

MHC Class-II Binding Peptide Prediction Results

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INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Thu Apr 15 00:09:52 2010
Length of input sequence	260 amino acids
Number of nanomers from input sequence	252
Number of nanomers with obligatory P1 anchor residue	54
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	26

ALLELE: DRB1_0101	Threshold for 3 % with score: 0.14	Highest Score achievable by any peptide: 6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	-0.2000	0
2	YEPEPGKPA	78	-0.5000	0
3	FEREYRTRL	214	-0.8100	0
4	VTPQATQAI	67	-0.9000	0
5	FLDLVENEL	30	-1.2000	0
6	VENELTRLI	34	-1.2100	0
7	INQGRAVLE	197	-1.3000	0
8	YRTRLKTYL	218	-1.3100	0

9	LTPADVHNV	2	-1.4000	0
10	LVENELTRL	33	-1.4700	0
11	MNEEQALKA	94	-1.5000	0
12	MGTINQORA	194	-1.6000	0
13	LAAGGGAGV	59	-1.7000	0
14	VAFSKPPIG	10	-1.8300	0
15	ILGEARHTA	138	-1.9000	0
16	LEQLRTFER	208	-1.9000	0
17	LRTFEREYR	211	-2.1200	0
18	IMGTINQOR	193	-2.6000	0
19	LTRLIEENS	38	-2.7000	0
20	VLSLAQDTA	105	-2.7000	0
21	INELDQELA	52	-2.9000	0
22	YLESQLEEL	225	-3.0000	0
23	LKTYLESQL	222	-3.1000	0
24	VHNVAFSKP	7	-3.1500	0
25	LEELGQRGS	230	-3.2100	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	LKAARVLSL	100	0.8000	13.33
2	VTPQATQAI	67	0.1000	1.67
3	VENELTRLI	34	-0.2100	0
4	INQORAVLE	197	-0.3000	0
5	LTPADVHNV	2	-0.4000	0
6	LVENELTRL	33	-0.4700	0
7	MNEEQALKA	94	-0.5000	0
8	MGTINQORA	194	-0.6000	0
9	LAAGGGAGV	59	-0.7000	0
10	FEREYRTRL	214	-0.8100	0
11	VAFSKPPIG	10	-0.8300	0
12	ILGEARHTA	138	-0.9000	0

13	LEQLRTFER	208	-0.9000	0
14	LRTFEREYR	211	-1.1200	0
15	FLDLVENEL	30	-1.2000	0
16	YEPEPGKPA	78	-1.5000	0
17	IMGTINQQR	193	-1.6000	0
18	LTRLIEENS	38	-1.7000	0
19	VLSLAQDTA	105	-1.7000	0
20	INELDQELA	52	-1.9000	0
21	LKTYLESQL	222	-2.1000	0
22	VHNVAFSKP	7	-2.1500	0
23	LEELGQRGS	230	-2.2100	0
24	LDLVENELT	31	-2.2500	0
25	LRQAQEKAD	172	-2.3000	0

ALLELE: DRB1_0301	Threshold for 3 % with score: 2.96	Highest Score achievable by any peptide: 9.5
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Rank	Sequence	At Position	Score	% of Highest Score
1	MLADARANA	127	4.3000	45.26
2	MLADAQSRS	160	4.1700	43.89
3	VAFSKPPIG	10	3.1000	32.63
4	LRTFEREYR	211	2.5000	26.32
5	LKAARVLSL	100	2.4600	25.89
6	YNEDEVDAF	22	2.4000	25.26
7	LTNTAKAES	116	1.9000	20.00
8	LEQLRTFER	208	1.9000	20.00
9	LAQDTADRL	108	1.6600	17.47
10	VTPQATQAI	67	1.6000	16.84
11	YRTRLKTYL	218	1.3600	14.32
12	LVENELTRL	33	1.1600	12.21
13	LTPADVHNV	2	1.0000	10.53
14	LQADAERKH	182	0.7000	7.37
15	INQQRAVLE	197	0.7000	7.37
16	MGTINQORA	194	0.6000	6.32

17	ILGEARHTA	138	0.4000	4.21
18	VLSLAQDTA	105	0.3000	3.16
19	VLEGRLEQL	203	0.2600	2.74
20	LTRLIEENS	38	0.2000	2.11
21	VENELTRLI	34	0.1000	1.05
22	LAAGGGAGV	59	0.1000	1.05
23	IMGTINQQR	193	0.1000	1.05
24	LRQRINELD	48	-0.2000	0
25	VHNVAFSKP	7	-0.3300	0

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	MLADARANA	127	3.3000	36.26
2	MLADAQSRS	160	2.7700	30.44
3	YNEDEVDAF	22	1.5000	16.48
4	YRTRLKTYL	218	1.4000	15.38
5	VAFSKPPIG	10	0.7000	7.69
6	LKAARVLSL	100	0.5000	5.49
7	LTNTAKAES	116	0.5000	5.49
8	LQADAERKH	182	0.2800	3.08
9	VTPQATQAI	67	-0.3000	0
10	LAQDTADRL	108	-0.3000	0
11	FEREYRTRL	214	-0.3000	0
12	MGTINQORA	194	-0.4000	0
13	YLESQLEEL	225	-0.5000	0
14	ILGEARHTA	138	-0.6000	0
15	LEQLRTFER	208	-0.6000	0
16	VLSLAQDTA	105	-0.7000	0
17	LVENELTRL	33	-0.8000	0
18	LTPADVHNV	2	-1.0000	0
19	VSAGMNEEQ	90	-1.1000	0
20	LTRLIEENS	38	-1.2000	0

21	FSKPPIGKR	12	-1.5000	0
22	INQQRAVLE	197	-1.7000	0
23	VLEGRLEQL	203	-1.7000	0
24	VENELTRLI	34	-1.8000	0

ALLELE: DRB1_0306	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	MLADARANA	127	4.3000	48.86
2	MLADAQSRS	160	3.5000	39.77
3	LKAARVLSL	100	2.0000	22.73
4	LTNTAKAES	116	1.5000	17.05
5	LRTFEREYR	211	1.4000	15.91
6	ILGEARHTA	138	1.2000	13.64
7	LAQDTADRL	108	1.0000	11.36
8	LQADAERKH	182	0.9800	11.14
9	LTPADVHNV	2	0.8000	9.09
10	YNEDEVDAF	22	0.8000	9.09
11	VTPQATQAI	67	0.8000	9.09
12	MGTINQQRA	194	0.7000	7.95
13	VLSLAQDTA	105	0.6000	6.82
14	YRTRLKTYL	218	0.4000	4.55
15	VAFSKPPIG	10	0.3000	3.41
16	VSAGMNEEQ	90	0.3000	3.41
17	LVENELTRL	33	0.2000	2.27
18	LTRLIEENS	38	0.2000	2.27
19	VLEGRLEQL	203	-0.3000	0
20	INELDQELA	52	-0.5000	0
21	MNEEQALKA	94	-0.7000	0
22	MPLTPADVH	0	-0.7200	0
23	INQQRAVLE	197	-0.8200	0
24	LRQRINELD	48	-0.9000	0
25	LAAGGGAGV	59	-0.9000	0

ALLELE: DRB1_0307	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	MLADARANA	127	4.3000	48.86
2	MLADAQSRS	160	3.5000	39.77
3	LKAARVLSL	100	2.0000	22.73
4	LTNTAKAES	116	1.5000	17.05
5	LRTFEREYR	211	1.4000	15.91
6	ILGEARHTA	138	1.2000	13.64
7	LAQDTADRL	108	1.0000	11.36
8	LQADAERKH	182	0.9800	11.14
9	LTPADVHNV	2	0.8000	9.09
10	YNEDEVDAF	22	0.8000	9.09
11	VTPQATQAI	67	0.8000	9.09
12	MGTINQORA	194	0.7000	7.95
13	VLSLAQDTA	105	0.6000	6.82
14	YRTRLKTYL	218	0.4000	4.55
15	VAFSKPPIG	10	0.3000	3.41
16	VSAGMNEEQ	90	0.3000	3.41
17	LVENELTRL	33	0.2000	2.27
18	LTRLIEENS	38	0.2000	2.27
19	VLEGRLEQL	203	-0.3000	0
20	INELDQELA	52	-0.5000	0
21	MNEEQALKA	94	-0.7000	0
22	MPLTPADVH	0	-0.7200	0
23	INQQRAVLE	197	-0.8200	0
24	LRQRINELD	48	-0.9000	0
25	LAAGGGAGV	59	-0.9000	0

ALLELE: DRB1_0308	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	MLADARANA	127	4.3000	48.86
2	MLADAQSRS	160	3.5000	39.77
3	LKAARVLSL	100	2.0000	22.73
4	LTNTAKAES	116	1.5000	17.05
5	LRTFEREYR	211	1.4000	15.91
6	ILGEARHTA	138	1.2000	13.64
7	LAQDTADRL	108	1.0000	11.36
8	LQADAERKH	182	0.9800	11.14
9	LTPADVHNV	2	0.8000	9.09
10	YNEDEVDAF	22	0.8000	9.09
11	VTPQATQAI	67	0.8000	9.09
12	MGTINQQRA	194	0.7000	7.95
13	VLSLAQDTA	105	0.6000	6.82
14	YRTRLKTYL	218	0.4000	4.55
15	VAFSKPPIG	10	0.3000	3.41
16	VSAGMNEEQ	90	0.3000	3.41
17	LVENELTRL	33	0.2000	2.27
18	LTRLIEENS	38	0.2000	2.27
19	VLEGRLEQL	203	-0.3000	0
20	INELDQELA	52	-0.5000	0
21	MNEEQALKA	94	-0.7000	0
22	MPLTPADVH	0	-0.7200	0
23	INQQRAVLE	197	-0.8200	0
24	LRQRINELD	48	-0.9000	0
25	LAAGGGAGV	59	-0.9000	0

ALLELE: DRB1_0309	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 9.5
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Rank	Sequence	At Position	Score	% of Highest Score
1	YNEDEVDAF	22	3.4000	35.79
2	MLADARANA	127	3.3000	34.74
3	MLADAQSRS	160	3.1700	33.37

4	YRTRLKTYL	218	2.3600	24.84
5	VAFSKPPIG	10	2.1000	22.11
6	LRTFEREYR	211	1.5000	15.79
7	LKAARVLSL	100	1.4600	15.37
8	LTNTAKAES	116	0.9000	9.47
9	LEQLRTFER	208	0.9000	9.47
10	LAQDTADRL	108	0.6600	6.95
11	FEREYRTRL	214	0.6600	6.95
12	VTPQATQAI	67	0.6000	6.32
13	YLESQLEEL	225	0.4600	4.84
14	LVENELTRL	33	0.1600	1.68
15	LQADAERKH	182	-0.3000	0
16	INQQRAVLE	197	-0.3000	0
17	MGTINQORA	194	-0.4000	0
18	ILGEARHTA	138	-0.6000	0
19	VLSLAQDTA	105	-0.7000	0
20	VLEGRLEQL	203	-0.7400	0
21	LTRLIEENS	38	-0.8000	0
22	VENELTRLI	34	-0.9000	0
23	LAAGGGAGV	59	-0.9000	0

ALLELE: DRB1_0311	Threshold for 3 % with score: 2.08	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	MLADARANA	127	4.3000	48.86
2	MLADAQSRS	160	3.5000	39.77
3	LKAARVLSL	100	2.0000	22.73
4	LTNTAKAES	116	1.5000	17.05
5	LRTFEREYR	211	1.4000	15.91
6	ILGEARHTA	138	1.2000	13.64
7	LAQDTADRL	108	1.0000	11.36
8	LQADAERKH	182	0.9800	11.14
9	LTPADVHNV	2	0.8000	9.09

10	YNEDEVDAF	22	0.8000	9.09
11	VTPQATQAI	67	0.8000	9.09
12	MGTINQORA	194	0.7000	7.95
13	VLSLAQDTA	105	0.6000	6.82
14	YRTRLKTYL	218	0.4000	4.55
15	VAFSKPPIG	10	0.3000	3.41
16	VSAGMNEEQ	90	0.3000	3.41
17	LVENELTRL	33	0.2000	2.27
18	LTRLIEENS	38	0.2000	2.27
19	VLEGRLEQL	203	-0.3000	0
20	INELDQELA	52	-0.5000	0
21	MNEEQALKA	94	-0.7000	0
22	MPLTPADVH	0	-0.7200	0
23	INQQRAVLE	197	-0.8200	0
24	LRQRINELD	48	-0.9000	0
25	LAAGGGAGV	59	-0.9000	0

ALLELE: DRB1_0401	Threshold for 3 % with score: 1.48	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	VTPQATQAI	67	1.7000	19.77
2	VENELTRLI	34	1.5000	17.44
3	IMGTTINQQR	193	1.3000	15.12
4	MNEEQALKA	94	0.8000	9.30
5	LKAARVLSL	100	0.7000	8.14
6	YNEDEVDAF	22	0.6000	6.98
7	MLADAQSRS	160	0.4000	4.65
8	LIEENSDLR	41	0.1000	1.16
9	YEPEPGKPA	78	0.1000	1.16
10	MPLTPADVH	0	-0.0200	0
11	LEQLRTFER	208	-0.2000	0
12	LTPADVHNV	2	-0.5000	0
13	ILGEARHTA	138	-0.7000	0

14	VLSLAQDTA	105	-0.8000	0
15	LRQRINELD	48	-0.9000	0
16	VSAGMNEEQ	90	-0.9000	0
17	LAQDTADRL	108	-0.9000	0
18	LTRLIEENS	38	-1.0000	0
19	MLADARANA	127	-1.0000	0
20	INQQRAVLE	197	-1.0200	0
21	VAFSKPPIG	10	-1.1000	0
22	IEENSDLRQ	42	-1.1000	0
23	MGTINQQRA	194	-1.2000	0
24	FEREYRTRL	214	-1.2000	0
25	YLESQLEEL	225	-1.3000	0

ALLELE: DRB1_0402	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 9.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	VTPQATQAI	67	2.6000	27.08
2	IMGTINQQR	193	2.2000	22.92
3	LKAARVLSL	100	2.0000	20.83
4	VENELTRLI	34	1.6000	16.67
5	LRQRINELD	48	1.6000	16.67
6	LGQRGSAAP	233	1.2000	12.50
7	LTPADVHNV	2	1.0000	10.42
8	LEQLRTFER	208	0.9000	9.38
9	MGTINQQRA	194	0.1800	1.88
10	LADAQSRSE	161	-0.3000	0
11	VSAGMNEEQ	90	-0.4000	0
12	LEELGQRGS	230	-0.8000	0
13	LEGRLEQLR	204	-1.0000	0
14	IGKRGYNED	17	-1.1000	0
15	IEENSDLRQ	42	-1.1000	0
16	INQQRAVLE	197	-1.1000	0
17	YRTRLKTYL	218	-1.1000	0

18	LVENELTRL	33	-1.5000	0
19	MNEEQALKA	94	-1.7000	0
20	LTNTAKAES	116	-1.7000	0
21	LQADAERKH	182	-1.7200	0
22	LRQAQEKAD	172	-1.9000	0
23	LSLAQDTAD	106	-2.0000	0
24	MPLTPADVH	0	-2.0200	0
25	LDLVENELT	31	-2.1000	0

ALLELE: DRB1_0404	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LEQLRTFER	208	1.9500	22.16
2	VTPQATQAI	67	1.7000	19.32
3	LKAARVLSL	100	1.3000	14.77
4	IMGTINQQR	193	0.5000	5.68
5	VENELTRLI	34	0.2000	2.27
6	LTPADVHNV	2	0.1000	1.14
7	VHNVAFSKP	7	-0.1000	0
8	MGTINQQRA	194	-0.1000	0
9	LDLVENELT	31	-0.4000	0
10	MLADAQSRS	160	-0.4000	0
11	VLSLAQDTA	105	-0.5000	0
12	LTRLIEENS	38	-0.7000	0
13	LRTFEREYR	211	-0.9000	0
14	INQQRAVLE	197	-1.0000	0
15	MNEEQALKA	94	-1.2000	0
16	LRQRINELD	48	-1.3000	0
17	LVENELTRL	33	-1.5000	0
18	MPLTPADVH	0	-1.5200	0
19	INELDQELA	52	-1.6000	0
20	VSAGMNEEQ	90	-1.6000	0
21	LSLAQDTAD	106	-1.7000	0

22	LEELGQRGS	230	-1.8000	0
23	VAFSKPPIG	10	-1.9000	0
24	IEENSDLRQ	42	-2.1000	0
25	LTNTAKAES	116	-2.1000	0

ALLELE: DRB1_0405	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 9.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	1.3000	13.83
2	INQQRAVLE	197	1.0000	10.64
3	LEQLRTFER	208	0.9500	10.11
4	VTPQATQAI	67	0.9000	9.57
5	LRQRINELD	48	0.4000	4.26
6	LADARANAE	128	-0.3000	0
7	LDLVENELT	31	-0.5000	0
8	IMGTINQQR	193	-0.5000	0
9	LTPADVHNV	2	-0.6000	0
10	VENELTRLI	34	-0.6000	0
11	VHNVAFSKP	7	-0.7000	0
12	VDAFLDLVE	27	-0.8000	0
13	LADAQSRSE	161	-0.9000	0
14	FLDLVENEL	30	-1.0000	0
15	MGTINQQRA	194	-1.1000	0
16	MPLTPADVH	0	-1.3000	0
17	MLADAQSRS	160	-1.4000	0
18	LVENELTRL	33	-1.5000	0
19	VLSLAQDTA	105	-1.5000	0
20	LRQAQEKAD	172	-1.5000	0
21	VAFSKPPIG	10	-1.6000	0
22	LTRLIEENS	38	-1.7000	0
23	LGEARHTAD	139	-1.7000	0
24	VSAGMNEEQ	90	-1.8000	0

ALLELE: DRB1_0408	Threshold for 3 % with score: 1.2	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LEQLRTFER	208	0.9500	10.80
2	VTPQATQAI	67	0.7000	7.95
3	LKAARVLSL	100	0.3000	3.41
4	IMGTINQQR	193	-0.5000	0
5	VENELTRLI	34	-0.8000	0
6	LTPADVHNV	2	-0.9000	0
7	VHNVAFSKP	7	-1.1000	0
8	MGTINQQRA	194	-1.1000	0
9	LDLVENELT	31	-1.4000	0
10	MLADAQSRS	160	-1.4000	0
11	VLSLAQDTA	105	-1.5000	0
12	LTRLIEENS	38	-1.7000	0
13	LRTFEREYR	211	-1.9000	0
14	FLDLVENEL	30	-2.0000	0
15	INQQRAVLE	197	-2.0000	0
16	MNEEQALKA	94	-2.2000	0
17	LRQRINELD	48	-2.3000	0
18	LVENELTRL	33	-2.5000	0
19	MPLTPADVH	0	-2.5200	0
20	INELDQELA	52	-2.6000	0
21	VSAGMNEEQ	90	-2.6000	0
22	LSLAQDTAD	106	-2.7000	0
23	YNEDEVDAF	22	-2.8000	0
24	LEELGQRGS	230	-2.8000	0
25	VAFSKPPIG	10	-2.9000	0

ALLELE: DRB1_0410	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	2.3000	24.47
2	INQQRAVLE	197	2.0000	21.28
3	LEQLRTFER	208	1.9500	20.74
4	VTPQATQAI	67	1.9000	20.21
5	LRQRINELD	48	1.4000	14.89
6	LSLAQDTAD	106	1.0000	10.64
7	LADARANAE	128	0.7000	7.45
8	LDLVENELT	31	0.5000	5.32
9	IMG TINQQR	193	0.5000	5.32
10	LTPADVHNV	2	0.4000	4.26
11	VENELTRLI	34	0.4000	4.26
12	VHNVAFSKP	7	0.3000	3.19
13	VDAFLDLVE	27	0.2000	2.13
14	LADAQSRSE	161	0.1000	1.06
15	MGTINQORA	194	-0.1000	0
16	MPLTPADVH	0	-0.3000	0
17	MLADAQSRS	160	-0.4000	0
18	LVENELTRL	33	-0.5000	0
19	VLSLAQDTA	105	-0.5000	0
20	LRQAQEKAD	172	-0.5000	0
21	VAFSKPPIG	10	-0.6000	0
22	LTRLIEENS	38	-0.7000	0
23	LGEARHTAD	139	-0.7000	0
24	VSAGMNEEQ	90	-0.8000	0
25	LRTFEREYR	211	-0.9000	0

ALLELE: DRB1_0421	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9
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Rank	Sequence	At Position	Score	% of Highest Score
1	IMG TINQQR	193	2.8000	31.11
2	VTPQATQAI	67	2.6000	28.89
3	YNEDEVDAF	22	2.5000	27.78

4	VENELTRLI	34	2.4000	26.67
5	LKAARVLSL	100	1.6600	18.44
6	LIEENSDLR	41	1.6000	17.78
7	LEQLRTFER	208	1.3000	14.44
8	MNEEQALKA	94	0.8000	8.89
9	MLADAQSRS	160	0.8000	8.89
10	LTPADVHNV	2	0.5000	5.56
11	INQQRVLE	197	0.3800	4.22
12	VAFSKPPIG	10	0.3000	3.33
13	LRQRINELD	48	0.2000	2.22
14	YEPEPGKPA	78	0.1000	1.11
15	LAQDTADRL	108	0.0600	0.67
16	FEREYRTRL	214	-0.2400	0
17	YLESQLEEL	225	-0.3400	0
18	LDQELAAGG	55	-0.4000	0
19	LVENELTRL	33	-0.4400	0
20	MPLTPADVH	0	-0.6000	0
21	LTRLIEENS	38	-0.6000	0
22	ILGEARHTA	138	-0.7000	0
23	VLSLAQDTA	105	-0.8000	0
24	MLADARANA	127	-1.0000	0
25	LTNTAKAES	116	-1.1000	0

ALLELE: DRB1_0423	Threshold for 3 % with score: 1.68	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LEQLRTFER	208	1.9500	22.16
2	VTPQATQAI	67	1.7000	19.32
3	LKAARVLSL	100	1.3000	14.77
4	IMGTINQQR	193	0.5000	5.68
5	VENELTRLI	34	0.2000	2.27
6	LTPADVHNV	2	0.1000	1.14
7	VHNVAFSKP	7	-0.1000	0

8	MGTINQQR	194	-0.1000	0
9	LDLVENELT	31	-0.4000	0
10	MLADAQSRS	160	-0.4000	0
11	VLSLAQDTA	105	-0.5000	0
12	LTRLIEENS	38	-0.7000	0
13	LRTFEREYR	211	-0.9000	0
14	INQQRVLE	197	-1.0000	0
15	MNEEQALKA	94	-1.2000	0
16	LRQRINELD	48	-1.3000	0
17	LVENELTRL	33	-1.5000	0
18	MPLTPADVH	0	-1.5200	0
19	INELDQELA	52	-1.6000	0
20	VSAGMNEEQ	90	-1.6000	0
21	LSLAQDTAD	106	-1.7000	0
22	LEELGQRGS	230	-1.8000	0
23	VAFSKPPIG	10	-1.9000	0
24	IEENSDLRQ	42	-2.1000	0
25	LTNTAKAES	116	-2.1000	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	VTPQATQAI	67	1.7000	19.77
2	VENELTRLI	34	1.5000	17.44
3	IMGTINQQR	193	1.3000	15.12
4	MNEEQALKA	94	0.8000	9.30
5	LKAARVLSL	100	0.7000	8.14
6	YNEDEVDAF	22	0.6000	6.98
7	MLADAQSRS	160	0.4000	4.65
8	LIEENSDLR	41	0.1000	1.16
9	YEPEPGKPA	78	0.1000	1.16
10	MPLTPADVH	0	-0.0200	0
11	LEQLRTER	208	-0.2000	0

12	LTPADVHNV	2	-0.5000	0
13	ILGEARHTA	138	-0.7000	0
14	VLSLAQDTA	105	-0.8000	0
15	LRQRINELD	48	-0.9000	0
16	VSAGMNEEQ	90	-0.9000	0
17	LAQDTADRL	108	-0.9000	0
18	LTRLIEENS	38	-1.0000	0
19	MLADARANA	127	-1.0000	0
20	INQQRAVLE	197	-1.0200	0
21	VAFSKPPIG	10	-1.1000	0
22	IEENSDLRQ	42	-1.1000	0
23	MGTINQQRA	194	-1.2000	0
24	FEREYRTRL	214	-1.2000	0
25	YLESQLEEL	225	-1.3000	0

ALLELE: DRB1_0701	Threshold for 3 % with score: 4.1	Highest Score achievable by any peptide: 11.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	5.8000	50.00
2	YLESQLEEL	225	4.7000	40.52
3	YRTRLKTYL	218	4.3000	37.07
4	FEREYRTRL	214	2.6000	22.41
5	LTPADVHNV	2	2.3000	19.83
6	VENELTRLI	34	2.2200	19.14
7	VTPQATQAI	67	2.2200	19.14
8	LVENELTRL	33	2.2000	18.97
9	IMGTINQQR	193	1.4000	12.07
10	FLDLVENEL	30	1.2000	10.34
11	VLEGRLEQL	203	1.1000	9.48
12	MGTINQQRA	194	0.6000	5.17
13	LKTYLESQ	222	0.5000	4.31
14	LRTFEREYR	211	0.4000	3.45
15	LDLVENELT	31	0.3000	2.59

16	VHNVAFSKP	7	0.2000	1.72
17	INQQRAVLE	197	-0.4000	0
18	LEQLRTFER	208	-0.4800	0
19	LAQDTADRL	108	-0.5000	0
20	LTNTAKAES	116	-0.5000	0
21	MPLTPADVH	0	-0.6000	0
22	MNEEQALKA	94	-0.6000	0
23	LAAGGGAGV	59	-0.7000	0
24	LRQRINELD	48	-0.8000	0

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	LKAARVLSL	100	5.8000	50.00
2	YLESQLEEL	225	4.7000	40.52
3	YRTRLKTYL	218	4.3000	37.07
4	FEREYRTRL	214	2.6000	22.41
5	LTPADVHNV	2	2.3000	19.83
6	VENELTRLI	34	2.2200	19.14
7	VTPQATQAI	67	2.2200	19.14
8	LVENELTRL	33	2.2000	18.97
9	IMGTINQQR	193	1.4000	12.07
10	FLDLVENEL	30	1.2000	10.34
11	VLEGRLEQL	203	1.1000	9.48
12	MGTINQQRA	194	0.6000	5.17
13	LKTYLESQL	222	0.5000	4.31
14	LRTFEREYR	211	0.4000	3.45
15	LDLVENELT	31	0.3000	2.59
16	VHNVAFSKP	7	0.2000	1.72
17	INQQRAVLE	197	-0.4000	0
18	LEQLRTFER	208	-0.4800	0
19	LAQDTADRL	108	-0.5000	0
20	LTNTAKAES	116	-0.5000	0

21	MPLTPADVH	0	-0.6000	0
22	MNEEQALKA	94	-0.6000	0
23	LAAGGGAGV	59	-0.7000	0
24	LRQRINELD	48	-0.8000	0

ALLELE: DRB1_0801	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	YRTRLKTYL	218	3.4000	39.53
2	LRQRINELD	48	1.5000	17.44
3	LKAARVLSL	100	1.0000	11.63
4	LGQRGSAAP	233	0.8000	9.30
5	LTNTAKAES	116	0.5000	5.81
6	FDQFNRGKN	251	0.3000	3.49
7	IGKRGYNED	17	0.1000	1.16
8	LKTYLESQL	222	-0.4000	0
9	ILGEARHTA	138	-0.7000	0
10	LRTFEREYR	211	-0.7000	0
11	LTPADVHNV	2	-0.8000	0
12	IPAYEPEPG	75	-0.9000	0
13	INQQRAVLE	197	-1.0000	0
14	VENELTRLI	34	-1.3000	0
15	LEQLRTER	208	-1.3000	0
16	LQADAERKH	182	-1.5000	0
17	VAFSKPPIG	10	-1.6000	0
18	FEREYRTRL	214	-1.6000	0
19	LEELGQRGS	230	-1.6000	0
20	LADAQSRSE	161	-1.7000	0
21	MGTINQQRA	194	-1.7000	0
22	VLSLAQDTA	105	-1.8000	0
23	MLADAQSRS	160	-1.9000	0

ALLELE: DRB1_0802	Threshold for 3 % with score: 1.0	Highest Score achievable by any peptide: 8
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Rank	Sequence	At Position	Score	% of Highest Score
1	YRTRLKTYL	218	2.4000	30.00
2	LTNTAKAES	116	0.5000	6.25
3	LGQRGSAAP	233	0.4000	5.00
4	ILGEARHTA	138	-0.7000	0
5	LRTFEREYR	211	-0.7000	0
6	LTPADVHNV	2	-1.1000	0
7	LRQRINELD	48	-1.2000	0
8	LEQLRTFER	208	-1.3000	0
9	LKTYLESQL	222	-1.4000	0
10	VENELTRLI	34	-1.5000	0
11	LEELGQRGS	230	-1.6000	0
12	MGTINQORA	194	-1.7000	0
13	FDQFNRGKN	251	-1.7000	0
14	VLSLAQDTA	105	-1.8000	0
15	MLADAQSRS	160	-1.9000	0
16	LEGRLEQLR	204	-2.0000	0
17	FSKPPIGKR	12	-2.1000	0
18	YEPEPGKPA	78	-2.1000	0
19	IPAYEPEPG	75	-2.2000	0
20	VTPQATQAI	67	-2.4000	0
21	IGKRGYNED	17	-2.6000	0
22	FEREYRTRL	214	-2.6000	0
23	LTRLIEENS	38	-2.7000	0

ALLELE: DRB1_0804	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LTNTAKAES	116	1.5000	18.75
2	YRTRLKTYL	218	1.4000	17.50

3	LGQRGSAAP	233	1.4000	17.50
4	LKAARVLSL	100	1.0000	12.50
5	MLADARANA	127	1.0000	12.50
6	ILGEARHTA	138	0.3000	3.75
7	LRTFEREYR	211	0.3000	3.75
8	LTPADVHNV	2	-0.1000	0
9	LRQRINELD	48	-0.2000	0
10	LEQLRTER	208	-0.3000	0
11	LKTYLESQL	222	-0.4000	0
12	VENELTRLI	34	-0.5000	0
13	LEELGQRGS	230	-0.6000	0
14	MGTINQORA	194	-0.7000	0
15	VLSLAQDTA	105	-0.8000	0
16	MLADAQSRS	160	-0.9000	0
17	LEGRLEQLR	204	-1.0000	0
18	IPAYEPEPG	75	-1.2000	0
19	VTPQATQAI	67	-1.4000	0
20	IGKRGYNED	17	-1.6000	0
21	LTRLIEENS	38	-1.7000	0
22	MNEEQALKA	94	-1.7000	0
23	LRQAQEKAD	172	-1.7000	0
24	LQADAERKH	182	-1.7200	0
25	VAFSKPPIG	10	-1.9000	0

ALLELE: DRB1_0806	Threshold for 3 % with score: 2.4	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRQRINELD	48	2.5000	29.07
2	YRTRLKTYL	218	2.4000	27.91
3	LKAARVLSL	100	2.0000	23.26
4	LGQRGSAAP	233	1.8000	20.93
5	LTNTAKAES	116	1.5000	17.44
6	IGKRGYNED	17	1.1000	12.79

7	MLADARANA	127	1.0000	11.63
8	LRQAQEKAD	172	1.0000	11.63
9	LKTYLESQL	222	0.6000	6.98
10	ILGEARHTA	138	0.3000	3.49
11	LRTFEREYR	211	0.3000	3.49
12	LTPADVHNV	2	0.2000	2.33
13	IPAYEPEPG	75	0.1000	1.16
14	VENELTRLI	34	-0.3000	0
15	LEQLRTFER	208	-0.3000	0
16	LQADAERKH	182	-0.5000	0
17	VAFSKPPIG	10	-0.6000	0
18	LEELGQRGS	230	-0.6000	0
19	LADAQSRSE	161	-0.7000	0
20	MGTINQORA	194	-0.7000	0
21	FDQFNRGKN	251	-0.7000	0
22	VLSLAQDTA	105	-0.8000	0
23	MLADAQSRS	160	-0.9000	0
24	LEGRLEQLR	204	-1.0000	0

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	YRTRLKTYL	218	5.2000	59.77
2	LRTFEREYR	211	1.0000	11.49
3	LKAARVLSL	100	0.6000	6.90
4	LRQRINELD	48	0.5000	5.75
5	LTNTAKAES	116	0.5000	5.75
6	LKTYLESQL	222	0.4000	4.60
7	LGQRGSAAP	233	0.4000	4.60
8	FEREYRTRL	214	0.2000	2.30
9	MLADAQSRS	160	-0.1000	0
10	ILGEARHTA	138	-0.2000	0
11	LEQLRTFER	208	-0.4500	0

12	LVENELTRL	33	-0.5000	0
13	IPAYEPEPG	75	-0.5000	0
14	LTPADVHNV	2	-0.6000	0
15	IGKRGYNED	17	-0.6000	0
16	VLSLAQDTA	105	-0.6000	0
17	MGTINQQRA	194	-0.7000	0
18	LTRLIEENS	38	-1.0000	0
19	LEGRLEQLR	204	-1.0000	0
20	FLDLVENEL	30	-1.3000	0
21	VTPQATQAI	67	-1.4000	0
22	VHNVAFSKP	7	-1.6000	0
23	INELDQELA	52	-1.7000	0
24	VENELTRLI	34	-1.8000	0

ALLELE: DRB1_0817	Threshold for 3 % with score: 2.8	Highest Score achievable by any peptide: 10.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	YRTRLKTYL	218	4.5000	44.55
2	LKAARVLSL	100	2.8000	27.72
3	LRQRINELD	48	2.6000	25.74
4	LGQRGSAAP	233	0.8000	7.92
5	LRQAQEKAD	172	0.6000	5.94
6	LTNTAKAES	116	0.5000	4.95
7	IGKRGYNED	17	0.4000	3.96
8	LRTFEREYR	211	0.4000	3.96
9	FDQFNRGKN	251	0.4000	3.96
10	IPAYEPEPG	75	0.2000	1.98
11	LTPADVHNV	2	-0.1000	0
12	LKTYLESQL	222	-0.4000	0
13	VAFSKPPIG	10	-0.4500	0
14	INQQRAVLE	197	-0.5000	0
15	FEREYRTRL	214	-0.5000	0
16	LEQLRTER	208	-0.8000	0

17	MNEEQALKA	94	-0.9000	0
18	VENELTRLI	34	-1.1000	0
19	LVENELTRL	33	-1.2000	0
20	LQADAERKH	182	-1.3000	0
21	VDAFLDLVE	27	-1.4000	0
22	LEELGQRGS	230	-1.4000	0
23	YEPEPGKPA	78	-1.5000	0

ALLELE: DRB1_1101	Threshold for 3 % with score: 1.1	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	1.8000	21.69
2	LTNTAKAES	116	0.9000	10.84
3	YRTRLKTYL	218	0.5000	6.02
4	LRTFEREYR	211	0.3000	3.61
5	LTPADVHNV	2	-0.4000	0
6	LEQLRTFER	208	-0.4000	0
7	MLADARANA	127	-0.7000	0
8	ILGEARHTA	138	-0.7000	0
9	MGTINQORA	194	-1.0000	0
10	LEELGQRGS	230	-1.0000	0
11	LTRLIEENS	38	-1.2000	0
12	VAFSKPPIG	10	-1.4500	0
13	MNEEQALKA	94	-1.6000	0
14	VTPQATQAI	67	-1.7000	0
15	VLSLAQDTA	105	-1.7000	0
16	FDQFNRGKN	251	-1.7000	0
17	INELDQELA	52	-1.9000	0
18	VENELTRLI	34	-2.0000	0
19	LRQAQEKAD	172	-2.1000	0
20	LVENELTRL	33	-2.2000	0
21	YEPEPGKPA	78	-2.2000	0
22	FEREYRTRL	214	-2.2000	0

23	IEENSDLRQ	42	-2.5000	0
24	FLDLVENEL	30	-2.6000	0
25	MLADAQSRS	160	-2.6000	0

ALLELE: DRB1_1102	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	2.0000	23.81
2	LKAARVLSL	100	1.7000	20.24
3	LTNTAKAES	116	1.4000	16.67
4	ILGEARHTA	138	1.4000	16.67
5	VENELTRLI	34	1.2000	14.29
6	LTPADVHNV	2	1.1000	13.10
7	VTPQATQAI	67	1.0000	11.90
8	LEQLRTER	208	0.9000	10.71
9	LEELGQRGS	230	0.9000	10.71
10	YRTRLKTYL	218	0.8000	9.52
11	MLADARANA	127	0.6000	7.14
12	VLSLAQDTA	105	-0.2000	0
13	LQADAERKH	182	-0.3200	0
14	INQQRAVLE	197	-0.4000	0
15	LTRLIEENS	38	-0.6000	0
16	LVENELTRL	33	-0.7000	0
17	LGQRGSAAP	233	-0.7000	0
18	VAFSKPPIG	10	-0.8000	0
19	MGTINQORA	194	-0.8000	0
20	LRQRINELD	48	-0.9000	0
21	MLADAQSRS	160	-0.9000	0
22	LRQAQEKAD	172	-0.9000	0
23	MNEEQALKA	94	-1.1000	0
24	INELDQELA	52	-1.3000	0
25	IPAYEPEPG	75	-1.6000	0

ALLELE: DRB1_1104	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	2.8000	33.73
2	LTNTAKAES	116	1.9000	22.89
3	LRTFEREYR	211	1.3000	15.66
4	LTPADVHNV	2	0.6000	7.23
5	LEQLRTFER	208	0.6000	7.23
6	MLADARANA	127	0.3000	3.61
7	ILGEARHTA	138	0.3000	3.61
8	LTRLIEENS	38	-0.2000	0
9	VAFSKPPIG	10	-0.4500	0
10	YRTRLKTYL	218	-0.5000	0
11	MNEEQALKA	94	-0.6000	0
12	VTPQATQAI	67	-0.7000	0
13	VLSLAQDTA	105	-0.7000	0
14	INELDQELA	52	-0.9000	0
15	VENELTRLI	34	-1.0000	0
16	LRQAQEKAD	172	-1.1000	0
17	LVENELTRL	33	-1.2000	0
18	IEENSCLRQ	42	-1.5000	0
19	MLADAQSRS	160	-1.6000	0
20	LGQRGSAAP	233	-1.6000	0
21	INQGRAVLE	197	-1.9000	0
22	IMGTINQQR	193	-2.0000	0
23	LRQRINELD	48	-2.1000	0

ALLELE: DRB1_1106	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	2.8000	33.73

2	LTNTAKAES	116	1.9000	22.89
3	LRTFEREYR	211	1.3000	15.66
4	LTPADVHNV	2	0.6000	7.23
5	LEQLRTER	208	0.6000	7.23
6	MLADARANA	127	0.3000	3.61
7	ILGEARHTA	138	0.3000	3.61
8	LTRLIEENS	38	-0.2000	0
9	VAFSKPPIG	10	-0.4500	0
10	YRTRLKTYL	218	-0.5000	0
11	MNEEQALKA	94	-0.6000	0
12	VTPQATQAI	67	-0.7000	0
13	VLSLAQDTA	105	-0.7000	0
14	INELDQELA	52	-0.9000	0
15	VENELTRLI	34	-1.0000	0
16	LRQAQEKAD	172	-1.1000	0
17	LVENELTRL	33	-1.2000	0
18	IEENSCLRQ	42	-1.5000	0
19	MLADAQSRS	160	-1.6000	0
20	LGQRGSAAP	233	-1.6000	0
21	INQQRVLE	197	-1.9000	0
22	IMGTINQQR	193	-2.0000	0
23	LRQRINELD	48	-2.1000	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	MLADARANA	127	4.3000	47.25
2	MLADAQSRS	160	3.7700	41.43
3	VAFSKPPIG	10	1.7000	18.68
4	LKAARVLSL	100	1.5000	16.48
5	LTNTAKAES	116	1.5000	16.48
6	LQADAERKH	182	1.2800	14.07
7	LRTFEREYR	211	1.0000	10.99

8	VTPQATQAI	67	0.7000	7.69
9	LAQDTADRL	108	0.7000	7.69
10	MGTINQORA	194	0.6000	6.59
11	YNEDEVDAF	22	0.5000	5.49
12	ILGEARHTA	138	0.4000	4.40
13	LEQLRTFER	208	0.4000	4.40
14	YRTRLKTYL	218	0.4000	4.40
15	VLSLAQDTA	105	0.3000	3.30
16	LVENELTRL	33	0.2000	2.20
17	VSAGMNEEQ	90	-0.1000	0
18	LTRLIEENS	38	-0.2000	0
19	INQQRVLE	197	-0.7000	0
20	VLEGRLEQL	203	-0.7000	0
21	VENELTRLI	34	-0.8000	0
22	INELDQELA	52	-0.9000	0
23	LAAGGGAGV	59	-0.9000	0
24	MPLTPADVH	0	-1.0200	0

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	YRTRLKTYL	218	1.8000	21.43
2	LRTFEREYR	211	1.0000	11.90
3	LKAARVLSL	100	0.7000	8.33
4	LTNTAKAES	116	0.4000	4.76
5	ILGEARHTA	138	0.4000	4.76
6	VENELTRLI	34	0.2000	2.38
7	LTPADVHNV	2	0.1000	1.19
8	LEQLRTFER	208	-0.1000	0
9	LEELGQRGS	230	-0.1000	0
10	MLADARANA	127	-0.4000	0
11	VLSLAQDTA	105	-1.2000	0
12	FEREYRTRL	214	-1.2000	0

13	LQADAERKH	182	-1.3200	0
14	YEPEPGKPA	78	-1.4000	0
15	INQQRAVLE	197	-1.4000	0
16	LTRLIEENS	38	-1.6000	0
17	LVENELTRL	33	-1.7000	0
18	LGQRGSAAP	233	-1.7000	0
19	VAFSKPPIG	10	-1.8000	0
20	MGTINQORA	194	-1.8000	0
21	LRQRINELD	48	-1.9000	0
22	MLADAQSRS	160	-1.9000	0
23	LRQAQEKAD	172	-1.9000	0
24	MNEEQALKA	94	-2.1000	0

ALLELE: DRB1_1120	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	YRTRLKTYL	218	2.7600	31.36
2	LRTFEREYR	211	2.5000	28.41
3	LKAARVLSL	100	1.6600	18.86
4	LEQLRTFER	208	1.4000	15.91
5	LTPADVHNV	2	1.1000	12.50
6	VENELTRLI	34	1.1000	12.50
7	VTPQATQAI	67	0.9000	10.23
8	LTNTAKAES	116	0.8000	9.09
9	ILGEARHTA	138	0.4000	4.55
10	LEELGQRGS	230	0.3000	3.41
11	FEREYRTRL	214	-0.2400	0
12	VAFSKPPIG	10	-0.4000	0
13	MLADARANA	127	-0.4000	0
14	LGQRGSAAP	233	-0.7000	0
15	LVENELTRL	33	-0.7400	0
16	LRQRINELD	48	-0.8000	0
17	LRQAQEKAD	172	-0.8000	0

18	YNEDEVDAF	22	-1.2000	0
19	LTRLIEENS	38	-1.2000	0
20	IPAYEPEPG	75	-1.2000	0
21	VLSLAQDTA	105	-1.2000	0
22	FLDLVENEL	30	-1.2400	0
23	IMGTINQQR	193	-1.3000	0
24	YEPEPGKPA	78	-1.4000	0

ALLELE: DRB1_1121	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	2.0000	23.81
2	LKAARVLSL	100	1.7000	20.24
3	LTNTAKAES	116	1.4000	16.67
4	ILGEARHTA	138	1.4000	16.67
5	VENELTRLI	34	1.2000	14.29
6	LTPADVHNV	2	1.1000	13.10
7	VTPQATQAI	67	1.0000	11.90
8	LEQLRTFER	208	0.9000	10.71
9	LEELGQRGS	230	0.9000	10.71
10	YRTRLKTYL	218	0.8000	9.52
11	MLADARANA	127	0.6000	7.14
12	VLSLAQDTA	105	-0.2000	0
13	LQADAERKH	182	-0.3200	0
14	INQQRAVLE	197	-0.4000	0
15	LTRLIEENS	38	-0.6000	0
16	LVENELTRL	33	-0.7000	0
17	LGQRGSAAP	233	-0.7000	0
18	VAFSKPPIG	10	-0.8000	0
19	MGTINQQRA	194	-0.8000	0
20	LRQRINELD	48	-0.9000	0
21	MLADAQSRS	160	-0.9000	0
22	LRQAQEKAD	172	-0.9000	0

23	MNEEQALKA	94	-1.1000	0
24	INELDQELA	52	-1.3000	0
25	IPAYEPEPG	75	-1.6000	0

ALLELE: DRB1_1128	Threshold for 3 % with score: 2.15	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	2.7600	31.72
2	LRTFEREYR	211	1.8000	20.69
3	YRTRLKTYL	218	1.4600	16.78
4	LTNTAKAES	116	1.3000	14.94
5	LEQLRTFER	208	1.1000	12.64
6	LTPADVHNV	2	0.6000	6.90
7	VAFSKPPIG	10	-0.0500	0
8	LEELGQRGS	230	-0.6000	0
9	MLADARANA	127	-0.7000	0
10	ILGEARHTA	138	-0.7000	0
11	LTRLIEENS	38	-0.8000	0
12	VTPQATQAI	67	-0.8000	0
13	FDQFNRGKN	251	-0.9000	0
14	LRQAQEKAD	172	-1.0000	0
15	MGTINQORA	194	-1.0000	0
16	VENELTRLI	34	-1.1000	0
17	FSKPPIGKR	12	-1.2000	0
18	LVENELTRL	33	-1.2400	0
19	FEREYRTRL	214	-1.2400	0
20	IMGTINQQR	193	-1.5000	0
21	INQRAVLE	197	-1.5000	0
22	MNEEQALKA	94	-1.6000	0
23	LGQRGSAAP	233	-1.6000	0
24	FLDLVENEL	30	-1.6400	0
25	VLSLAQDTA	105	-1.7000	0

ALLELE: DRB1_1301	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	3.5000	39.77
2	LKAARVLSL	100	2.6600	30.23
3	LEQLRTER	208	2.4000	27.27
4	LTPADVHNV	2	2.1000	23.86
5	VENELTRLI	34	2.1000	23.86
6	VTPQATQAI	67	1.9000	21.59
7	LTNTAKAES	116	1.8000	20.45
8	YRTRLKTYL	218	1.7600	20.00
9	ILGEARHTA	138	1.4000	15.91
10	LEELGQRGS	230	1.3000	14.77
11	INQQRAVLE	197	1.0000	11.36
12	VAFSKPPIG	10	0.6000	6.82
13	MLADARANA	127	0.6000	6.82
14	LGQRGSAAP	233	0.3000	3.41
15	LVENELTRL	33	0.2600	2.95
16	LRQRINELD	48	0.2000	2.27
17	LRQAQEKAD	172	0.2000	2.27
18	LTRLIEENS	38	-0.2000	0
19	IPAYEPEPG	75	-0.2000	0
20	VLSLAQDTA	105	-0.2000	0
21	IMGTINQQR	193	-0.3000	0
22	MLADAQSRS	160	-0.5000	0
23	LADAQSRSE	161	-0.5000	0
24	MGTINQORA	194	-0.8000	0
25	LEGRLEQLR	204	-0.8000	0

ALLELE: DRB1_1302	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	YRTRLKTYL	218	2.7600	31.36
2	LRTFEREYR	211	2.5000	28.41
3	LKAARVLSL	100	1.6600	18.86
4	LEQLRTFER	208	1.4000	15.91
5	LTPADVHNV	2	1.1000	12.50
6	VENELRLI	34	1.1000	12.50
7	VTPQATQAI	67	0.9000	10.23
8	LTNTAKAES	116	0.8000	9.09
9	ILGEARHTA	138	0.4000	4.55
10	LEELGQRGS	230	0.3000	3.41
11	FEREYRTRL	214	-0.2400	0
12	VAFSKPPIG	10	-0.4000	0
13	MLADARANA	127	-0.4000	0
14	LGQRGSAAP	233	-0.7000	0
15	LVENELTRL	33	-0.7400	0
16	LRQRINELD	48	-0.8000	0
17	LRQAQEKAD	172	-0.8000	0
18	YNEDEVDAF	22	-1.2000	0
19	LTRLIEENS	38	-1.2000	0
20	IPAYEPEPG	75	-1.2000	0
21	VLSLAQDTA	105	-1.2000	0
22	FLDLVENEL	30	-1.2400	0
23	IMGTINQQR	193	-1.3000	0
24	YEPEPGKPA	78	-1.4000	0

ALLELE: DRB1_1304	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	2.7000	30.00
2	INQQRAVLE	197	2.6000	28.89
3	LRTFEREYR	211	2.0000	22.22
4	LRQRINELD	48	1.8000	20.00

5	LRQAQEKAD	172	1.8000	20.00
6	YRTRLKTYL	218	1.8000	20.00
7	LTPADVHNV	2	1.4000	15.56
8	VENELTRLI	34	1.4000	15.56
9	LTNTAKAES	116	1.4000	15.56
10	ILGEARHTA	138	1.4000	15.56
11	VTPQATQAI	67	1.2000	13.33
12	LADAQSRSE	161	1.1000	12.22
13	LQADAERKH	182	0.9000	10.00
14	LEQLRTFER	208	0.9000	10.00
15	LEELGQRGS	230	0.9000	10.00
16	VAEARQRAD	150	0.7000	7.78
17	MLADARANA	127	0.6000	6.67
18	VAFSKPPIG	10	0.5000	5.56
19	IGKRGYNED	17	0.4000	4.44
20	LVENELTRL	33	0.3000	3.33
21	LADARANAE	128	0.1000	1.11
22	VLSLAQDTA	105	-0.2000	0
23	IPAYEPEPG	75	-0.3000	0
24	LGQRGSAAP	233	-0.3000	0
25	LTRLIEENS	38	-0.6000	0

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	LKAARVLSL	100	2.7600	31.72
2	LRTFEREYR	211	1.8000	20.69
3	YRTRLKTYL	218	1.4600	16.78
4	LTNTAKAES	116	1.3000	14.94
5	LEQLRTFER	208	1.1000	12.64
6	LTPADVHNV	2	0.6000	6.90
7	VAFSKPPIG	10	-0.0500	0
8	LEELGQRGS	230	-0.6000	0

9	MLADARANA	127	-0.7000	0
10	ILGEARHTA	138	-0.7000	0
11	LTRLIEENS	38	-0.8000	0
12	VTPQATQAI	67	-0.8000	0
13	FDQFNRGKN	251	-0.9000	0
14	LRQAQEKAD	172	-1.0000	0
15	MGTINQQRA	194	-1.0000	0
16	VENELTRLI	34	-1.1000	0
17	FSKPPIGKR	12	-1.2000	0
18	LVENELTRL	33	-1.2400	0
19	FEREYRTRL	214	-1.2400	0
20	IMGTINQQR	193	-1.5000	0
21	INQQRAVLE	197	-1.5000	0
22	MNEEQALKA	94	-1.6000	0
23	LGQRGSAAP	233	-1.6000	0
24	FLDLVENEL	30	-1.6400	0
25	VLSLAQDTA	105	-1.7000	0

ALLELE: DRB1_1307		Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8	
Rank	Sequence	At Position	Score	% of Highest Score
1	LTNTAKAES	116	0.9000	13.24
2	YRTRLKTYL	218	-0.6000	0
3	MLADARANA	127	-0.7000	0
4	LRTFEREYR	211	-0.8000	0
5	LEQLRTFER	208	-0.9000	0
6	LTPADVHNV	2	-1.1000	0
7	MGTINQQRA	194	-1.1000	0
8	LEELGQRGS	230	-1.2000	0
9	VLSLAQDTA	105	-1.4000	0
10	ILGEARHTA	138	-1.4000	0
11	VTPQATQAI	67	-1.8000	0
12	FDQFNRGKN	251	-1.8000	0

13	VENELTRLI	34	-2.2000	0
14	LTRLIEENS	38	-2.3000	0
15	VAFSKPPIG	10	-2.6000	0
16	MLADAQSRS	160	-2.6000	0
17	LGQRGSAAP	233	-2.6000	0
18	LRQAQEKAD	172	-2.7000	0
19	FSKPPIGKR	12	-2.8000	0
20	YEPEPGKPA	78	-2.8000	0
21	FLDLVENEL	30	-2.9000	0
22	INELDQELA	52	-3.0000	0
23	IMGTINQQR	193	-3.1000	0
24	VHNVAFSKP	7	-3.3000	0

ALLELE: DRB1_1311	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	2.8000	33.73
2	LTNTAKAES	116	1.9000	22.89
3	LRTFEREYR	211	1.3000	15.66
4	LTPADVHNV	2	0.6000	7.23
5	LEQLRTFER	208	0.6000	7.23
6	MLADARANA	127	0.3000	3.61
7	ILGEARHTA	138	0.3000	3.61
8	LTRLIEENS	38	-0.2000	0
9	VAFSKPPIG	10	-0.4500	0
10	YRTRLKTYL	218	-0.5000	0
11	MNEEQALKA	94	-0.6000	0
12	VTPQATQAI	67	-0.7000	0
13	VLSLAQDTA	105	-0.7000	0
14	INELDQELA	52	-0.9000	0
15	VENELTRLI	34	-1.0000	0
16	LRQAQEKAD	172	-1.1000	0
17	LVENELTRL	33	-1.2000	0

18	IEENSDLRQ	42	-1.5000	0
19	MLADAQSRS	160	-1.6000	0
20	LGQRGSAAP	233	-1.6000	0
21	INQQRAVLE	197	-1.9000	0
22	IMGTINQQR	193	-2.0000	0
23	LRQRINELD	48	-2.1000	0

ALLELE: DRB1_1321	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.9
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Rank	Sequence	At Position	Score	% of Highest Score
1	LKAARVLSL	100	2.8000	31.46
2	YRTRLKTYL	218	1.5000	16.85
3	LTNTAKAES	116	0.9000	10.11
4	LRQAQEKAD	172	0.6000	6.74
5	LRTFEREYR	211	0.3000	3.37
6	FDQFNRGKN	251	0.3000	3.37
7	INQQRAVLE	197	0.1000	1.12
8	LTPADVHNV	2	-0.1000	0
9	VAFSKPPIG	10	-0.1500	0
10	LRQRINELD	48	-0.4000	0
11	LEQLRTFER	208	-0.4000	0
12	MLADARANA	127	-0.7000	0
13	ILGEARHTA	138	-0.7000	0
14	MGTINQORA	194	-1.0000	0
15	LEELGQRGS	230	-1.0000	0
16	LVENELTRL	33	-1.2000	0
17	LTRLIEENS	38	-1.2000	0
18	FEREYRTRL	214	-1.2000	0
19	VDAFLDLVE	27	-1.5000	0
20	VTPQATQAI	67	-1.5000	0
21	LADAQSRSE	161	-1.5000	0
22	FLDLVENEL	30	-1.6000	0
23	MNEEQALKA	94	-1.6000	0

24	IEENSDLRQ	42	-1.7000	0
25	VLSLAQDTA	105	-1.7000	0

ALLELE: DRB1_1322	Threshold for 3 % with score: 1.8	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	2.0000	23.81
2	LKAARVLSL	100	1.7000	20.24
3	LTNTAKAES	116	1.4000	16.67
4	ILGEARHTA	138	1.4000	16.67
5	VENELTRLI	34	1.2000	14.29
6	LTPADVHNV	2	1.1000	13.10
7	VTPQATQAI	67	1.0000	11.90
8	LEQLRTER	208	0.9000	10.71
9	LEELGQRGS	230	0.9000	10.71
10	YRTRLKTYL	218	0.8000	9.52
11	MLADARANA	127	0.6000	7.14
12	VLSLAQDTA	105	-0.2000	0
13	LQADAERKH	182	-0.3200	0
14	INQGRAVLE	197	-0.4000	0
15	LTRLIEENS	38	-0.6000	0
16	LVENELTRL	33	-0.7000	0
17	LGQRGSAAP	233	-0.7000	0
18	VAFSKPPIG	10	-0.8000	0
19	MGTINQORA	194	-0.8000	0
20	LRQRINELD	48	-0.9000	0
21	MLADAQSRS	160	-0.9000	0
22	LRQAQEKAD	172	-0.9000	0
23	MNEEQALKA	94	-1.1000	0
24	INELDQELA	52	-1.3000	0
25	IPAYEPEPG	75	-1.6000	0

ALLELE: DRB1_1323	Threshold for 3 % with score: 1.3	Highest Score achievable by any peptide: 8.4
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Rank	Sequence	At Position	Score	% of Highest Score
1	YRTRLKTYL	218	1.8000	21.43
2	LRTFEREYR	211	1.0000	11.90
3	LKAARVLSL	100	0.7000	8.33
4	LTNTAKAES	116	0.4000	4.76
5	ILGEARHTA	138	0.4000	4.76
6	VENELTRLI	34	0.2000	2.38
7	LTPADVHNV	2	0.1000	1.19
8	LEQLRTFER	208	-0.1000	0
9	LEELGQRGS	230	-0.1000	0
10	MLADARANA	127	-0.4000	0
11	VLSLAQDTA	105	-1.2000	0
12	FEREYRTRL	214	-1.2000	0
13	LQADAERKH	182	-1.3200	0
14	YEPEPGKPA	78	-1.4000	0
15	INQQRAVLE	197	-1.4000	0
16	LTRLIEENS	38	-1.6000	0
17	LVENELTRL	33	-1.7000	0
18	LGQRGSAAP	233	-1.7000	0
19	VAFSKPPIG	10	-1.8000	0
20	MGTINQORA	194	-1.8000	0
21	LRQRINELD	48	-1.9000	0
22	MLADAQSRS	160	-1.9000	0
23	LRQAQEKAD	172	-1.9000	0
24	MNEEQALKA	94	-2.1000	0

ALLELE: DRB1_1327	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	3.5000	39.77

2	LKAARVLSL	100	2.6600	30.23
3	LEQLRTFER	208	2.4000	27.27
4	LTPADVHNV	2	2.1000	23.86
5	VENELTRLI	34	2.1000	23.86
6	VTPQATQAI	67	1.9000	21.59
7	LTNTAKAES	116	1.8000	20.45
8	YRTRLKTYL	218	1.7600	20.00
9	ILGEARHTA	138	1.4000	15.91
10	LEELGQRGS	230	1.3000	14.77
11	INQQRAVLE	197	1.0000	11.36
12	VAFSKPPIG	10	0.6000	6.82
13	MLADARANA	127	0.6000	6.82
14	LGQRGSAAP	233	0.3000	3.41
15	LVENELTRL	33	0.2600	2.95
16	LRQRINELD	48	0.2000	2.27
17	LRQAQEKAD	172	0.2000	2.27
18	LTRLIEENS	38	-0.2000	0
19	IPAYEPEPG	75	-0.2000	0
20	VLSLAQDTA	105	-0.2000	0
21	IMGTINQQR	193	-0.3000	0
22	MLADAQSRS	160	-0.5000	0
23	LADAQSRSE	161	-0.5000	0
24	MGTINQQRA	194	-0.8000	0
25	LEGRLEQLR	204	-0.8000	0

ALLELE: DRB1_1328	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 8.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	3.5000	39.77
2	LKAARVLSL	100	2.6600	30.23
3	LEQLRTFER	208	2.4000	27.27
4	LTPADVHNV	2	2.1000	23.86
5	VENELTRLI	34	2.1000	23.86

6	VTPQATQAI	67	1.9000	21.59
7	LTNTAKAES	116	1.8000	20.45
8	YRTRLKTYL	218	1.7600	20.00
9	ILGEARHTA	138	1.4000	15.91
10	LEELGQRGS	230	1.3000	14.77
11	INQQRAVLE	197	1.0000	11.36
12	VAFSKPPIG	10	0.6000	6.82
13	MLADARANA	127	0.6000	6.82
14	LGQRGSAAP	233	0.3000	3.41
15	LVENELTRL	33	0.2600	2.95
16	LRQRINELD	48	0.2000	2.27
17	LRQAQEKAD	172	0.2000	2.27
18	LTRLIEENS	38	-0.2000	0
19	IPAYEPEPG	75	-0.2000	0
20	VLSLAQDTA	105	-0.2000	0
21	IMGTINQQR	193	-0.3000	0
22	MLADAQSRS	160	-0.5000	0
23	LADAQSRSE	161	-0.5000	0
24	MGTINQQRA	194	-0.8000	0
25	LEGRLEQLR	204	-0.8000	0

ALLELE: DRB1_1501	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	3.9000	39.80
2	LKTYLESQL	222	3.4000	34.69
3	LKAARVLSL	100	3.2000	32.65
4	ILGEARHTA	138	2.2000	22.45
5	YRTRLKTYL	218	1.8000	18.37
6	LVENELTRL	33	1.6000	16.33
7	MLADARANA	127	1.6000	16.33
8	LEQLRTER	208	0.9600	9.80
9	LTPADVHNV	2	0.9000	9.18

10	MNEEQALKA	94	0.9000	9.18
11	FEREYRTRL	214	0.9000	9.18
12	LAAGGGAGV	59	0.8000	8.16
13	VDAFLDLVE	27	0.7000	7.14
14	LRQRINELD	48	0.5000	5.10
15	VHNVAFSKP	7	0.4000	4.08
16	IMGTTNQQR	193	0.4000	4.08
17	IPAYEPEPG	75	0.3000	3.06
18	VLSLAQDTA	105	0.2000	2.04
19	LGQRGSAAP	233	0.2000	2.04
20	VENELTRLI	34	0.1600	1.63
21	IGKRGYNED	17	-0.1000	0
22	FDQFNRGKN	251	-0.1000	0
23	VTPQATQAI	67	-0.1400	0
24	VAFSKPPIG	10	-0.2000	0

ALLELE: DRB1_1502	Threshold for 3 % with score: 3.25	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	2.9000	29.59
2	YRTRLKTYL	218	2.8000	28.57
3	LKTYLESQL	222	2.4000	24.49
4	LKAARVLSL	100	2.2000	22.45
5	FEREYRTRL	214	1.9000	19.39
6	ILGEARHTA	138	1.2000	12.24
7	FDQFNRGKN	251	0.9000	9.18
8	LVENELTRL	33	0.6000	6.12
9	MLADARANA	127	0.6000	6.12
10	FLDLVENEL	30	0.4000	4.08
11	LEQLRTFER	208	-0.0400	0
12	LTPADVHNV	2	-0.1000	0
13	MNEEQALKA	94	-0.1000	0
14	LAAGGGAGV	59	-0.2000	0

15	VDAFLDLVE	27	-0.3000	0
16	LRQRINELD	48	-0.5000	0
17	YLESQLEEL	225	-0.5000	0
18	VHNVAFSKP	7	-0.6000	0
19	IMGTINQQR	193	-0.6000	0
20	IPAYEPEPG	75	-0.7000	0
21	VLSLAQDTA	105	-0.8000	0
22	LGQRGSAAP	233	-0.8000	0
23	VENELTRLI	34	-0.8400	0
24	MGTINQQR	194	-1.0000	0

ALLELE: DRB1_1506	Threshold for 3 % with score: 3.1	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRTFEREYR	211	3.9000	39.80
2	LKTYLESQL	222	3.4000	34.69
3	LKAARVLSL	100	3.2000	32.65
4	ILGEARHTA	138	2.2000	22.45
5	YRTRLKTYL	218	1.8000	18.37
6	LVENELTRL	33	1.6000	16.33
7	MLADARANA	127	1.6000	16.33
8	LEQLRTFER	208	0.9600	9.80
9	LTPADVHNV	2	0.9000	9.18
10	MNEEQALKA	94	0.9000	9.18
11	FEREYRTRL	214	0.9000	9.18
12	LAAGGGAGV	59	0.8000	8.16
13	VDAFLDLVE	27	0.7000	7.14
14	LRQRINELD	48	0.5000	5.10
15	VHNVAFSKP	7	0.4000	4.08
16	IMGTINQQR	193	0.4000	4.08
17	IPAYEPEPG	75	0.3000	3.06
18	VLSLAQDTA	105	0.2000	2.04
19	LGQRGSAAP	233	0.2000	2.04

20	VENELTRLI	34	0.1600	1.63
21	IGKRGYNED	17	-0.1000	0
22	FDQFNRGKN	251	-0.1000	0
23	VTPQATQAI	67	-0.1400	0
24	VAFSKPPIG	10	-0.2000	0

ALLELE: DRB5_0101	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LEQLRTFER	208	2.9000	29.59
2	IMGTINQQR	193	2.5000	25.51
3	LRTFEREYR	211	0.9000	9.18
4	LKAARVLSL	100	0.7000	7.14
5	YRTRLKTYL	218	0.6000	6.12
6	FLDLVENEL	30	0.1000	1.02
7	MGTINQQRA	194	0.1000	1.02
8	FSKPPIGKR	12	-0.1000	0
9	FEREYRTL	214	-0.2000	0
10	VTPQATQAI	67	-0.3000	0
11	YEPEPGKPA	78	-0.3000	0
12	MPLTPADVH	0	-0.7000	0
13	VAFSKPPIG	10	-0.7000	0
14	LEELGQRGS	230	-0.9000	0
15	LTPADVHNV	2	-1.0000	0
16	LTNTAKAES	116	-1.0000	0
17	LVENELTRL	33	-1.2000	0
18	ILGEARHTA	138	-1.2000	0
19	LEGRLEQLR	204	-1.2000	0
20	VHNVAFSKP	7	-1.3000	0
21	YLESQLEEL	225	-1.3000	0
22	LRQAQEKAD	172	-1.4000	0
23	LQADAERKH	182	-1.4000	0
24	LKTYLESQL	222	-1.4000	0

ALLELE: DRB5_0105	Threshold for 3 % with score: 2.3	Highest Score achievable by any peptide: 9.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	LEQLRTFER	208	2.9000	29.59
2	IMGTINQQR	193	2.5000	25.51
3	LRTFEREYR	211	0.9000	9.18
4	LKAARVLSL	100	0.7000	7.14
5	YRTRLKTYL	218	0.6000	6.12
6	FLDLVENEL	30	0.1000	1.02
7	MGTINQQRA	194	0.1000	1.02
8	FSKPPIGKR	12	-0.1000	0
9	FEREYRTRL	214	-0.2000	0
10	VTPQATQAI	67	-0.3000	0
11	YEPEPGKPA	78	-0.3000	0
12	MPLTPADVH	0	-0.7000	0
13	VAFSKPPIG	10	-0.7000	0
14	LEELGQRGS	230	-0.9000	0
15	LTPADVHNV	2	-1.0000	0
16	LTNTAKAES	116	-1.0000	0
17	LVENELTRL	33	-1.2000	0
18	ILGEARHTA	138	-1.2000	0
19	LEGRLEQLR	204	-1.2000	0
20	VHNVAFSKP	7	-1.3000	0
21	YLESQLEEL	225	-1.3000	0
22	LRQAQEKAD	172	-1.4000	0
23	LQADAERKH	182	-1.4000	0
24	LKTYLESQL	222	-1.4000	0