	YQSWSKPNP	43	0.7000	7.14
25	LRRKQARQA	161	0.7000	7.14

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

DRB1_1506	score: 3.1	peptide: 9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	WRHFIAMRA	191	5.5000	56.12
2	IVVTGNYRA	182	3.7000	37.76
3	VGHFSVLEH	66	3.6000	36.73
4	LVEFAGRAC	34	3.3000	33.67
5	IRRLAIECL	207	3.2500	33.16
6	LIRHRHFSY	92	2.9000	29.59
7	VSFYITGIS	77	2.6600	27.14
8	VVVPPGMED	115	2.6000	26.53
9	YRAWRHFIA	188	2.5000	25.51
10	VQLIAKTDF	8	2.3000	23.47
11	IRHRHFSYS	93	2.3000	23.47
12	LRHILTEAA	127	2.2600	23.06
13	ITGISRSCT	81	1.9000	19.39
14	LRQLAAVAP	215	1.9000	19.39
15	LRHIIDVGH	60	1.8000	18.37
16	LRVQLIAKT	6	1.7500	17.86
17	LRRKQARQA	161	1.7000	17.35
18	MRASEHADV	197	1.7000	17.35
19	IECLRQLAA	212	1.7000	17.35
20	IAMRASEHA	195	1.5000	15.31
21	LIAKTDFLA	10	1.4000	14.29
22	VLEHASVSF	71	1.4000	14.29
23	IIDVGHFSV	63	1.2000	12.24
24	ISRSCTHEL	84	1.1600	11.84
25	FYITGISRS	79	1.1500	11.73

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	FIAMRASEH	194	3.6000	36.73
2	VQLIAKTDF	8	2.5000	25.51
3	WRHFIAMRA	191	2.2000	22.45
4	FYITGISRS	79	1.8000	18.37
5	IVVTGNYRA	182	1.8000	18.37
6	LRRKQARQA	161	1.5000	15.31
7	IRRLAIECL	207	1.5000	15.31
8	LAAVAPAVF	218	1.5000	15.31

9	LRHIIDVGH	60	1.4000	14.29
10	FSYSQLSQR	98	1.3000	13.27
11	YRAWRHFIA	188	1.1000	11.22
12	LIRHRHFSY	92	1.0000	10.20
13	LRHILTEAA	127	1.0000	10.20
14	LAIECLRQL	210	0.8000	8.16
15	LRQLAAVAP	215	0.7000	7.14
16	ISRSCTHEL	84	0.6000	6.12
17	LAKLEAKFA	146	0.5000	5.10
18	FAGRACYQS	37	0.4000	4.08
19	LVEFAGRAC	34	0.3000	3.06
20	YITGISRSC	80	0.3000	3.06
21	FEVTTLADG	229	0.3000	3.06
22	VEFAGRACY	35	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FIAMRASEH	194	3.6000	36.73
2	VQLIAKTDF	8	2.5000	25.51
3	WRHFIAMRA	191	2.2000	22.45
4	FYITGISRS	79	1.8000	18.37
5	IVVTGNYRA	182	1.8000	18.37
6	LRRKQARQA	161	1.5000	15.31
7	IRRLAIECL	207	1.5000	15.31
8	LAAVAPAVF	218	1.5000	15.31
9	LRHIIDVGH	60	1.4000	14.29
10	FSYSQLSQR	98	1.3000	13.27
11	YRAWRHFIA	188	1.1000	11.22
12	LIRHRHFSY	92	1.0000	10.20
13	LRHILTEAA	127	1.0000	10.20
14	LAIECLRQL	210	0.8000	8.16
15	LRQLAAVAP	215	0.7000	7.14
16	ISRSCTHEL	84	0.6000	6.12
17	LAKLEAKFA	146	0.5000	5.10
18	FAGRACYQS	37	0.4000	4.08
19	LVEFAGRAC	34	0.3000	3.06
20	YITGISRSC	80	0.3000	3.06
21	FEVTTLADG	229	0.3000	3.06
22	VEFAGRACY	35	-0.1000	0