

MHC Class-II Binding Peptide Prediction Results

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INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Tue Apr 20 23:54:47 2010
Length of input sequence	314 amino acids
Number of nanomers from input sequence	306
Number of nanomers with obligatory P1 anchor residue	81
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	31

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	VRGLKALLA	94	2.6000	43.33
2	IRRVASARV	168	1.5500	25.83
3	LKALLATVV	97	1.3900	23.17
4	VQRQYPSAL	176	1.1000	18.33
5	VGRIAAPSV	255	1.0700	17.83
6	VGIGLGLAL	109	0.8000	13.33
7	LQVLTALHP	241	0.8000	13.33
8	VLAVVGIGL	105	0.7500	12.50

9	IIGIGAVSR	130	0.5000	8.33
10	IVIIGIGAV	128	0.4000	6.67
11	VIIIGIGAVS	129	0.3000	5.00
12	LRITIVERV	184	0.3000	5.00
13	LTLADGRVV	268	0.0900	1.50
14	LLQIDTQQV	153	-0.2000	0
15	LHPEVASQV	247	-0.2000	0
16	LYFTPAMSA	117	-0.2100	0
17	IGLGLALYF	111	-0.3000	0
18	ITIVERVPV	186	-0.3500	0
19	VVRGLKALL	93	-0.4000	0
20	YPSALRITI	180	-0.8000	0
21	VVLAVVGIG	104	-0.9000	0
22	LTALHPEVA	244	-0.9000	0
23	VASQVGRIA	251	-0.9100	0
24	LLTQPGRTY	294	-1.0100	0
25	VVGIGLGLA	108	-1.3000	0
26	VVIWGTTDR	275	-1.3100	0
27	IVERVPVVV	188	-1.4000	0
28	LLATVVLAV	100	-1.5000	0
29	VSREEVLDA	136	-1.8000	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6
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Rank	Sequence	At Position	Score	% of Highest Score
1	VRGLKALLA	94	3.6000	60.00
2	IRRVASARV	168	2.5500	42.50
3	LKALLATVV	97	2.3900	39.83
4	VQRQYPSAL	176	2.1000	35.00
5	VGRIAAPSV	255	2.0700	34.50
6	VGIGLGLAL	109	1.8000	30.00
7	LQVLTALHP	241	1.8000	30.00
8	VLAVVGIGL	105	1.7500	29.17

9	IIGIGAVSR	130	1.5000	25.00
10	IVIIGIGAV	128	1.4000	23.33
11	VIIIGIGAVS	129	1.3000	21.67
12	LRITIVERV	184	1.3000	21.67
13	LTLADGRVV	268	1.0900	18.17
14	VRPATPLLQ	147	1.0000	16.67
15	LLQIDTQQV	153	0.8000	13.33
16	LHPEVASQV	247	0.8000	13.33
17	LYFTPAMSA	117	0.7900	13.17
18	IGLGLALYF	111	0.7000	11.67
19	ITIVERVPV	186	0.6500	10.83
20	VVRGLKALL	93	0.6000	10.00
21	VVLAVVGIG	104	0.1000	1.67
22	LTALHPEVA	244	0.1000	1.67
23	VASQVGRIA	251	0.0900	1.50
24	LLTQPGRTY	294	-0.0100	0
25	VVGIGLGLA	108	-0.3000	0
26	VVIWGTTDR	275	-0.3100	0
27	IVERVPVVV	188	-0.4000	0
28	LLATVVLAV	100	-0.5000	0
29	VSREEVLDA	136	-0.8000	0
30	IVSEQNPAK	79	-0.8300	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	IVIIGIGAV	128	5.2000	54.74
2	VVLAVVGIG	104	4.8000	50.53
3	LQIDTQQVA	154	4.6000	48.42
4	VVRGLKALL	93	4.5600	48.00
5	LRITIVERV	184	4.0000	42.11
6	VVIWGTTDR	275	3.8000	40.00
7	VIIIGIGAVS	129	3.5000	36.84

8	IGIGAVSRE	131	3.4700	36.53
9	VVKDFSDGP	195	3.4000	35.79
10	VVGIGLGLA	108	3.1000	32.63
11	IGLGLALYF	111	3.1000	32.63
12	IRRVASARV	168	3.1000	32.63
13	VRPATPLLQ	147	3.0000	31.58
14	ITIVERVPV	186	3.0000	31.58
15	VATIRRVAS	165	2.8000	29.47
16	VGRIAAPSV	255	2.7000	28.42
17	VRGLKALLA	94	2.6000	27.37
18	LALYFTPAM	115	2.6000	27.37
19	IIGIGAVSR	130	2.5000	26.32
20	LLQIDTQQV	153	2.5000	26.32
21	FATDPPPPA	213	2.5000	26.32
22	VQRQYPSAL	176	2.4300	25.58
23	FDVDNPGPS	225	2.2000	23.16
24	VERVPVVVK	189	2.0000	21.05
25	VGIGLGLAL	109	1.9600	20.63
26	VLTALHPEV	243	1.9000	20.00
27	LYFTPAMSA	117	1.8000	18.95
28	VPVVVKDFS	192	1.8000	18.95
29	VIWGTTDRC	276	1.8000	18.95
30	LLATVVLAV	100	1.7000	17.89
31	LAVVGIGLG	106	1.7000	17.89

ALLELE: DRB1_0305	Threshold for 3 % with score: 1.7	Highest Score achievable by any peptide: 9.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	LQIDTQQVA	154	3.6000	39.56
2	FATDPPPPA	213	3.5000	38.46
3	IVIIGIGAV	128	3.2000	35.16
4	FDVDNPGPS	225	2.8000	30.77
5	VRPATPLLQ	147	2.7000	29.67

6	VVRGLKALL	93	2.6000	28.57
7	VVLAVVGIG	104	2.4000	26.37
8	FDRDGVDF	206	2.3000	25.27
9	VVGIGLGLA	108	2.1000	23.08
10	VIIIGIGAVS	129	2.1000	23.08
11	LRITIVERV	184	2.0000	21.98
12	VRGLKALLA	94	1.6000	17.58
13	VATIRRVAS	165	1.4000	15.38
14	VVKDFSDGP	195	1.4000	15.38
15	VVIWGTTDR	275	1.3000	14.29
16	IRRVASARV	168	1.1000	12.09
17	IGIGAVSRE	131	1.0700	11.76
18	ITIVERVPV	186	1.0000	10.99
19	VERVPVVVK	189	0.9000	9.89
20	LYFTPAMSA	117	0.8000	8.79
21	VASARVQRQ	171	0.8000	8.79
22	YPSALRITI	180	0.8000	8.79
23	VIWGTTDRC	276	0.8000	8.79
24	VGRIAAPSV	255	0.7000	7.69
25	LLQIDTQQV	153	0.5000	5.49
26	VQRQYPSAL	176	0.4700	5.16
27	VPVVVKDFS	192	0.4000	4.40
28	IGLGLALYF	111	0.2000	2.20
29	IVSEQNPAK	79	0.1000	1.10
30	LALYFTPAM	115	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	LQIDTQQVA	154	4.7000	53.41
2	VRPATLLQ	147	4.2000	47.73
3	VVRGLKALL	93	3.6000	40.91
4	LRITIVERV	184	3.4000	38.64

5	VRGLKALLA	94	3.1000	35.23
6	VIIIGIGAVS	129	3.1000	35.23
7	IVIIGIGAV	128	2.8000	31.82
8	VVKDFSDGP	195	2.7000	30.68
9	VVIWGTTDR	275	2.3000	26.14
10	VATIRRVAS	165	2.2800	25.91
11	IRRVASARV	168	2.1000	23.86
12	VIWGTTDRC	276	2.1000	23.86
13	VVLAVVGIG	104	2.0000	22.73
14	VASARVQRQ	171	1.9000	21.59
15	ITIVERVPV	186	1.8800	21.36
16	IGIGAVSRE	131	1.8000	20.45
17	VERVPVVVK	189	1.7800	20.23
18	VVGIGLGLA	108	1.7000	19.32
19	IGLGLALYF	111	1.7000	19.32
20	VPVVVKDFS	192	1.7000	19.32
21	LLQIDTQQV	153	1.6000	18.18
22	FDRDGVDF	206	1.6000	18.18
23	VGIGLGLAL	109	1.5000	17.05
24	LYFTPAMSA	117	1.5000	17.05
25	VSREEVLDA	136	1.3000	14.77
26	LLATVVLA	100	1.2000	13.64
27	VQRQYPSAL	176	1.2000	13.64
28	FATDPPPPA	213	1.1000	12.50
29	LQVLTALHP	241	1.1000	12.50
30	IGAVSREEV	133	1.0000	11.36
31	IIGIGAVSR	130	0.8800	10.00

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	LQIDTQQVA	154	4.7000	53.41
2	VRPATPLLQ	147	4.2000	47.73

3	VVRGLKALL	93	3.6000	40.91
4	LRITIVERV	184	3.4000	38.64
5	VRGLKALLA	94	3.1000	35.23
6	VIIGIGAVS	129	3.1000	35.23
7	IVIIGIGAV	128	2.8000	31.82
8	VVKDFSDGP	195	2.7000	30.68
9	VVIWGTTDR	275	2.3000	26.14
10	VATIRRVAS	165	2.2800	25.91
11	IRRVASARV	168	2.1000	23.86
12	VIWGTTDRC	276	2.1000	23.86
13	VVLAVVGIG	104	2.0000	22.73
14	VASARVQRQ	171	1.9000	21.59
15	ITIVERVPV	186	1.8800	21.36
16	IGIGAVSRE	131	1.8000	20.45
17	VERVPVVVK	189	1.7800	20.23
18	VVGIGLGLA	108	1.7000	19.32
19	IGLGLALYF	111	1.7000	19.32
20	VPVVVKDFS	192	1.7000	19.32
21	LLQIDTQQV	153	1.6000	18.18
22	FDRDGVDF	206	1.6000	18.18
23	VGIGLGLAL	109	1.5000	17.05
24	LYFTPAMSA	117	1.5000	17.05
25	VSREEVLDA	136	1.3000	14.77
26	LLATVVLA	100	1.2000	13.64
27	VQRQYPSAL	176	1.2000	13.64
28	FATDPPPPA	213	1.1000	12.50
29	LQVLTALHP	241	1.1000	12.50
30	IGAVSREEV	133	1.0000	11.36
31	IIGIGAVSR	130	0.8800	10.00

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	LQIDTQQVA	154	4.7000	53.41
2	VRPATPLLQ	147	4.2000	47.73
3	VVRGLKALL	93	3.6000	40.91
4	LRITIVERV	184	3.4000	38.64
5	VRGLKALLA	94	3.1000	35.23
6	VIIIGIGAVS	129	3.1000	35.23
7	IVIIGIGAV	128	2.8000	31.82
8	VVKDFSDGP	195	2.7000	30.68
9	VVIWGTTDR	275	2.3000	26.14
10	VATIRRVAS	165	2.2800	25.91
11	IRRVASARV	168	2.1000	23.86
12	VIWGTTDRC	276	2.1000	23.86
13	VVLAVVGIG	104	2.0000	22.73
14	VASARVQRQ	171	1.9000	21.59
15	ITIVERVPV	186	1.8800	21.36
16	IGIGAVSRE	131	1.8000	20.45
17	VERVPVVVK	189	1.7800	20.23
18	VVGIGLGLA	108	1.7000	19.32
19	IGLGLALYF	111	1.7000	19.32
20	VPVVVKDFS	192	1.7000	19.32
21	LLQIDTQQV	153	1.6000	18.18
22	FDRDGVDF	206	1.6000	18.18
23	VGIGLGLAL	109	1.5000	17.05
24	LYFTPAMSA	117	1.5000	17.05
25	VSREEVLDA	136	1.3000	14.77
26	LLATVVLAV	100	1.2000	13.64
27	VQRQYPSAL	176	1.2000	13.64
28	FATDPPPPA	213	1.1000	12.50
29	LQVLTALHP	241	1.1000	12.50
30	IGAVSREEV	133	1.0000	11.36
31	IIGIGAVSR	130	0.8800	10.00

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

2.4

9.5

Rank	Sequence	At Position	Score	% of Highest Score
1	IVIIGIGAV	128	4.2000	44.21
2	VVLAVVGIG	104	3.8000	40.00
3	LQIDTQQVA	154	3.6000	37.89
4	VVRGLKALL	93	3.5600	37.47
5	FATDPPPPA	213	3.5000	36.84
6	FDVDNPGPS	225	3.2000	33.68
7	LRITIVERV	184	3.0000	31.58
8	VVIWGTTDR	275	2.8000	29.47
9	VIIGIGAVS	129	2.5000	26.32
10	IGIGAVSRE	131	2.4700	26.00
11	VVKDFSDGP	195	2.4000	25.26
12	FDRDGV DFA	206	2.3000	24.21
13	VVGIGLGLA	108	2.1000	22.11
14	IGLGLALYF	111	2.1000	22.11
15	IRRVASARV	168	2.1000	22.11
16	VRPATPLLQ	147	2.0000	21.05
17	ITIVERVPV	186	2.0000	21.05
18	VATIRRVAS	165	1.8000	18.95
19	YPSALRITI	180	1.7000	17.89
20	VGRIAAPSV	255	1.7000	17.89
21	VRGLKALLA	94	1.6000	16.84
22	LALYFTPAM	115	1.6000	16.84
23	IIGIGAVSR	130	1.5000	15.79
24	LLQIDTQQV	153	1.5000	15.79
25	VQRQYPSAL	176	1.4300	15.05
26	VERVPVVVK	189	1.0000	10.53
27	VGIGLGLAL	109	0.9600	10.11
28	VTALHPEV	243	0.9000	9.47
29	LYFTPAMSA	117	0.8000	8.42
30	VPVVVKDFS	192	0.8000	8.42
31	VIWGTTDRC	276	0.8000	8.42

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	LQIDTQQVA	154	4.7000	53.41
2	VRPATPLLQ	147	4.2000	47.73
3	VVRGLKALL	93	3.6000	40.91
4	LRITIVERV	184	3.4000	38.64
5	VRGLKALLA	94	3.1000	35.23
6	VIIIGIGAVS	129	3.1000	35.23
7	IVIIGIGAV	128	2.8000	31.82
8	VVKDFSDGP	195	2.7000	30.68
9	VVIWGTDDR	275	2.3000	26.14
10	VATIRRVAS	165	2.2800	25.91
11	IRRVASARV	168	2.1000	23.86
12	VIWGTDDRC	276	2.1000	23.86
13	VVLAVVGIG	104	2.0000	22.73
14	VASARVQRQ	171	1.9000	21.59
15	ITIVERVPV	186	1.8800	21.36
16	IGIGAVSRE	131	1.8000	20.45
17	VERVPVVVK	189	1.7800	20.23
18	VVGIGLGLA	108	1.7000	19.32
19	IGLGLALYF	111	1.7000	19.32
20	VPVVVKDFS	192	1.7000	19.32
21	LLQIDTQQV	153	1.6000	18.18
22	FDRDGVDFDA	206	1.6000	18.18
23	VGIGLGLAL	109	1.5000	17.05
24	LYFTPAMSA	117	1.5000	17.05
25	VSREEVLDA	136	1.3000	14.77
26	LLATVVLA	100	1.2000	13.64
27	VQRQYPSAL	176	1.2000	13.64
28	FATDPPPPA	213	1.1000	12.50
29	LQVLTALHP	241	1.1000	12.50
30	IGAVSREEV	133	1.0000	11.36

31	IIGIGAVSR	130	0.8800	10.00
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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	LRITIVERV	184	3.8000	44.19
2	IVSEQNPAK	79	3.1000	36.05
3	VRGLKALLA	94	2.9000	33.72
4	VRPATPLLQ	147	2.7000	31.40
5	VSREEVLDA	136	2.5000	29.07
6	LYFTPAMSA	117	2.2000	25.58
7	VVIWGTTDR	275	2.2000	25.58
8	LLQIDTQQV	153	2.0000	23.26
9	VVKDFSDGP	195	1.9000	22.09
10	LLATVVLA V	100	1.6000	18.60
11	LQIDTQQVA	154	1.6000	18.60
12	FDRDGV DFA	206	1.4000	16.28
13	IVIIGIGAV	128	1.3000	15.12
14	IRRVASARV	168	1.3000	15.12
15	LQVLTALHP	241	0.9000	10.47
16	VVLAVVGIG	104	0.7000	8.14
17	FATDPPPPA	213	0.7000	8.14
18	LHPEVASQV	247	0.7000	8.14
19	LAALLTQPG	291	0.7000	8.14
20	VASARVQRQ	171	0.6000	6.98
21	VQRQYPSAL	176	0.5000	5.81
22	IIGIGAVSR	130	0.1800	2.09
23	LKALLATVV	97	0.1000	1.16
24	VIWGTTDRC	276	0.1000	1.16
25	VVGIGLGLA	108	-0.3000	0
26	FTPAMSARE	119	-0.4000	0
27	VGRIAAPSV	255	-0.4000	0
28	VERVPVVVK	189	-0.4200	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	VVIWGTTDR	275	6.2000	64.58
2	VRPATPLLQ	147	4.0000	41.67
3	LLQIDTQQV	153	3.3800	35.21
4	VRGLKALLA	94	2.8000	29.17
5	VASARVQRQ	171	2.7000	28.13
6	IRRVASARV	168	2.5000	26.04
7	LRITIVERV	184	2.2000	22.92
8	LYFTPAMSA	117	2.0000	20.83
9	LLATVVLA V	100	1.7000	17.71
10	IVERVPVVV	188	1.4000	14.58
11	LAALLTQPG	291	1.4000	14.58
12	LDAARVRPA	142	1.3000	13.54
13	LALYFTPAM	115	1.1000	11.46
14	VIIGIGAVS	129	1.1000	11.46
15	VVLAVVGIG	104	0.9000	9.38
16	VERVPVVVK	189	0.9000	9.38
17	IGLGLALYF	111	0.8000	8.33
18	LQVLTALHP	241	0.8000	8.33
19	IVIIGIGAV	128	0.7800	8.12
20	IIGIGAVSR	130	0.5800	6.04
21	MSAREIVII	123	0.5000	5.21
22	LTLADGRVV	268	0.5000	5.21
23	VVVKDFSDG	194	0.2000	2.08
24	VIWGTTDRC	276	0.2000	2.08
25	IGIGAVSRE	131	0.1000	1.04
26	VQRQYPSAL	176	0.1000	1.04

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

8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVIWGTTDR	275	4.8500	55.11
2	VRGLKALLA	94	3.7000	42.05
3	IRRVASARV	168	3.7000	42.05
4	VRPATPLLQ	147	3.3000	37.50
5	LLQIDTQQV	153	3.1000	35.23
6	IVIIGIGAV	128	2.7000	30.68
7	LRITIVERV	184	2.3000	26.14
8	LKALLATVV	97	1.8000	20.45
9	VVLAVVGIG	104	1.8000	20.45
10	VERVPVVVK	189	1.8000	20.45
11	LQVLTALHP	241	1.7000	19.32
12	LAALLTQPG	291	1.7000	19.32
13	LYFTPAMSA	117	1.5000	17.05
14	VASARVQRQ	171	1.4000	15.91
15	VQRQYPSAL	176	1.4000	15.91
16	IIGIGAVSR	130	1.3000	14.77
17	IVSEQNPAK	79	1.2000	13.64
18	VVGIGLGLA	108	1.1000	12.50
19	LALYFTPAM	115	1.1000	12.50
20	LLATVVVLAV	100	0.6000	6.82
21	VGRIAAPSV	255	0.6000	6.82
22	VASITLTLA	263	0.6000	6.82
23	VSREEVLDA	136	0.5000	5.68
24	LTALHPEVA	244	0.3000	3.41
25	LQIDTQQVA	154	-0.1000	0
26	LHPEVASQV	247	-0.2000	0
27	LPYFDVDNP	222	-0.3000	0
28	VVVKDFSDG	194	-0.5000	0
29	VVKDFSDGP	195	-0.5000	0
30	VIIGIGAVS	129	-0.6000	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	VVIWGTTDR	275	3.8500	40.96
2	VRPATPLLQ	147	3.1000	32.98
3	IRRVASARV	168	3.0000	31.91
4	VRGLKALLA	94	2.7000	28.72
5	FTPAMSARE	119	2.6000	27.66
6	LLQIDTQQV	153	2.4000	25.53
7	VVLAVVGIG	104	2.1000	22.34
8	IVIIGIGAV	128	2.0000	21.28
9	LAALLTQPG	291	2.0000	21.28
10	LRITIVERV	184	1.6000	17.02
11	VQRQYPSAL	176	1.4000	14.89
12	IGIGAVSRE	131	1.3000	13.83
13	LALYFTPAM	115	1.2000	12.77
14	VASARVQRQ	171	1.2000	12.77
15	LKALLATVV	97	1.1000	11.70
16	LQVLTALHP	241	1.1000	11.70
17	LYFTPAMSA	117	0.5000	5.32
18	IIGIGAVSR	130	0.3000	3.19
19	VVGIGLGLA	108	0.1000	1.06
20	VERVPVVVK	189	0.1000	1.06
21	LLATVVLAV	100	-0.1000	0
22	VGRIAAPSV	255	-0.1000	0
23	VVVKDFSDG	194	-0.2000	0
24	VASITLTLA	263	-0.4000	0
25	IVSEQNPAK	79	-0.5000	0
26	VSREEVLDA	136	-0.5000	0
27	YFDVDNPGP	224	-0.6000	0
28	LTALHPEVA	244	-0.7000	0
29	LPYFDVDNP	222	-0.9000	0
30	LHPEVASQV	247	-0.9000	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	VVIWGTTDR	275	3.8500	43.75
2	VRGLKALLA	94	2.7000	30.68
3	IRRVASARV	168	2.7000	30.68
4	VRPATPLLQ	147	2.3000	26.14
5	LLQIDTQQV	153	2.1000	23.86
6	IVIIGIGAV	128	1.7000	19.32
7	LRITIVERV	184	1.3000	14.77
8	LKALLATVV	97	0.8000	9.09
9	VVLAVVGIG	104	0.8000	9.09
10	VERVPVVVK	189	0.8000	9.09
11	LQVLTALHP	241	0.7000	7.95
12	LAALLTQPG	291	0.7000	7.95
13	LYFTPAMSA	117	0.5000	5.68
14	VASARVQRQ	171	0.4000	4.55
15	VQRQYPSAL	176	0.4000	4.55
16	IIGIGAVSR	130	0.3000	3.41
17	IVSEQNPAK	79	0.2000	2.27
18	VVGIGLGLA	108	0.1000	1.14
19	LALYFTPAM	115	0.1000	1.14
20	LLATVVLAV	100	-0.4000	0
21	FTPAMSARE	119	-0.4000	0
22	VGRIAAPSV	255	-0.4000	0
23	VASITLTLA	263	-0.4000	0
24	VSREEVLDA	136	-0.5000	0
25	LTALHPEVA	244	-0.7000	0
26	YFDVDNPGP	224	-1.0000	0
27	LQIDTQQVA	154	-1.1000	0
28	LHPEVASQV	247	-1.2000	0
29	LPYFDVDNP	222	-1.3000	0
30	VVVKDFSDG	194	-1.5000	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	VVIWGTTDR	275	4.8500	51.60
2	VRPATPLLQ	147	4.1000	43.62
3	IRRVASARV	168	4.0000	42.55
4	VRGLKALLA	94	3.7000	39.36
5	LLQIDTQQV	153	3.4000	36.17
6	VVLAVVGIG	104	3.1000	32.98
7	IVIIGIGAV	128	3.0000	31.91
8	LAALLTQPG	291	3.0000	31.91
9	LRITIVERV	184	2.6000	27.66
10	VQRQYPSAL	176	2.4000	25.53
11	IGIGAVSRE	131	2.3000	24.47
12	LALYFTPAM	115	2.2000	23.40
13	VASARVQRQ	171	2.2000	23.40
14	LKALLATVV	97	2.1000	22.34
15	LQVLTALHP	241	2.1000	22.34
16	FTPAMSARE	119	1.6000	17.02
17	LYFTPAMSA	117	1.5000	15.96
18	IIGIGAVSR	130	1.3000	13.83
19	VVGIGLGLA	108	1.1000	11.70
20	VERVPVVVK	189	1.1000	11.70
21	LLATVVLA	100	0.9000	9.57
22	VGRIAAPSV	255	0.9000	9.57
23	VVVKDFSDG	194	0.8000	8.51
24	VASITLTLA	263	0.6000	6.38
25	IVSEQNPAK	79	0.5000	5.32
26	VSREEVLDA	136	0.5000	5.32
27	LTALHPEVA	244	0.3000	3.19
28	LPYFDVDNP	222	0.1000	1.06
29	LHPEVASQV	247	0.1000	1.06
30	VLAVVGIGL	105	0.0800	0.85

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	LRITIVERV	184	4.8000	53.33
2	VVIWGTTDR	275	3.7000	41.11
3	IVSEQNPAK	79	3.2000	35.56
4	LLQIDTQQV	153	3.0000	33.33
5	VRGLKALLA	94	2.9000	32.22
6	VVKDFSDGP	195	2.9000	32.22
7	LLATVVLA V	100	2.6000	28.89
8	VSREEVLDA	136	2.5000	27.78
9	IVIIGIGAV	128	2.3000	25.56
10	IRRVASARV	168	2.3000	25.56
11	LYFTPAMSA	117	2.2000	24.44
12	VVLAVVGIG	104	2.1000	23.33
13	LAALLTQPG	291	2.1000	23.33
14	VRPATPLLQ	147	2.0000	22.22
15	LQVLTALHP	241	1.9000	21.11
16	LHPEVASQV	247	1.7000	18.89
17	IIGIGAVSR	130	1.6800	18.67
18	LQIDTQQVA	154	1.6000	17.78
19	VQRQYPSAL	176	1.4600	16.22
20	FDRDGVDF A	206	1.4000	15.56
21	LKALLATVV	97	1.1000	12.22
22	FTPAMSARE	119	1.0000	11.11
23	ITLTLADGR	266	0.9000	10.00
24	LALYFTPAM	115	0.7000	7.78
25	FATDPPPPA	213	0.7000	7.78
26	VGRIAAPSV	255	0.6000	6.67
27	IGLGLALYF	111	0.5000	5.56
28	FDVDNPGPS	225	0.4000	4.44
29	VIWGTTDRC	276	0.1000	1.11

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	VVIWGTTDR	275	4.8500	55.11
2	VRGLKALLA	94	3.7000	42.05
3	IRRVASARV	168	3.7000	42.05
4	VRPATPLLQ	147	3.3000	37.50
5	LLQIDTQQV	153	3.1000	35.23
6	IVIIGIGAV	128	2.7000	30.68
7	LRITIVERV	184	2.3000	26.14
8	LKALLATVV	97	1.8000	20.45
9	VVLAVVGIG	104	1.8000	20.45
10	VERVPVVVK	189	1.8000	20.45
11	LQVLTALHP	241	1.7000	19.32
12	LAALLTQPG	291	1.7000	19.32
13	LYFTPAMSA	117	1.5000	17.05
14	VASARVQRQ	171	1.4000	15.91
15	VQRQYPSAL	176	1.4000	15.91
16	IIGIGAVSR	130	1.3000	14.77
17	IVSEQNPAK	79	1.2000	13.64
18	VVGIGLGLA	108	1.1000	12.50
19	LALYFTPAM	115	1.1000	12.50
20	LLATVVVLAV	100	0.6000	6.82
21	VGRIAAPSV	255	0.6000	6.82
22	VASITLTLA	263	0.6000	6.82
23	VSREEVLDA	136	0.5000	5.68
24	LTALHPEVA	244	0.3000	3.41
25	LQIDTQQVA	154	-0.1000	0
26	LHPEVASQV	247	-0.2000	0
27	LPYFDVDNP	222	-0.3000	0
28	VVVKDFSDG	194	-0.5000	0
29	VVKDFSDGP	195	-0.5000	0

30	VIIGIGAVS	129	-0.6000	0
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ALLELE: DRB1_0426	Threshold for 3 % with score: 1.6	Highest Score achievable by any peptide: 8.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRITIVERV	184	3.8000	44.19
2	IVSEQNPAK	79	3.1000	36.05
3	VRGLKALLA	94	2.9000	33.72
4	VRPATPLLQ	147	2.7000	31.40
5	VSREEVLDA	136	2.5000	29.07
6	LYFTPAMSA	117	2.2000	25.58
7	VVIWGTTDR	275	2.2000	25.58
8	LLQIDTQQV	153	2.0000	23.26
9	VVKDFSDGP	195	1.9000	22.09
10	LLATVVLA V	100	1.6000	18.60
11	LQIDTQQVA	154	1.6000	18.60
12	FDRDGVDF A	206	1.4000	16.28
13	IVIIGIGAV	128	1.3000	15.12
14	IRRVASARV	168	1.3000	15.12
15	LQVLTALHP	241	0.9000	10.47
16	VVLAVVGIG	104	0.7000	8.14
17	FATDPPPPA	213	0.7000	8.14
18	LHPEVASQV	247	0.7000	8.14
19	LAALLTQPG	291	0.7000	8.14
20	VASARVQRQ	171	0.6000	6.98
21	VQRQYPSAL	176	0.5000	5.81
22	IIGIGAVSR	130	0.1800	2.09
23	LKALLATVV	97	0.1000	1.16
24	VIWGTTDRC	276	0.1000	1.16
25	VVGIGLGLA	108	-0.3000	0
26	FTPAMSARE	119	-0.4000	0
27	VGRIAAPSV	255	-0.4000	0
28	VERVPVVVK	189	-0.4200	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	LRITIVERV	184	7.1000	61.21
2	VLAVVGIGL	105	6.1000	52.59
3	LLATVVLAV	100	5.7000	49.14
4	IRRVASARV	168	5.4000	46.55
5	IVIIGIGAV	128	5.2000	44.83
6	VGIGLGLAL	109	4.9000	42.24
7	YPSALRITI	180	4.4000	37.93
8	LLQIDTQQV	153	4.1200	35.52
9	LYFTPAMSA	117	3.9000	33.62
10	ITIVERVPV	186	3.9000	33.62
11	IGLGLALYF	111	3.7000	31.90
12	VGRIAAPSV	255	3.1000	26.72
13	VVRGLKALL	93	3.0000	25.86
14	VRGLKALLA	94	2.8000	24.14
15	VQRQYPSAL	176	2.7000	23.28
16	VRPATPLLQ	147	2.3000	19.83
17	LKALLATVV	97	2.2000	18.97
18	IIGIGAVSR	130	2.2000	18.97
19	IGAVSREEV	133	2.2000	18.97
20	MSAREIVII	123	2.1000	18.10
21	LTLADGRVV	268	2.1000	18.10
22	IVERVPVVV	188	1.9000	16.38
23	VVLAVVGIG	104	1.6000	13.79
24	VVIWGTTDR	275	1.5200	13.10
25	VVGIGLGLA	108	1.5000	12.93
26	LQVLTALHP	241	1.5000	12.93
27	VERVPVVVK	189	1.3000	11.21
28	IAAPSVASI	258	1.3000	11.21
29	LHPEVASQV	247	1.1000	9.48

30	LATVVLAHV	101	1.0000	8.62
31	LGLALYFTP	113	1.0000	8.62

ALLELE: DRB1_0703	Threshold for 3 % with score: 4.0	Highest Score achievable by any peptide: 11.6
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Rank	Sequence	At Position	Score	% of Highest Score
1	LRITIVERV	184	7.1000	61.21
2	VLAVVGIGL	105	6.1000	52.59
3	LLATVVLAHV	100	5.7000	49.14
4	IRRVASARV	168	5.4000	46.55
5	IVIIGIGAV	128	5.2000	44.83
6	VGIGLGLAL	109	4.9000	42.24
7	YPSALRITI	180	4.4000	37.93
8	LLQIDTQQV	153	4.1200	35.52
9	LYFTPAMSA	117	3.9000	33.62
10	ITIVERVPV	186	3.9000	33.62
11	IGLGLALYF	111	3.7000	31.90
12	VGRIAAPSV	255	3.1000	26.72
13	VVRGLKALL	93	3.0000	25.86
14	VRGLKALLA	94	2.8000	24.14
15	VQRQYPSAL	176	2.7000	23.28
16	VRPATPLLQ	147	2.3000	19.83
17	LKALLATVV	97	2.2000	18.97
18	IIGIGAVSR	130	2.2000	18.97
19	IGAVSREEV	133	2.2000	18.97
20	MSAREIVII	123	2.1000	18.10
21	LTLADGRVV	268	2.1000	18.10
22	IVERVPVVV	188	1.9000	16.38
23	VVLAVVGIG	104	1.6000	13.79
24	VVIWGTTDR	275	1.5200	13.10
25	VVGIGLGLA	108	1.5000	12.93
26	LQVLTALHP	241	1.5000	12.93
27	VERVPVVVK	189	1.3000	11.21

28	IAAPSVASI	258	1.3000	11.21
29	LHPEVASQV	247	1.1000	9.48
30	LATVVLAVV	101	1.0000	8.62
31	LGLALYFTP	113	1.0000	8.62

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	VVLAVVGIG	104	3.1000	36.05
2	VRPATPLLQ	147	3.0000	34.88
3	IVIIGIGAV	128	2.7000	31.40
4	LALYFTPAM	115	2.5000	29.07
5	VVRGLKALL	93	2.1000	24.42
6	VRGLKALLA	94	1.8000	20.93
7	WGTDRCEE	278	1.8000	20.93
8	IRRVASARV	168	1.7000	19.77
9	FTPAMSARE	119	1.5000	17.44
10	VVVKDFSDG	194	1.5000	17.44
11	VVGIGLGLA	108	1.3000	15.12
12	IGIGAVSRE	131	1.2000	13.95
13	IVERVPVVV	188	1.2000	13.95
14	VIIGIGAVS	129	0.6000	6.98
15	MSAREIVII	123	0.5000	5.81
16	VASARVQRQ	171	0.5000	5.81
17	LAVVGIGLG	106	0.3000	3.49
18	ITIVERVPV	186	0.3000	3.49
19	LQVLTALHP	241	0.2000	2.33
20	LRITIVERV	184	0.1000	1.16
21	VATIRRVAS	165	-0.1000	0
22	YPSALRITI	180	-0.2000	0
23	LAALLTQPG	291	-0.4000	0
24	LLATVVLAV	100	-0.5000	0
25	LLQIDTQQV	153	-0.5000	0

26	LYFTPAMSA	117	-0.6000	0
27	VSREEVLDA	136	-0.7000	0
28	LQIDTQQVA	154	-0.8000	0
29	VERVPVVVK	189	-0.8000	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	IVIIGIGAV	128	2.4000	30.00
2	VRPATPLLQ	147	2.2000	27.50
3	VRGLKALLA	94	1.8000	22.50
4	VVLAVVGIG	104	1.8000	22.50
5	LALYFTPAM	115	1.4000	17.50
6	IRRVASARV	168	1.4000	17.50
7	VVGIGLGLA	108	1.3000	16.25
8	VVRGLKALL	93	1.1000	13.75
9	IVERVPVVV	188	0.9000	11.25
10	VIIGIGAVS	129	0.6000	7.50
11	MSAREIVII	123	0.3000	3.75
12	VVVKDFSDG	194	0.2000	2.50
13	VATIRRVAS	165	-0.1000	0
14	VERVPVVVK	189	-0.1000	0
15	IEQARRAAK	64	-0.2000	0
16	LRITIVERV	184	-0.2000	0
17	LQVLTALHP	241	-0.2000	0
18	VASARVQRQ	171	-0.3000	0
19	YPSALRITI	180	-0.4000	0
20	LYFTPAMSA	117	-0.6000	0
21	VSREEVLDA	136	-0.7000	0
22	LLATVVLA	100	-0.8000	0
23	LLQIDTQQV	153	-0.8000	0
24	LQIDTQQVA	154	-0.8000	0
25	LAVVGIGLG	106	-1.0000	0

26	VPVVVKDFS	192	-1.1000	0
27	FDVDNPGPS	225	-1.1000	0
28	IAAPSVASI	258	-1.1000	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	IVIIGIGAV	128	3.4000	42.50
2	VRPATPLLQ	147	3.2000	40.00
3	VRGLKALLA	94	2.8000	35.00
4	VVLAVVGIG	104	2.8000	35.00
5	LALYFTPAM	115	2.4000	30.00
6	IRRVASARV	168	2.4000	30.00
7	VVGIGLGLA	108	2.3000	28.75
8	VVRGLKALL	93	2.1000	26.25
9	IVERVPVVV	188	1.9000	23.75
10	VIIGIGAVS	129	1.6000	20.00
11	MSAREIVII	123	1.3000	16.25
12	VVVKDFS	194	1.2000	15.00
13	ITIVERVPV	186	1.0000	12.50
14	VVIWGTTDR	275	1.0000	12.50
15	VATIRRVAS	165	0.9000	11.25
16	VERVPVVVK	189	0.9000	11.25
17	IEQARRAAK	64	0.8000	10.00
18	LRITIVERV	184	0.8000	10.00
19	LQVLTALHP	241	0.8000	10.00
20	VASARVQRQ	171	0.7000	8.75
21	LYFTPAMSA	117	0.4000	5.00
22	VSREEVLDA	136	0.3000	3.75
23	LLATVVLA	100	0.2000	2.50
24	LLQIDTQQV	153	0.2000	2.50
25	LQIDTQQVA	154	0.2000	2.50
26	VPVVVKDFS	192	-0.1000	0

27	IAAPSVASI	258	-0.1000	0
28	LATVVLAVV	101	-0.2000	0
29	VGRIAAPSV	255	-0.4000	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	VVLAVVGIG	104	4.1000	47.67
2	VRPATPLLQ	147	4.0000	46.51
3	IVIIGIGAV	128	3.7000	43.02
4	LALYFTPAM	115	3.5000	40.70
5	VVRGLKALL	93	3.1000	36.05
6	VRGLKALLA	94	2.8000	32.56
7	IRRVASARV	168	2.7000	31.40
8	VVVKDFSDG	194	2.5000	29.07
9	VVGIGLGLA	108	2.3000	26.74
10	IGIGAVSRE	131	2.2000	25.58
11	IVERVPVVV	188	2.2000	25.58
12	VIIIGIGAVS	129	1.6000	18.60
13	MSAREIVII	123	1.5000	17.44
14	VASARVQRQ	171	1.5000	17.44
15	LAVVGIGLG	106	1.3000	15.12
16	ITIVERVPV	186	1.3000	15.12
17	LQVLTALHP	241	1.2000	13.95
18	LRITIVERV	184	1.1000	12.79
19	VVIWGTDDR	275	1.0000	11.63
20	VATIRRVAS	165	0.9000	10.47
21	WGTDDRCEE	278	0.8000	9.30
22	LAALLTQPG	291	0.6000	6.98
23	LLATVVLAV	100	0.5000	5.81
24	FTPAMSARE	119	0.5000	5.81
25	LLQIDTQQV	153	0.5000	5.81
26	LYFTPAMSA	117	0.4000	4.65

27	VSREEVLDA	136	0.3000	3.49
28	LQIDTQQVA	154	0.2000	2.33
29	VERVPVVVK	189	0.2000	2.33
30	IEQARRAAK	64	0.1000	1.16
31	LATVVLAVV	101	0.1000	1.16

ALLELE: DRB1_0813	Threshold for 3 % with score: 1.9	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
1	VRPATPLLQ	147	2.8000	32.18
2	VVIWGTTDR	275	2.8000	32.18
3	VRGLKALLA	94	2.4000	27.59
4	VVVKDFSDG	194	2.0000	22.99
5	IVERVPVVV	188	1.9000	21.84
6	IVIIGIGAV	128	1.7000	19.54
7	LALYFTPAM	115	1.6000	18.39
8	LRITIVERV	184	1.5000	17.24
9	IRRVASARV	168	1.4000	16.09
10	MSAREIVII	123	1.3000	14.94
11	VVRGLKALL	93	1.1000	12.64
12	VVLAVVGIG	104	1.1000	12.64
13	ITIVERVPV	186	1.0000	11.49
14	VATIRRVAS	165	0.9000	10.34
15	VERVPVVVK	189	0.9000	10.34
16	VASARVQRQ	171	0.7000	8.05
17	VVGIGLGLA	108	0.6000	6.90
18	VIIIGIGAVS	129	0.6000	6.90
19	LKALLATVV	97	0.5000	5.75
20	YPSALRITI	180	0.4800	5.52
21	LYFTPAMSA	117	0.4000	4.60
22	LQVLTALHP	241	0.4000	4.60
23	LLQIDTQQV	153	0.2000	2.30
24	LQIDTQQVA	154	0.2000	2.30

25	VPVVVKDFS	192	0.1000	1.15
26	VASITLTLA	263	0.1000	1.15
27	VSREEVLDA	136	-0.1000	0
28	VQRQYPSAL	176	-0.1000	0
29	IEQARRAAK	64	-0.2000	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	VRPATPLLQ	147	4.8000	47.52
2	LALYFTPAM	115	3.6500	36.14
3	VRGLKALLA	94	3.6000	35.64
4	VVLAVVGIG	104	3.2000	31.68
5	IVIIGIGAV	128	2.8000	27.72
6	VVRGLKALL	93	2.1000	20.79
7	LQVLTALHP	241	2.0000	19.80
8	WGTTDRCEE	278	1.8000	17.82
9	IRRVASARV	168	1.7000	16.83
10	IVERVPVVV	188	1.7000	16.83
11	FTPAMSARE	119	1.5000	14.85
12	VVVKDFSDBG	194	1.5000	14.85
13	VVGIGLGLA	108	1.4000	13.86
14	YPSALRITI	180	1.4000	13.86
15	LLATVVLA	100	1.3000	12.87
16	IGIGAVSRE	131	1.2000	11.88
17	LRITIVERV	184	1.2000	11.88
18	VSREEVLDA	136	1.1000	10.89
19	VVIWGTTDR	275	1.1000	10.89
20	LYFTPAMSA	117	1.0000	9.90
21	MSAREIVII	123	1.0000	9.90
22	IGLGLALYF	111	0.9000	8.91
23	VGIGLGLAL	109	0.8000	7.92
24	ITIVERVPV	186	0.8000	7.92

25	VIIGIGAVS	129	0.6000	5.94
26	VASARVQRQ	171	0.6000	5.94
27	VLAVVGIGL	105	0.4000	3.96
28	LAVVGIGLG	106	0.4000	3.96
29	VATIRRVAS	165	0.4000	3.96
30	VGRIAAPSV	255	0.0500	0.50

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	VRGLKALLA	94	4.0000	48.19
2	VRPATPLLQ	147	4.0000	48.19
3	IVIIGIGAV	128	3.1000	37.35
4	VVGIGLGLA	108	2.0000	24.10
5	LQVLTALHP	241	2.0000	24.10
6	VVLAVVGIG	104	1.9000	22.89
7	IRRVASARV	168	1.5000	18.07
8	LLATVVLAV	100	1.4000	16.87
9	LYFTPAMSA	117	1.4000	16.87
10	LRITIVERV	184	1.3000	15.66
11	YPSALRITI	180	1.2000	14.46
12	VATIRRVAS	165	1.0000	12.05
13	VVIWGTDDR	275	1.0000	12.05
14	ITIVERVPV	186	0.6000	7.23
15	VERVPVVVK	189	0.5000	6.02
16	VVRGLKALL	93	0.4000	4.82
17	VSREEVLDA	136	0.4000	4.82
18	VGRIAAPSV	255	0.3500	4.22
19	VIIGIGAVS	129	-0.1000	0
20	LLQIDTQQV	153	-0.1000	0
21	IEQARRAAK	64	-0.2000	0
22	VASARVQRQ	171	-0.2000	0
23	LALYFTPAM	115	-0.3500	0

24	IIGIGAVSR	130	-0.4000	0
25	VLAVVGIGL	105	-0.5000	0
26	IGLGLALYF	111	-0.7000	0
27	LTALHPEVA	244	-0.7000	0
28	LKALLATVV	97	-0.8000	0
29	LAVVGIGLG	106	-0.8000	0
30	WGTTDRCEE	278	-0.8000	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	VRPATPLLQ	147	3.9000	46.43
2	VRGLKALLA	94	3.2000	38.10
3	VVIWGTTDR	275	3.2000	38.10
4	LRITIVERV	184	2.1000	25.00
5	VVLAVVGIG	104	1.8000	21.43
6	VVRGLKALL	93	1.6000	19.05
7	IVIIGIGAV	128	1.5000	17.86
8	VASARVQRQ	171	1.5000	17.86
9	LALYFTPAM	115	1.3000	15.48
10	VASQVGRIA	251	1.3000	15.48
11	IRRVASARV	168	1.2000	14.29
12	LQVLTALHP	241	1.2000	14.29
13	VIIIGIGAVS	129	1.1000	13.10
14	LDAARVRPA	142	1.1000	13.10
15	VQRQYPSAL	176	1.1000	13.10
16	LLTQPGRTY	294	1.1000	13.10
17	VATIRRVAS	165	1.0000	11.90
18	VSREEVLDA	136	0.9000	10.71
19	IEQARRAAK	64	0.8000	9.52
20	LLATVVLA	100	0.8000	9.52
21	ITIVERVPV	186	0.8000	9.52
22	IVERVPVVV	188	0.8000	9.52

23	LTLADGRVV	268	0.8000	9.52
24	VERVPVVVK	189	0.7000	8.33
25	LYFTPAMSA	117	0.6000	7.14
26	LQIDTQQVA	154	0.6000	7.14
27	VVGIGLGLA	108	0.4000	4.76
28	MSAREIVII	123	0.2000	2.38
29	LLQIDTQQV	153	0.1000	1.19
30	VVVKDFSDG	194	0.1000	1.19

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	VRGLKALLA	94	5.0000	60.24
2	VRPATPLLQ	147	5.0000	60.24
3	IVIIGIGAV	128	4.1000	49.40
4	VVGIGLGLA	108	3.0000	36.14
5	LQVLTALHP	241	3.0000	36.14
6	VVLAVVGIG	104	2.9000	34.94
7	IRRVASARV	168	2.5000	30.12
8	LLATVVLA	100	2.4000	28.92
9	LYFTPAMSA	117	2.4000	28.92
10	LRITIVERV	184	2.3000	27.71
11	VATIRRVAS	165	2.0000	24.10
12	VVIWGTTDR	275	2.0000	24.10
13	ITIVERVPV	186	1.6000	19.28
14	VERVPVVVK	189	1.5000	18.07
15	VVRGLKALL	93	1.4000	16.87
16	VSREEVLDA	136	1.4000	16.87
17	VGRIAAPSV	255	1.3500	16.27
18	VIIIGIGAVS	129	0.9000	10.84
19	LLQIDTQQV	153	0.9000	10.84
20	IEQARRAAK	64	0.8000	9.64
21	VASARVQRQ	171	0.8000	9.64

22	LALYFTPAM	115	0.6500	7.83
23	IIGIGAVSR	130	0.6000	7.23
24	VLAVVGIGL	105	0.5000	6.02
25	IGLGLALYF	111	0.3000	3.61
26	LTALHPEVA	244	0.3000	3.61
27	LKALLATVV	97	0.2000	2.41
28	LAVVGIGLG	106	0.2000	2.41
29	YPSALRITI	180	0.2000	2.41
30	VTALHPEV	243	0.1500	1.81
31	VGIGLGLAL	109	0.1000	1.20

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	VRGLKALLA	94	5.0000	60.24
2	VRPATPLLQ	147	5.0000	60.24
3	IVIIGIGAV	128	4.1000	49.40
4	VVGIGLGLA	108	3.0000	36.14
5	LQVLTALHP	241	3.0000	36.14
6	VVLAVVGIG	104	2.9000	34.94
7	IRRVASARV	168	2.5000	30.12
8	LLATVVLAV	100	2.4000	28.92
9	LYFTPAMSA	117	2.4000	28.92
10	LRITIVERV	184	2.3000	27.71
11	VATIRRVAS	165	2.0000	24.10
12	VVIWGTTDR	275	2.0000	24.10
13	ITIVERVPV	186	1.6000	19.28
14	VERVPVVVK	189	1.5000	18.07
15	VVRGLKALL	93	1.4000	16.87
16	VSREEVLDA	136	1.4000	16.87
17	VGRIAAPSV	255	1.3500	16.27
18	VIIIGIGAVS	129	0.9000	10.84
19	LLQIDTQQV	153	0.9000	10.84

20	IEQARRAAK	64	0.8000	9.64
21	VASARVQRQ	171	0.8000	9.64
22	LALYFTPAM	115	0.6500	7.83
23	IIGIGAVSR	130	0.6000	7.23
24	VLAVVGIGL	105	0.5000	6.02
25	IGLGLALYF	111	0.3000	3.61
26	LTALHPEVA	244	0.3000	3.61
27	LKALLATVV	97	0.2000	2.41
28	LAVVGIGLG	106	0.2000	2.41
29	YPSALRITI	180	0.2000	2.41
30	VTALHPEV	243	0.1500	1.81
31	VGIGLGLAL	109	0.1000	1.20

ALLELE: DRB1_1107	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 9.1
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Rank	Sequence	At Position	Score	% of Highest Score
1	LQIDTQQVA	154	4.6000	50.55
2	IVIIGIGAV	128	4.2000	46.15
3	VRPATPLLQ	147	3.7000	40.66
4	VVRGLKALL	93	3.6000	39.56
5	VVLAVVGIG	104	3.4000	37.36
6	VVGIGLGLA	108	3.1000	34.07
7	VIIIGIGAVS	129	3.1000	34.07
8	LRITIVERV	184	3.0000	32.97
9	VRGLKALLA	94	2.6000	28.57
10	FATDPPPPA	213	2.5000	27.47
11	VATIRRVAS	165	2.4000	26.37
12	VVKDFSDGP	195	2.4000	26.37
13	VVIWGTTDR	275	2.3000	25.27
14	IRRVASARV	168	2.1000	23.08
15	IGIGAVSRE	131	2.0700	22.75
16	ITIVERVPV	186	2.0000	21.98
17	VERVPVVVK	189	1.9000	20.88

18	LYFTPAMSA	117	1.8000	19.78
19	VASARVQRQ	171	1.8000	19.78
20	FDVDNPGPS	225	1.8000	19.78
21	VIWGTTDRC	276	1.8000	19.78
22	VGRIAAPSV	255	1.7000	18.68
23	LLQIDTQQV	153	1.5000	16.48
24	VQRQYPSAL	176	1.4700	16.15
25	VPVVVKDFS	192	1.4000	15.38
26	FDRDGVDF	206	1.3000	14.29
27	IGLGLALYF	111	1.2000	13.19
28	IVSEQNPAK	79	1.1000	12.09
29	LALYFTPAM	115	1.1000	12.09
30	VGIGLGLAL	109	1.0000	10.99
31	IIGIGAVSR	130	1.0000	10.99

ALLELE: DRB1_1114	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	VRPATPLLQ	147	2.9000	34.52
2	VRGLKALLA	94	2.2000	26.19
3	VVIWGTTDR	275	2.2000	26.19
4	LRITIVERV	184	1.1000	13.10
5	VVLAVVGIG	104	0.8000	9.52
6	VVRGLKALL	93	0.6000	7.14
7	IVIIGIGAV	128	0.5000	5.95
8	VASARVQRQ	171	0.5000	5.95
9	LALYFTPAM	115	0.3000	3.57
10	VASQVGRIA	251	0.3000	3.57
11	IRRVASARV	168	0.2000	2.38
12	LQVLTALHP	241	0.2000	2.38
13	VIIGIGAVS	129	0.1000	1.19
14	LDAARVRPA	142	0.1000	1.19
15	VQRQYPSAL	176	0.1000	1.19

16	LLTQPGRTY	294	0.1000	1.19
17	VSREEVLDA	136	-0.1000	0
18	YPSALRITI	180	-0.1000	0
19	IEQARRAAK	64	-0.2000	0
20	LLATVVLAV	100	-0.2000	0
21	ITIVERVPV	186	-0.2000	0
22	IVERVPVVV	188	-0.2000	0
23	LTLADGRVV	268	-0.2000	0
24	VERVPVVVK	189	-0.3000	0
25	LYFTPAMSA	117	-0.4000	0
26	LQIDTQQVA	154	-0.4000	0
27	VVGIGLGLA	108	-0.6000	0
28	MSAREIVII	123	-0.8000	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	VVIWGTTDR	275	3.7000	42.05
2	VRGLKALLA	94	2.2000	25.00
3	VVLAVVGIG	104	2.2000	25.00
4	VRPATPLLQ	147	2.2000	25.00
5	LRITIVERV	184	2.1000	23.86
6	LALYFTPAM	115	1.8000	20.45
7	VVRGLKALL	93	1.5600	17.73
8	FEGPRRRAR	40	1.5000	17.05
9	IVIIGIGAV	128	1.5000	17.05
10	LLTQPGRTY	294	1.4000	15.91
11	IRRVASARV	168	1.2000	13.64
12	LQVLTALHP	241	1.2000	13.64
13	VQRQYPSAL	176	1.0600	12.05
14	LLATVVLAV	100	0.8000	9.09
15	YPSALRITI	180	0.8000	9.09
16	ITIVERVPV	186	0.8000	9.09

17	IVERVPVVV	188	0.8000	9.09
18	LTLADGRVV	268	0.8000	9.09
19	VIIGIGAVS	129	0.5000	5.68
20	VVVKDFSDG	194	0.5000	5.68
21	VATIRRVAS	165	0.4000	4.55
22	IGLGLALYF	111	0.3000	3.41
23	VASQVGRIA	251	0.3000	3.41
24	LAALLTQPG	291	0.2000	2.27
25	MSAREIVII	123	0.1000	1.14
26	IIGIGAVSR	130	0.1000	1.14
27	LDAARVRPA	142	0.1000	1.14
28	LLQIDTQQV	153	0.1000	1.14
29	WGTTDRCEE	278	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	VRPATLLQ	147	3.9000	46.43
2	VRGLKALLA	94	3.2000	38.10
3	VVIWGTTDR	275	3.2000	38.10
4	LRITIVERV	184	2.1000	25.00
5	VVLAVVGIG	104	1.8000	21.43
6	VVRGLKALL	93	1.6000	19.05
7	IVIIGIGAV	128	1.5000	17.86
8	VASARVQRQ	171	1.5000	17.86
9	LALYFTPAM	115	1.3000	15.48
10	VASQVGRIA	251	1.3000	15.48
11	IRRVASARV	168	1.2000	14.29
12	LQVLTALHP	241	1.2000	14.29
13	VIIGIGAVS	129	1.1000	13.10
14	LDAARVRPA	142	1.1000	13.10
15	VQRQYPSAL	176	1.1000	13.10
16	LLTQPGRTY	294	1.1000	13.10

17	VATIRRVAS	165	1.0000	11.90
18	VSREEVLDA	136	0.9000	10.71
19	IEQARRAAK	64	0.8000	9.52
20	LLATVVLAV	100	0.8000	9.52
21	ITIVERVPV	186	0.8000	9.52
22	IVERVPVVV	188	0.8000	9.52
23	LTLADGRVV	268	0.8000	9.52
24	VERVPVVVK	189	0.7000	8.33
25	LYFTPAMSA	117	0.6000	7.14
26	LQIDTQQVA	154	0.6000	7.14
27	VVGIGLGLA	108	0.4000	4.76
28	MSAREIVII	123	0.2000	2.38
29	LLQIDTQQV	153	0.1000	1.19
30	VVVKDFSDG	194	0.1000	1.19

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	IVIIGIGAV	128	4.1000	47.13
2	VRGLKALLA	94	4.0000	45.98
3	VVLAVVGIG	104	3.3000	37.93
4	VRPATPLLQ	147	3.3000	37.93
5	LQVLTALHP	241	3.0000	34.48
6	IRRVASARV	168	2.5000	28.74
7	VVIWGTTDR	275	2.5000	28.74
8	LLATVVLAV	100	2.4000	27.59
9	LRITIVERV	184	2.3000	26.44
10	YPSALRITI	180	2.1000	24.14
11	VVGIGLGLA	108	2.0000	22.99
12	ITIVERVPV	186	1.6000	18.39
13	LYFTPAMSA	117	1.4000	16.09
14	VATIRRVAS	165	1.4000	16.09
15	VVRGLKALL	93	1.3600	15.63

16	VGRIAAPSV	255	1.3500	15.52
17	IGLGLALYF	111	1.2000	13.79
18	LALYFTPAM	115	1.1500	13.22
19	IIGIGAVSR	130	1.1000	12.64
20	LLQIDTQQV	153	0.9000	10.34
21	LAVVGIGLG	106	0.6000	6.90
22	VERVPVVVK	189	0.6000	6.90
23	WGTDRCEE	278	0.6000	6.90
24	VLAVVGIGL	105	0.4600	5.29
25	VSREEVLDA	136	0.4000	4.60
26	VIIIGIGAVS	129	0.3000	3.45
27	LKALLATVV	97	0.2000	2.30
28	LAALLTQPG	291	0.2000	2.30
29	VTALHPEV	243	0.1500	1.72
30	VGIGLGLAL	109	0.0600	0.69

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	VVIWGTTDR	275	4.7000	53.41
2	VRGLKALLA	94	3.2000	36.36
3	VVLAVVGIG	104	3.2000	36.36
4	VRPATPLLQ	147	3.2000	36.36
5	LRITIVERV	184	3.1000	35.23
6	LALYFTPAM	115	2.8000	31.82
7	VVRGLKALL	93	2.5600	29.09
8	IVIIGIGAV	128	2.5000	28.41
9	LLTQPGRTY	294	2.4000	27.27
10	IRRVASARV	168	2.2000	25.00
11	LQVLTALHP	241	2.2000	25.00
12	VQRQYPSAL	176	2.0600	23.41
13	LLATVVLA	100	1.8000	20.45
14	ITIVERVPV	186	1.8000	20.45

15	IVERVPVVV	188	1.8000	20.45
16	LTLADGRVV	268	1.8000	20.45
17	VIIIGIGAVS	129	1.5000	17.05
18	VVVKDFSDG	194	1.5000	17.05
19	VATIRRVAS	165	1.4000	15.91
20	IGLGLALYF	111	1.3000	14.77
21	VASQVGRIA	251	1.3000	14.77
22	LAALLTQPG	291	1.2000	13.64
23	MSAREIVII	123	1.1000	12.50
24	IIGIGAVSR	130	1.1000	12.50
25	LDAARVRPA	142	1.1000	12.50
26	LLQIDTQQV	153	1.1000	12.50
27	IDTQQVADR	156	1.0000	11.36
28	IEQARRAAK	64	0.9000	10.23
29	LKALLATVV	97	0.9000	10.23
30	VSREEVLDA	136	0.9000	10.23
31	VASARVQRQ	171	0.8000	9.09

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	VVIWGTTDR	275	3.7000	42.05
2	VRGLKALLA	94	2.2000	25.00
3	VVLAVVGIG	104	2.2000	25.00
4	VRPATPLLQ	147	2.2000	25.00
5	LRITIVERV	184	2.1000	23.86
6	LALYFTPAM	115	1.8000	20.45
7	VVRGLKALL	93	1.5600	17.73
8	FEGPRRRAR	40	1.5000	17.05
9	IVIIGIGAV	128	1.5000	17.05
10	LLTQPGRTY	294	1.4000	15.91
11	IRRVASARV	168	1.2000	13.64
12	LQVLTALHP	241	1.2000	13.64

13	VQRQYPSAL	176	1.0600	12.05
14	LLATVVLA	100	0.8000	9.09
15	YPSALRITI	180	0.8000	9.09
16	ITIVERVPV	186	0.8000	9.09
17	IVERVPVVV	188	0.8000	9.09
18	LTLADGRVV	268	0.8000	9.09
19	VIIGIGAVS	129	0.5000	5.68
20	VVVKDFSDG	194	0.5000	5.68
21	VATIRRVAS	165	0.4000	4.55
22	IGLGLALYF	111	0.3000	3.41
23	VASQVGRIA	251	0.3000	3.41
24	LAALLTQPG	291	0.2000	2.27
25	MSAREIVII	123	0.1000	1.14
26	IIGIGAVSR	130	0.1000	1.14
27	LDAARVRPA	142	0.1000	1.14
28	LLQIDTQQV	153	0.1000	1.14
29	WGTTRDCEE	278	0.1000	1.14

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	VRPATPLLQ	147	4.7000	52.22
2	VRGLKALLA	94	3.2000	35.56
3	VVIWGTTRD	275	3.2000	35.56
4	VVLAVVGIG	104	3.1000	34.44
5	VVRGLKALL	93	2.6000	28.89
6	LALYFTPAM	115	2.4000	26.67
7	LRITIVERV	184	2.4000	26.67
8	VASARVQRQ	171	2.3000	25.56
9	LLTQPGRTY	294	2.2000	24.44
10	IGIGAVSRE	131	2.1000	23.33
11	VQRQYPSAL	176	2.1000	23.33
12	IVIIGIGAV	128	1.8000	20.00

13	LQVLTALHP	241	1.6000	17.78
14	IRRVASARV	168	1.5000	16.67
15	VVVKDFSDG	194	1.4000	15.56
16	VASQVGRIA	251	1.3000	14.44
17	LLATVVLA V	100	1.1000	12.22
18	VIIIGIGAVS	129	1.1000	12.22
19	LDAARVRPA	142	1.1000	12.22
20	ITIVERVPV	186	1.1000	12.22
21	IVERVPVVV	188	1.1000	12.22
22	LTLADGRVV	268	1.1000	12.22
23	LAALLTQPG	291	1.1000	12.22
24	VATIRRVAS	165	1.0000	11.11
25	VSREEVLDA	136	0.9000	10.00
26	WGTTDRCEE	278	0.7000	7.78
27	LYFTPAMSA	117	0.6000	6.67
28	LQIDTQQVA	154	0.6000	6.67
29	FTPAMSARE	119	0.5000	5.56
30	VVGIGLGLA	108	0.4000	4.44
31	MSAREIVII	123	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	IVIIGIGAV	128	4.1000	47.13
2	VRGLKALLA	94	4.0000	45.98
3	VVLAVVGIG	104	3.3000	37.93
4	VRPATPLLQ	147	3.3000	37.93
5	LQVLTALHP	241	3.0000	34.48
6	IRRVASARV	168	2.5000	28.74
7	VVIWGTDDR	275	2.5000	28.74
8	LLATVVLA V	100	2.4000	27.59
9	LRITIVERV	184	2.3000	26.44
10	YPSALRITI	180	2.1000	24.14

11	VVGIGLGLA	108	2.0000	22.99
12	ITIVERVPV	186	1.6000	18.39
13	LYFTPAMSA	117	1.4000	16.09
14	VATIRRVAS	165	1.4000	16.09
15	VVRGLKALL	93	1.3600	15.63
16	VGRIAAPSV	255	1.3500	15.52
17	IGLGLALYF	111	1.2000	13.79
18	LALYFTPAM	115	1.1500	13.22
19	IIGIGAVSR	130	1.1000	12.64
20	LLQIDTQQV	153	0.9000	10.34
21	LAVVGIGLG	106	0.6000	6.90
22	VERVPVVVK	189	0.6000	6.90
23	WGTTRCEE	278	0.6000	6.90
24	VLAVVGIGL	105	0.4600	5.29
25	VSREEVLDA	136	0.4000	4.60
26	VIIGIGAVS	129	0.3000	3.45
27	LKALLATVV	97	0.2000	2.30
28	LAALLTQPG	291	0.2000	2.30
29	VTALHPEV	243	0.1500	1.72
30	VGIGLGLAL	109	0.0600	0.69

ALLELE: DRB1_1307	Threshold for 3 % with score: 0.6	Highest Score achievable by any peptide: 6.8
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Rank	Sequence	At Position	Score	% of Highest Score
1	IVIIGIGAV	128	3.0000	44.12
2	VRGLKALLA	94	2.2000	32.35
3	VRPATPLLQ	147	2.2000	32.35
4	VVGIGLGLA	108	1.9000	27.94
5	VVLAVVGIG	104	1.8000	26.47
6	IRRVASARV	168	1.5000	22.06
7	VATIRRVAS	165	0.5000	7.35
8	VVRGLKALL	93	0.4000	5.88
9	LRITIVERV	184	0.2000	2.94

10	LQVLTALHP	241	0.2000	2.94
11	ITIVERVPV	186	0.1000	1.47
12	VIIGIGAVS	129	-0.1000	0
13	VVIWGTTDR	275	-0.1000	0
14	IEQARRAAK	64	-0.2000	0
15	LYFTPAMSA	117	-0.2000	0
16	LLQIDTQQV	153	-0.2000	0
17	VASARVQRQ	171	-0.3000	0
18	LLATVVVLAV	100	-0.4000	0
19	YPSALRITI	180	-0.4000	0
20	VGRIAAPSV	255	-0.8000	0
21	WGTTDRCEE	278	-0.8000	0
22	LAVVGIGLG	106	-0.9000	0
23	IIGIGAVSR	130	-0.9000	0
24	VPVVVKDFS	192	-1.0000	0
25	LATVVVLAVV	101	-1.1000	0
26	VQRQYPSAL	176	-1.3000	0
27	LAALLTQPG	291	-1.3000	0
28	VSREEVLDA	136	-1.4000	0
29	LALYFTPAM	115	-1.5000	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	VRGLKALLA	94	5.0000	60.24
2	VRPATPLLQ	147	5.0000	60.24
3	IVIIGIGAV	128	4.1000	49.40
4	VVGIGLGLA	108	3.0000	36.14
5	LQVLTALHP	241	3.0000	36.14
6	VVLAVVGIG	104	2.9000	34.94
7	IRRVASARV	168	2.5000	30.12
8	LLATVVVLAV	100	2.4000	28.92
9	LYFTPAMSA	117	2.4000	28.92

10	LRITIVERV	184	2.3000	27.71
11	VATIRRVAS	165	2.0000	24.10
12	VVIWGTTDR	275	2.0000	24.10
13	ITIVERVPV	186	1.6000	19.28
14	VERVPVVVK	189	1.5000	18.07
15	VVRGLKALL	93	1.4000	16.87
16	VSREEVLDA	136	1.4000	16.87
17	VGRIAAPSV	255	1.3500	16.27
18	VIIIGAVS	129	0.9000	10.84
19	LLQIDTQQV	153	0.9000	10.84
20	IEQARRAAK	64	0.8000	9.64
21	VASARVQRQ	171	0.8000	9.64
22	LALYFTPAM	115	0.6500	7.83
23	IIGIGAVSR	130	0.6000	7.23
24	VLAVVGIGL	105	0.5000	6.02
25	IGLGLALYF	111	0.3000	3.61
26	LTALHPEVA	244	0.3000	3.61
27	LKALLATVV	97	0.2000	2.41
28	LAVVGIGLG	106	0.2000	2.41
29	YPSALRITI	180	0.2000	2.41
30	VTALHPEV	243	0.1500	1.81
31	VGIGLGLAL	109	0.1000	1.20

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	VRPATPLLQ	147	4.8000	53.93
2	VRGLKALLA	94	4.0000	44.94
3	IVIIGIGAV	128	3.4000	38.20
4	VVLAVVGIG	104	3.2000	35.96
5	LQVLTALHP	241	2.4000	26.97
6	WGTTDRCEE	278	2.2000	24.72
7	VVGIGLGLA	108	2.0000	22.47

8	IRRVASARV	168	1.8000	20.22
9	LLATVVVLAV	100	1.7000	19.10
10	LRITIVERV	184	1.6000	17.98
11	FTPAMSARE	119	1.5000	16.85
12	VVRGLKALL	93	1.4000	15.73
13	LYFTPAMSA	117	1.4000	15.73
14	YPSALRITI	180	1.4000	15.73
15	VATIRRVAS	165	1.0000	11.24
16	VVIWGTTDR	275	1.0000	11.24
17	ITIVERVPV	186	0.9000	10.11
18	LALYFTPAM	115	0.7500	8.43
19	VGRIAPS	255	0.6500	7.30
20	VASARVQRQ	171	0.6000	6.74
21	VLAVVGIGL	105	0.5000	5.62
22	LAVVGIGLG	106	0.5000	5.62
23	IGIGAVSRE	131	0.5000	5.62
24	VSREEVLDA	136	0.4000	4.49
25	IGLGLALYF	111	0.2000	2.25
26	LLQIDTQQV	153	0.2000	2.25
27	VGIGLGLAL	109	0.1000	1.12
28	LAALLTQPG	291	0.1000	1.12
29	VIIGIGAVS	129	-0.1000	0
30	VERVPVVVK	189	-0.2000	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	VRPATPLLQ	147	3.9000	46.43
2	VRGLKALLA	94	3.2000	38.10
3	VVIWGTTDR	275	3.2000	38.10
4	LRITIVERV	184	2.1000	25.00
5	VVLAVVGIG	104	1.8000	21.43
6	VVRGLKALL	93	1.6000	19.05

7	IVIIGIGAV	128	1.5000	17.86
8	VASARVQRQ	171	1.5000	17.86
9	LALYFTPAM	115	1.3000	15.48
10	VASQVGRIA	251	1.3000	15.48
11	IRRVASARV	168	1.2000	14.29
12	LQVLTALHP	241	1.2000	14.29
13	VIIIGIGAVS	129	1.1000	13.10
14	LDAARVRPA	142	1.1000	13.10
15	VQRQYPSAL	176	1.1000	13.10
16	LLTQPGRTY	294	1.1000	13.10
17	VATIRRVAS	165	1.0000	11.90
18	VSREEVLDA	136	0.9000	10.71
19	IEQARRAAK	64	0.8000	9.52
20	LLATVVLA V	100	0.8000	9.52
21	ITIVERVPV	186	0.8000	9.52
22	IVERVPVVV	188	0.8000	9.52
23	LTLADGRVV	268	0.8000	9.52
24	VERVPVVVK	189	0.7000	8.33
25	LYFTPAMSA	117	0.6000	7.14
26	LQIDTQQVA	154	0.6000	7.14
27	VVGIGLGLA	108	0.4000	4.76
28	MSAREIVII	123	0.2000	2.38
29	LLQIDTQQV	153	0.1000	1.19
30	VVVKDFSDG	194	0.1000	1.19

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	VRPATPLLQ	147	2.9000	34.52
2	VRGLKALLA	94	2.2000	26.19
3	VVIWGTTDR	275	2.2000	26.19
4	LRITIVERV	184	1.1000	13.10
5	VVLAVVGIG	104	0.8000	9.52

6	VVRGLKALL	93	0.6000	7.14
7	IVIIGIGAV	128	0.5000	5.95
8	VASARVQRQ	171	0.5000	5.95
9	LALYFTPAM	115	0.3000	3.57
10	VASQVGRIA	251	0.3000	3.57
11	IRRVASARV	168	0.2000	2.38
12	LQVLTALHP	241	0.2000	2.38
13	VIIIGIGAVS	129	0.1000	1.19
14	LDAARVRPA	142	0.1000	1.19
15	VQRQYPSAL	176	0.1000	1.19
16	LLTQPGRTY	294	0.1000	1.19
17	VSREEVLDA	136	-0.1000	0
18	YPSALRITI	180	-0.1000	0
19	IEQARRAAK	64	-0.2000	0
20	LLATVVLAV	100	-0.2000	0
21	ITIVERVPV	186	-0.2000	0
22	IVERVPVVV	188	-0.2000	0
23	LTLADGRVV	268	-0.2000	0
24	VERVPVVVK	189	-0.3000	0
25	LYFTPAMSA	117	-0.4000	0
26	LQIDTQQVA	154	-0.4000	0
27	VVGIGLGLA	108	-0.6000	0
28	MSAREIVII	123	-0.8000	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	VVIWGTTDR	275	4.7000	53.41
2	VRGLKALLA	94	3.2000	36.36
3	VVLAVVGIG	104	3.2000	36.36
4	VRPATPLLQ	147	3.2000	36.36
5	LRITIVERV	184	3.1000	35.23
6	LALYFTPAM	115	2.8000	31.82

7	VVRGLKALL	93	2.5600	29.09
8	IVIIGIGAV	128	2.5000	28.41
9	LLTQPGRTY	294	2.4000	27.27
10	IRRVASARV	168	2.2000	25.00
11	LQVLTALHP	241	2.2000	25.00
12	VQRQYPSAL	176	2.0600	23.41
13	LLATVVLA	100	1.8000	20.45
14	ITIVERVPV	186	1.8000	20.45
15	IVERVPVVV	188	1.8000	20.45
16	LTLADGRVV	268	1.8000	20.45
17	VIIIGIGAVS	129	1.5000	17.05
18	VVVKDFSDG	194	1.5000	17.05
19	VATIRRVAS	165	1.4000	15.91
20	IGLGLALYF	111	1.3000	14.77
21	VASQVGRIA	251	1.3000	14.77
22	LAALLTQPG	291	1.2000	13.64
23	MSAREIVII	123	1.1000	12.50
24	IIGIGAVSR	130	1.1000	12.50
25	LDAARVRPA	142	1.1000	12.50
26	LLQIDTQQV	153	1.1000	12.50
27	IDTQQVADR	156	1.0000	11.36
28	IEQARRAAK	64	0.9000	10.23
29	LKALLATVV	97	0.9000	10.23
30	VSREEVLDA	136	0.9000	10.23
31	VASARVQRQ	171	0.8000	9.09

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	VVIWGTDDR	275	4.7000	53.41
2	VRGLKALLA	94	3.2000	36.36
3	VVLAVVGIG	104	3.2000	36.36
4	VRPATPLLQ	147	3.2000	36.36

5	LRITIVERV	184	3.1000	35.23
6	LALYFTPAM	115	2.8000	31.82
7	VVRGLKALL	93	2.5600	29.09
8	IVIIGIGAV	128	2.5000	28.41
9	LLTQPGRTY	294	2.4000	27.27
10	IRRVASARV	168	2.2000	25.00
11	LQVLTALHP	241	2.2000	25.00
12	VQRQYPSAL	176	2.0600	23.41
13	LLATVVLA	100	1.8000	20.45
14	ITIVERVPV	186	1.8000	20.45
15	IVERVPVVV	188	1.8000	20.45
16	LTLADGRVV	268	1.8000	20.45
17	VIIGIGAVS	129	1.5000	17.05
18	VVVKDFSDG	194	1.5000	17.05
19	VATIRRVAS	165	1.4000	15.91
20	IGLGLALYF	111	1.3000	14.77
21	VASQVGRIA	251	1.3000	14.77
22	LAALLTQPG	291	1.2000	13.64
23	MSAREIVII	123	1.1000	12.50
24	IIGIGAVSR	130	1.1000	12.50
25	LDAARVRPA	142	1.1000	12.50
26	LLQIDTQQV	153	1.1000	12.50
27	IDTQQVADR	156	1.0000	11.36
28	IEQARRAAK	64	0.9000	10.23
29	LKALLATVV	97	0.9000	10.23
30	VSREEVLDA	136	0.9000	10.23
31	VASARVQRQ	171	0.8000	9.09

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	VGIGLGLAL	109	4.9000	50.00
2	VRGLKALLA	94	4.8000	48.98

3	IVIIGIGAV	128	4.5500	46.43
4	IRRVASARV	168	4.0000	40.82
5	LALYFTPAM	115	3.8400	39.18
6	VLAVVGIGL	105	3.7000	37.76
7	ITIVERVPV	186	3.3000	33.67
8	VVIWGTDDR	275	3.1600	32.24
9	VVGIGLGLA	108	3.1000	31.63
10	LYFTPAMSA	117	3.1000	31.63
11	VVRGLKALL	93	3.0000	30.61
12	IGLGLALYF	111	3.0000	30.61
13	LQVLTALHP	241	3.0000	30.61
14	VIIIGIGAVS	129	2.8000	28.57
15	LRITIVERV	184	2.7000	27.55
16	LLATVVLA	100	2.6000	26.53
17	VRPATPLLQ	147	2.6000	26.53
18	VGRIAAPSV	255	2.4000	24.49
19	LGLALYFTP	113	2.2000	22.45
20	LKALLATVV	97	2.1000	21.43
21	VVLAVVGIG	104	2.0000	20.41
22	YPSALRITI	180	1.9000	19.39
23	VQRQYPSAL	176	1.7000	17.35
24	VATIRRVAS	165	1.6000	16.33
25	LLQIDTQQV	153	1.5600	15.92
26	IVERVPVVV	188	1.5000	15.31
27	VSREEVLDA	136	1.4000	14.29
28	IGAVSREEV	133	1.3000	13.27
29	LTLADGRVV	268	1.3000	13.27
30	IIGIGAVSR	130	1.2000	12.24
31	LQIDTQQVA	154	1.2000	12.24

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	VGIGLGLAL	109	3.9000	39.80
2	VRGLKALLA	94	3.8000	38.78
3	IVIIGIGAV	128	3.5500	36.22
4	IRRVASARV	168	3.0000	30.61
5	YPSALRITI	180	2.9000	29.59
6	LALYFTPAM	115	2.8400	28.98
7	VLAVVGIGL	105	2.7000	27.55
8	ITIVERVPV	186	2.3000	23.47
9	VVIWGTTDR	275	2.1600	22.04
10	VVGIGLGLA	108	2.1000	21.43
11	LYFTPAMSA	117	2.1000	21.43
12	VVRGLKALL	93	2.0000	20.41
13	IGLGLALYF	111	2.0000	20.41
14	LQVLTALHP	241	2.0000	20.41
15	VIIIGIGAVS	129	1.8000	18.37
16	LRITIVERV	184	1.7000	17.35
17	LLATVVLA	100	1.6000	16.33
18	VRPATPLLQ	147	1.6000	16.33
19	VGRIAAPSV	255	1.4000	14.29
20	LGLALYFTP	113	1.2000	12.24
21	LKALLATVV	97	1.1000	11.22
22	VVLAVVGIG	104	1.0000	10.20
23	VQRQYPSAL	176	0.7000	7.14
24	VATIRRVAS	165	0.6000	6.12
25	LLQIDTQQV	153	0.5600	5.71
26	IVERVPVVV	188	0.5000	5.10
27	VSREEVLDA	136	0.4000	4.08
28	IGAVSREEV	133	0.3000	3.06
29	LTLADGRVV	268	0.3000	3.06
30	IIGIGAVSR	130	0.2000	2.04
31	LQIDTQQVA	154	0.2000	2.04

ALLELE: DRB1_1506	Threshold for 3 % with score:	Highest Score achievable by any peptide:
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3.1

9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VGIGLGLAL	109	4.9000	50.00
2	VRGLKALLA	94	4.8000	48.98
3	IVIIGIGAV	128	4.5500	46.43
4	IRRVASARV	168	4.0000	40.82
5	LALYFTPAM	115	3.8400	39.18
6	VLAVVGIGL	105	3.7000	37.76
7	ITIVERVPV	186	3.3000	33.67
8	VVIWGTTDR	275	3.1600	32.24
9	VVGIGLGLA	108	3.1000	31.63
10	LYFTPAMSA	117	3.1000	31.63
11	VVRGLKALL	93	3.0000	30.61
12	IGLGLALYF	111	3.0000	30.61
13	LQVLTALHP	241	3.0000	30.61
14	VIIIGIGAVS	129	2.8000	28.57
15	LRITIVERV	184	2.7000	27.55
16	LLATVVLA	100	2.6000	26.53
17	VRPATPLLQ	147	2.6000	26.53
18	VGRIAPS	255	2.4000	24.49
19	LGLALYFTP	113	2.2000	22.45
20	LKALLATVV	97	2.1000	21.43
21	VVLAVVGIG	104	2.0000	20.41
22	YPSALRITI	180	1.9000	19.39
23	VQRQYPSAL	176	1.7000	17.35
24	VATIRRVAS	165	1.6000	16.33
25	LLQIDTQQV	153	1.5600	15.92
26	IVERVPVVV	188	1.5000	15.31
27	VSREEVLDA	136	1.4000	14.29
28	IGAVSREEV	133	1.3000	13.27
29	LTLADGRVV	268	1.3000	13.27
30	IIGIGAVSR	130	1.2000	12.24
31	LQIDTQQVA	154	1.2000	12.24

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	IIGIGAVSR	130	3.8000	38.78
2	VLAVVGIGL	105	3.3000	33.67
3	VVIWGTTDR	275	3.2000	32.65
4	VRPATPLLQ	147	3.0000	30.61
5	IVIIGIGAV	128	2.9000	29.59
6	VRGLKALLA	94	2.6000	26.53
7	IRRVASARV	168	2.3000	23.47
8	VVGIGLGLA	108	2.2000	22.45
9	VERVPVVVK	189	2.0000	20.41
10	VVLAVVGIG	104	1.8000	18.37
11	LLTQPGRTY	294	1.6000	16.33
12	VQRQYPSAL	176	1.5000	15.31
13	LYFTPAMSA	117	1.4000	14.29
14	FEGPRRRAR	40	1.3000	13.27
15	ITLTLADGR	266	1.3000	13.27
16	LQVLTALHP	241	1.1000	11.22
17	VGIGLGLAL	109	1.0000	10.20
18	LLQIDTQQV	153	1.0000	10.20
19	IVSEQNPAK	79	0.8000	8.16
20	LKALLATVV	97	0.8000	8.16
21	YPSALRITI	180	0.8000	8.16
22	LTLADGRVV	268	0.8000	8.16
23	IGLGLALYF	111	0.7000	7.14
24	VGRIAAPSV	255	0.7000	7.14
25	LRITIVERV	184	0.6000	6.12
26	IEQARRAAK	64	0.5000	5.10
27	VIIIGIGAVS	129	0.4000	4.08
28	LAVVGIGLG	106	0.2000	2.04
29	LGLALYFTP	113	0.2000	2.04
30	YFTPAMSAR	118	0.1000	1.02

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	IIGIGAVSR	130	3.8000	38.78
2	VLAVVGIGL	105	3.3000	33.67
3	VVIWGTTDR	275	3.2000	32.65
4	VRPATPLLQ	147	3.0000	30.61
5	IVIIGIGAV	128	2.9000	29.59
6	VRGLKALLA	94	2.6000	26.53
7	IRRVASARV	168	2.3000	23.47
8	VVGIGLGLA	108	2.2000	22.45
9	VERVPVVVK	189	2.0000	20.41
10	VVLAVVGIG	104	1.8000	18.37
11	LLTQPGRTY	294	1.6000	16.33
12	VQRQYPSAL	176	1.5000	15.31
13	LYFTPAMSA	117	1.4000	14.29
14	FEGPRRRAR	40	1.3000	13.27
15	ITLTLADGR	266	1.3000	13.27
16	LQVLTALHP	241	1.1000	11.22
17	VGIGLGLAL	109	1.0000	10.20
18	LLQIDTQQV	153	1.0000	10.20
19	IVSEQNPAK	79	0.8000	8.16
20	LKALLATVV	97	0.8000	8.16
21	YPSALRITI	180	0.8000	8.16
22	LTLADGRVV	268	0.8000	8.16
23	IGLGLALYF	111	0.7000	7.14
24	VGRIAAPSV	255	0.7000	7.14
25	LRITIVERV	184	0.6000	6.12
26	IEQARRAAK	64	0.5000	5.10
27	VIIIGIGAVS	129	0.4000	4.08
28	LAVVGIGLG	106	0.2000	2.04
29	LGLALYFTP	113	0.2000	2.04

30

YFTPAMSAR

118

0.1000

1.02