

MHC Class-II Binding Peptide Prediction Results

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INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Fri Feb 5 17:22:06 2010
Length of input sequence	250 amino acids
Number of nanomers from input sequence	242
Number of nanomers with obligatory P1 anchor residue	112
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	25

ALLELE:
DRB1_0101

Threshold for 3 % with score:
0.14

Highest Score achievable by any
peptide: 6

Rank	Sequence	At Position	Score	% of Highest Score
1	YVLALALFV	130	3.7000	61.67
2	IVIALAFYL	38	3.4000	56.67
3	FVLPLAVTI	85	2.6000	43.33
4	VFILISNWL	95	2.2000	36.67
5	VTLLAPINL	164	1.8000	30.00
6	LRLFGNIFA	184	1.7800	29.67
7	IKLLKGHVT	157	1.6000	26.67
8	LIALFPPYI	199	1.5700	26.17
9	FILISNWLA	96	1.4200	23.67
10	INYVLALAL	128	1.3500	22.50
11	YIMWAPNAI	206	1.3000	21.67
12	LVALIALFP	196	1.2000	20.00
13	FVGAIQAFI	221	1.2000	20.00
14	FGNIFAGGI	187	1.1000	18.33

15	FVFVCYHTA	137	0.9500	15.83
16	LFVFVCYHT	136	0.6800	11.33
17	LYFSQAMEL	236	0.5900	9.83
18	WLAVLPVQY	102	0.5500	9.17
19	FVCYHTAGI	139	0.5000	8.33
20	YLRAKVTST	45	0.4900	8.17
21	FIFALLTIL	228	0.4900	8.17
22	IALFPPYIM	200	0.4600	7.67
23	MRIAPFVLP	80	0.2000	3.33
24	IAGLIVIAL	34	0.1000	1.67

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	IVIALAFYL	38	4.4000	73.33
2	VFILISNWL	95	3.2000	53.33
3	VTLLAPINL	164	2.8000	46.67
4	LRLFGNIFA	184	2.7800	46.33
5	YVLALALFV	130	2.7000	45.00
6	FVLPLAVTI	85	2.6000	43.33
7	IKLLKGHVT	157	2.6000	43.33
8	LIALFPPYI	199	2.5700	42.83
9	INYVLALAL	128	2.3500	39.17
10	LVALIALFP	196	2.2000	36.67
11	LFVFVCYHT	136	1.6800	28.00
12	LYFSQAMEL	236	1.5900	26.50
13	IALFPPYIM	200	1.4600	24.33
14	FILISNWL	96	1.4200	23.67
15	MRIAPFVLP	80	1.2000	20.00
16	FVGAIQAFI	221	1.2000	20.00
17	IAGLIVIAL	34	1.1000	18.33
18	FGNIFAGGI	187	1.1000	18.33
19	LLKSAADI	120	1.0000	16.67
20	LVEEVAKPI	172	1.0000	16.67
21	FVFVCYHTA	137	0.9500	15.83
22	MRNQVESAI	70	0.9000	15.00
23	VGAIQAFIF	222	0.9000	15.00

24	VESAIGMRI	74	0.7900	13.17
25	VLPLAVTIF	86	0.7900	13.17

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	IVIALAFYL	38	4.0600	42.74
2	VNTDTVLST	24	4.0000	42.11
3	LYFSQAMEL	236	3.4600	36.42
4	WRRGIVGHP	148	3.4000	35.79
5	VLPLAVTIF	86	3.3000	34.74
6	LFVGAIQAF	220	3.3000	34.74
7	ILVALIALF	195	3.1000	32.63
8	ISLSLRLFG	180	3.0000	31.58
9	LIALFPPYI	199	2.9000	30.53
10	ITIQMRNQV	66	2.7100	28.53
11	LIVIALAFY	37	2.6000	27.37
12	IQMRNQVES	68	2.6000	27.37
13	YVLALALFV	130	2.6000	27.37
14	VLALALFVF	131	2.6000	27.37
15	LLKGHVTL	159	2.5600	26.95
16	FYLRKVTS	44	2.5000	26.32
17	VGAIQAFIF	222	2.4000	25.26
18	ILISNWLAV	97	2.3000	24.21
19	LLKSAADI	120	2.3000	24.21
20	LKGHVTLA	160	2.3000	24.21
21	IFALLTILY	229	2.3000	24.21
22	MRIAPFVLP	80	2.2000	23.16
23	IFAGGILVA	190	2.2000	23.16
24	FVFILISNW	94	2.1700	22.84
25	VFILISNWL	95	2.0700	21.79

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	WRRGIVGHP	148	3.4000	37.36
2	FVFILISNW	94	3.1700	34.84
3	FYLRKAVTS	44	3.1000	34.07
4	YVLALALFV	130	2.6000	28.57
5	VNTDTVLST	24	2.3000	25.27
6	IVIALAFYL	38	2.1000	23.08
7	FVLPLAVTI	85	2.0000	21.98
8	FVGAIQAFI	221	1.7000	18.68
9	YIMWAPNAI	206	1.6100	17.69
10	YLRKAVTST	45	1.6000	17.58
11	FVCYHTAGI	139	1.6000	17.58
12	LYFSQAMEL	236	1.5000	16.48
13	FILISNWLA	96	1.4000	15.38
14	LKGHVTLA	160	1.3000	14.29
15	FGNIFAGGI	187	1.3000	14.29
16	IQMRNQVES	68	1.2000	13.19
17	IFAGGILVA	190	1.2000	13.19
18	LRLFGNIFA	184	1.0000	10.99
19	LIALFPPYI	199	1.0000	10.99
20	FIFALLTIL	228	1.0000	10.99
21	LFPPYIMWA	202	0.9000	9.89
22	FALLTILYF	230	0.9000	9.89
23	ITIQMRNQV	66	0.7100	7.80
24	LFFEAITIQ	61	0.7000	7.69
25	WLAVLPVQY	102	0.7000	7.69

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	VNTDTVLST	24	3.8000	43.18
2	LKGHVTLA	160	2.8000	31.82
3	IFAGGILVA	190	2.7000	30.68
4	ITIQMRNQV	66	2.4000	27.27
5	VQYTDKHGH	108	2.3800	27.05
6	LYFSQAMEL	236	2.2000	25.00
7	YVLALALFV	130	2.1000	23.86

8	ISLSLRLFG	180	2.1000	23.86
9	IQMRNQVES	68	2.0800	23.64
10	FYLRAKVTS	44	1.9800	22.50
11	FVFILISNW	94	1.9000	21.59
12	VFILISNWL	95	1.8000	20.45
13	ILISNWLAV	97	1.8000	20.45
14	LFFEAITIQ	61	1.7000	19.32
15	IVGHPIKLL	152	1.7000	19.32
16	LRLFGNIFA	184	1.6800	19.09
17	IVIALAFYL	38	1.6000	18.18
18	LLKGHVTL	159	1.6000	18.18
19	LFPPYIMWA	202	1.6000	18.18
20	LVALIALFP	196	1.5000	17.05
21	LFVGAIQAF	220	1.5000	17.05
22	VLPLAVTIF	86	1.4000	15.91
23	LLKSAADI	120	1.4000	15.91
24	VGHPIKLLK	153	1.4000	15.91
25	LIVIALAFY	37	1.3000	14.77

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	VNTDTVLST	24	3.8000	43.18
2	LKGHVTLA	160	2.8000	31.82
3	IFAGGILVA	190	2.7000	30.68
4	ITIQMRNQV	66	2.4000	27.27
5	VQYTDKHHG	108	2.3800	27.05
6	LYFSQAMEL	236	2.2000	25.00
7	YVLALALFV	130	2.1000	23.86
8	ISLSLRLFG	180	2.1000	23.86
9	IQMRNQVES	68	2.0800	23.64
10	FYLRAKVTS	44	1.9800	22.50
11	FVFILISNW	94	1.9000	21.59
12	VFILISNWL	95	1.8000	20.45
13	ILISNWLAV	97	1.8000	20.45
14	LFFEAITIQ	61	1.7000	19.32
15	IVGHPIKLL	152	1.7000	19.32

16	LRLFGNIFA	184	1.6800	19.09
17	IVIALAFYL	38	1.6000	18.18
18	LLKGHVTLL	159	1.6000	18.18
19	LFPPYIMWA	202	1.6000	18.18
20	LVALIALFP	196	1.5000	17.05
21	LFVGAIQAF	220	1.5000	17.05
22	VLPLAVTIF	86	1.4000	15.91
23	LLKSAADI	120	1.4000	15.91
24	VGHPIKLLK	153	1.4000	15.91
25	LIVIALAFY	37	1.3000	14.77

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	VNTDTVLST	24	3.8000	43.18
2	LKGHVTLA	160	2.8000	31.82
3	IFAGGILVA	190	2.7000	30.68
4	ITIQMRNQV	66	2.4000	27.27
5	VQYTDKHHG	108	2.3800	27.05
6	LYFSQAMEL	236	2.2000	25.00
7	YVLALALFV	130	2.1000	23.86
8	ISLSLRLFG	180	2.1000	23.86
9	IQMRNQVES	68	2.0800	23.64
10	FYLRAKVT	44	1.9800	22.50
11	FVFILISNW	94	1.9000	21.59
12	VFILISNWL	95	1.8000	20.45
13	ILISNWLAV	97	1.8000	20.45
14	LFFEAITIQ	61	1.7000	19.32
15	IVGHPIKLL	152	1.7000	19.32
16	LRLFGNIFA	184	1.6800	19.09
17	IVIALAFYL	38	1.6000	18.18
18	LLKGHVTLL	159	1.6000	18.18
19	LFPPYIMWA	202	1.6000	18.18
20	LVALIALFP	196	1.5000	17.05
21	LFVGAIQAF	220	1.5000	17.05
22	VLPLAVTIF	86	1.4000	15.91
23	LLKSAADI	120	1.4000	15.91

24	VGHPIKLLK	153	1.4000	15.91
25	LIVIALAFY	37	1.3000	14.77

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	WRRGIVGHP	148	4.4000	46.32
2	YVLALALFV	130	3.6000	37.89
3	FYLRAKVTS	44	3.5000	36.84
4	FVFILISNW	94	3.1700	33.37
5	IVIALAFYL	38	3.0600	32.21
6	VNTDTVLST	24	3.0000	31.58
7	FVLPLAVTI	85	2.9000	30.53
8	FALLTILYF	230	2.8000	29.47
9	FVGAIQAFI	221	2.6000	27.37
10	YIMWAPNAI	206	2.5100	26.42
11	FVCYHTAGI	139	2.5000	26.32
12	LYFSQAMEL	236	2.4600	25.89
13	YLRAKVTST	45	2.3000	24.21
14	VLPLAVTIF	86	2.3000	24.21
15	LFVGAIQAF	220	2.3000	24.21
16	FGNIFAGGI	187	2.2000	23.16
17	ILVALIALF	195	2.1000	22.11
18	WLAVLPVQY	102	2.0000	21.05
19	ISLSLRLFG	180	2.0000	21.05
20	FIFALLTIL	228	1.9600	20.63
21	FFEAITIQM	62	1.9000	20.00
22	LIALFPPYI	199	1.9000	20.00
23	WLGMTVNTD	19	1.7100	18.00
24	ITIQMRNQV	66	1.7100	18.00
25	FEAITIQMR	63	1.7000	17.89

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	VNTDTVLST	24	3.8000	43.18
2	LKGHVTLA	160	2.8000	31.82
3	IFAGGILVA	190	2.7000	30.68
4	ITIQMRNQV	66	2.4000	27.27
5	VQYTDKHHG	108	2.3800	27.05
6	LYFSQAMEL	236	2.2000	25.00
7	YVLALALFV	130	2.1000	23.86
8	ISLSLRLFG	180	2.1000	23.86
9	IQMRNQVES	68	2.0800	23.64
10	FYLRKVTS	44	1.9800	22.50
11	FVFILISNW	94	1.9000	21.59
12	VFILISNWL	95	1.8000	20.45
13	ILISNWLAV	97	1.8000	20.45
14	LFFEAITIQ	61	1.7000	19.32
15	IVGHPIKLL	152	1.7000	19.32
16	LRLFGNIFA	184	1.6800	19.09
17	IVIALAFYL	38	1.6000	18.18
18	LLKGHVTLA	159	1.6000	18.18
19	LFPPYIMWA	202	1.6000	18.18
20	LVALIALFP	196	1.5000	17.05
21	LFVGAIQAF	220	1.5000	17.05
22	VLPLAVTIF	86	1.4000	15.91
23	LLKSAADI	120	1.4000	15.91
24	VGHPIKLLK	153	1.4000	15.91
25	LIVIALAFY	37	1.3000	14.77

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	LKGHVTLA	160	4.0000	46.51
2	YVLALALFV	130	3.1000	36.05
3	FILISNWLA	96	2.8000	32.56
4	VFILISNWL	95	2.7000	31.40
5	LRLFGNIFA	184	2.6800	31.16
6	LFFEAITIQ	61	2.4000	27.91
7	FVFILISNW	94	2.4000	27.91

8	FVCYHTAGI	139	2.1000	24.42
9	WLGMTVNTD	19	1.9000	22.09
10	LGMTVNTDT	20	1.6000	18.60
11	VNTDTVLST	24	1.6000	18.60
12	YIMWAPNAI	206	1.6000	18.60
13	IFALLTILY	229	1.5800	18.37
14	LPVQYTDKH	106	1.4800	17.21
15	FALLTILYF	230	1.4000	16.28
16	YLRAKVTST	45	1.3000	15.12
17	ILISNWLAV	97	1.3000	15.12
18	LVALIALFP	196	1.3000	15.12
19	LYFSQAMEL	236	1.3000	15.12
20	FVLPLAVTI	85	1.2800	14.88
21	FFEAITIQM	62	1.1800	13.72
22	IVGHPIKLL	152	1.0000	11.63
23	VLPLAVTIF	86	0.9000	10.47
24	LVEEVAKPI	172	0.8000	9.30
25	LPLAVTIFV	87	0.7800	9.07

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	LKGHVTLA	160	5.4000	56.25
2	LRLFGNIFA	184	5.3000	55.21
3	FILISNWL	96	3.8800	40.42
4	YIMWAPNAI	206	3.4000	35.42
5	IVIALAFYL	38	3.1000	32.29
6	IQMRNQVES	68	3.0000	31.25
7	YVLALALFV	130	2.4000	25.00
8	IVGHPIKLL	152	2.4000	25.00
9	VFILISNWL	95	2.3000	23.96
10	FVCYHTAGI	139	2.3000	23.96
11	LPLAVTIFV	87	2.2000	22.92
12	LRAKVTSTD	46	2.1000	21.88
13	IALFPPYIM	200	1.8000	18.75
14	IWRRGIVGH	147	1.7800	18.54
15	LGMTVNTDT	20	1.6000	16.67

16	IFALLTILY	229	1.6000	16.67
17	MRIAPFVLP	80	1.5000	15.62
18	VGEHHTATW	11	1.4000	14.58
19	IMWAPNAIW	207	1.4000	14.58
20	LFVFVCYHT	136	1.3000	13.54
21	IGMRIAPFV	78	1.2000	12.50
22	LVALIALFP	196	1.2000	12.50
23	IFAGGILVA	190	1.0000	10.42
24	VTIFVFILI	91	0.9000	9.38
25	INYVLALAL	128	0.9000	9.38

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	LRLFGNIFA	184	5.5800	63.41
2	VFILISNWL	95	4.0000	45.45
3	FILISNWLA	96	2.8000	31.82
4	IFALLTILY	229	2.7800	31.59
5	VLPLAVTIF	86	2.6000	29.55
6	IVIALAFYL	38	2.5500	28.98
7	LKGHVTLA	160	2.5000	28.41
8	FVFILISNW	94	2.4000	27.27
9	FVCYHTAGI	139	2.3000	26.14
10	LVALIALFP	196	2.1000	23.86
11	WLGMTVNTD	19	1.9000	21.59
12	LTILYFSQA	233	1.9000	21.59
13	YIMWAPNAI	206	1.8500	21.02
14	LPLAVTIFV	87	1.7800	20.23
15	YVLALALFV	130	1.7000	19.32
16	LGMTVNTDT	20	1.5000	17.05
17	LRAKVTSTD	46	1.4000	15.91
18	INYVLALAL	128	1.4000	15.91
19	IALFPPYIM	200	1.4000	15.91
20	IMWAPNAIW	207	1.4000	15.91
21	LFPEAITIQ	61	1.3000	14.77
22	MRIAPFVLP	80	1.2000	13.64
23	IAGLIVIAL	34	1.1800	13.41

24	VTIFVFILI	91	1.1800	13.41
25	VTLLAPINL	164	1.0800	12.27

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	WLGMTVNTD	19	5.6000	59.57
2	LRLFGNIFA	184	4.5800	48.72
3	FVFILISNW	94	4.3000	45.74
4	VFILISNWL	95	4.0000	42.55
5	FILISNWL	96	3.8000	40.43
6	FVCYHTAGI	139	3.5000	37.23
7	LRAKVTSTD	46	3.1000	32.98
8	YIMWAPNAI	206	3.0500	32.45
9	YVLALALFV	130	3.0000	31.91
10	IFALLTILY	229	2.8800	30.64
11	YLRAKVTST	45	2.7000	28.72
12	IVIALAFYL	38	2.5500	27.13
13	VLPLAVTIF	86	2.5000	26.60
14	FFEAITIQM	62	2.2800	24.26
15	FALLTILYF	230	2.1000	22.34
16	FVLPLAVTI	85	1.6000	17.02
17	LLAPINLVE	166	1.6000	17.02
18	ILYFSQAME	235	1.6000	17.02
19	WLAVLPVQY	102	1.5000	15.96
20	FVFVCYHTA	137	1.5000	15.96
21	LKGVHTLLA	160	1.5000	15.96
22	LVALIALFP	196	1.5000	15.96
23	IALFPPYIM	200	1.5000	15.96
24	LGMTVNTDT	20	1.4000	14.89
25	INYVLALAL	128	1.4000	14.89

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	LRLFGNIFA	184	4.5800	52.05
2	FILISNWL	96	3.8000	43.18
3	FVFILISNW	94	3.4000	38.64
4	FVCYHTAGI	139	3.3000	37.50
5	VFILISNWL	95	3.0000	34.09
6	WLGMTVNTD	19	2.9000	32.95
7	YIMWAPNAI	206	2.8500	32.39
8	YVLALALFV	130	2.7000	30.68
9	YLRKVTST	45	1.8000	20.45
10	IFALLTILY	229	1.7800	20.23
11	VLPLAVTIF	86	1.6000	18.18
12	IVIALAFYL	38	1.5500	17.61
13	FVFVCYHTA	137	1.5000	17.05
14	LKGHVTLA	160	1.5000	17.05
15	FVLPLAVTI	85	1.4000	15.91
16	FALLTILYF	230	1.2000	13.64
17	FFEAITIQM	62	1.1800	13.41
18	LVALIALFP	196	1.1000	12.50
19	LTILYFSQA	233	0.9000	10.23
20	LPLAVTIFV	87	0.7800	8.86
21	FGNIFAGGI	187	0.6000	6.82
22	LGMTVNTDT	20	0.5000	5.68
23	FVGAIQAFI	221	0.5000	5.68
24	LRAKVTSTD	46	0.4000	4.55
25	WLAVLPVQY	102	0.4000	4.55

ALLELE:
DRB1_0410

Threshold for 3 % with score:
2.6

Highest Score achievable by any
peptide: 9.4

Rank	Sequence	At Position	Score	% of Highest Score
1	LRLFGNIFA	184	5.5800	59.36
2	VFILISNWL	95	5.0000	53.19
3	WLGMTVNTD	19	4.6000	48.94
4	LRAKVTSTD	46	4.1000	43.62
5	IFALLTILY	229	3.8800	41.28
6	IVIALAFYL	38	3.5500	37.77
7	VLPLAVTIF	86	3.5000	37.23

8	FVFILISNW	94	3.3000	35.11
9	FILISNWLA	96	2.8000	29.79
10	LLAPINLVE	166	2.6000	27.66
11	ILYFSQAME	235	2.6000	27.66
12	FVCYHTAGI	139	2.5000	26.60
13	LKGHVTLA	160	2.5000	26.60
14	LVALIALFP	196	2.5000	26.60
15	IALFPPYIM	200	2.5000	26.60
16	LGMTVNTDT	20	2.4000	25.53
17	INYVLALAL	128	2.4000	25.53
18	IMWAPNAIW	207	2.3000	24.47
19	IAGLIVIAL	34	2.1800	23.19
20	LFFEAITIQ	61	2.1000	22.34
21	LPLAVTIFV	87	2.0800	22.13
22	VTLLAPINL	164	2.0800	22.13
23	YIMWAPNAI	206	2.0500	21.81
24	LPVQYTDKH	106	2.0000	21.28
25	YVLALALFV	130	2.0000	21.28

ALLELE:
DRB1_0421

Threshold for 3 % with score:
2.3

Highest Score achievable by any
peptide: 9

Rank	Sequence	At Position	Score	% of Highest Score
1	YVLALALFV	130	4.1000	45.56
2	LKGHVTLA	160	4.0000	44.44
3	VFILISNWL	95	3.6600	40.67
4	FALLTILYF	230	3.3000	36.67
5	WLGMTVNTD	19	3.0000	33.33
6	FVCYHTAGI	139	3.0000	33.33
7	IFALLTILY	229	2.8800	32.00
8	VLPLAVTIF	86	2.8000	31.11
9	FILISNWLA	96	2.8000	31.11
10	FFEAITIQM	62	2.6800	29.78
11	LRLFGNIFA	184	2.6800	29.78
12	YIMWAPNAI	206	2.5000	27.78
13	FVFILISNW	94	2.4000	26.67
14	LGMTVNTDT	20	2.3000	25.56
15	VNTDTVLST	24	2.3000	25.56

16	ILISNWLAV	97	2.3000	25.56
17	LVALIALFP	196	2.3000	25.56
18	LYFSQAMEL	236	2.2600	25.11
19	FVLPLAVTI	85	2.1800	24.22
20	YLRKVTST	45	2.0000	22.22
21	IVGHPIKLL	152	1.9600	21.78
22	LPLAVTIFV	87	1.7800	19.78
23	LFFEAITIQ	61	1.7000	18.89
24	LVEEVAKPI	172	1.7000	18.89
25	IVIALAFYL	38	1.5600	17.33

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	LRLFGNIFA	184	5.5800	63.41
2	VFILISNWL	95	4.0000	45.45
3	FILISNWLA	96	2.8000	31.82
4	IFALLTILY	229	2.7800	31.59
5	VLPLAVTIF	86	2.6000	29.55
6	IVIALAFYL	38	2.5500	28.98
7	LKGHVTLA	160	2.5000	28.41
8	FVFILISNW	94	2.4000	27.27
9	FVCYHTAGI	139	2.3000	26.14
10	LVALIALFP	196	2.1000	23.86
11	WLGMTVNTD	19	1.9000	21.59
12	LTYLYFSQA	233	1.9000	21.59
13	YIMWAPNAI	206	1.8500	21.02
14	LPLAVTIFV	87	1.7800	20.23
15	YVLALALFV	130	1.7000	19.32
16	LGMTVNTDT	20	1.5000	17.05
17	LRAKVTSTD	46	1.4000	15.91
18	INYVLALAL	128	1.4000	15.91
19	IALFPPYIM	200	1.4000	15.91
20	IMWAPNAIW	207	1.4000	15.91
21	LFFEAITIQ	61	1.3000	14.77
22	MRIAPFVLP	80	1.2000	13.64
23	IAGLIVIAL	34	1.1800	13.41

24	VTIFVFILI	91	1.1800	13.41
25	VTLLAPINL	164	1.0800	12.27

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	LKGHVTLA	160	4.0000	46.51
2	YVLALALFV	130	3.1000	36.05
3	FILISNWLA	96	2.8000	32.56
4	VFILISNWL	95	2.7000	31.40
5	LRLFGNIFA	184	2.6800	31.16
6	LFFEAITIQ	61	2.4000	27.91
7	FVFILISNW	94	2.4000	27.91
8	FVCYHTAGI	139	2.1000	24.42
9	WLGMTVNTD	19	1.9000	22.09
10	LGMTVNTDT	20	1.6000	18.60
11	VNTDTVLST	24	1.6000	18.60
12	YIMWAPNAI	206	1.6000	18.60
13	IFALLTILY	229	1.5800	18.37
14	LPVQYTDKH	106	1.4800	17.21
15	FALLTILYF	230	1.4000	16.28
16	YLRKVTST	45	1.3000	15.12
17	ILISNWLAV	97	1.3000	15.12
18	LVALIALFP	196	1.3000	15.12
19	LYFSQAMEL	236	1.3000	15.12
20	FVLPLAVTI	85	1.2800	14.88
21	FFEAITIQM	62	1.1800	13.72
22	IVGHPIKLL	152	1.0000	11.63
23	VLPLAVTIF	86	0.9000	10.47
24	LVEEVAKPI	172	0.8000	9.30
25	LPLAVTIFV	87	0.7800	9.07

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	IVIALAFYL	38	8.1000	69.83
2	LYFSQAMEL	236	7.4000	63.79
3	YVLALALFV	130	7.3000	62.93
4	INYVLALAL	128	7.1000	61.21
5	FVLPLAVTI	85	6.9000	59.48
6	ILISNWLAV	97	6.3000	54.31
7	VFILISNWL	95	5.9000	50.86
8	VTIFVFILI	91	5.7000	49.14
9	YIMWAPNAI	206	5.7000	49.14
10	FGNIFAGGI	187	5.5000	47.41
11	FIFALLTIL	228	5.3000	45.69
12	LAVTIFVFI	89	5.1000	43.97
13	LLKSAADI	120	4.9000	42.24
14	IVGHPIKLL	152	4.8000	41.38
15	VGAIQAFIF	222	4.8000	41.38
16	FVFILISNW	94	4.7000	40.52
17	FVGAIQAFI	221	4.6000	39.66
18	FVCYHTAGI	139	4.5200	38.97
19	VLSTAIAGL	29	4.5000	38.79
20	VTLLAPINL	164	4.5000	38.79
21	IAGLIVIAL	34	4.3000	37.07
22	LRLFGNIFA	184	4.2000	36.21
23	WLAVLPVQY	102	4.1000	35.34
24	FILISNWLA	96	4.0000	34.48
25	VAKPISLSL	176	4.0000	34.48

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	IVIALAFYL	38	8.1000	69.83
2	LYFSQAMEL	236	7.4000	63.79
3	YVLALALFV	130	7.3000	62.93
4	INYVLALAL	128	7.1000	61.21
5	FVLPLAVTI	85	6.9000	59.48
6	ILISNWLAV	97	6.3000	54.31
7	VFILISNWL	95	5.9000	50.86

8	VTIFVFILI	91	5.7000	49.14
9	YIMWAPNAI	206	5.7000	49.14
10	FGNIFAGGI	187	5.5000	47.41
11	FIFALLTIL	228	5.3000	45.69
12	LAVTIFVFI	89	5.1000	43.97
13	LLKSAADI	120	4.9000	42.24
14	IVGHPIKLL	152	4.8000	41.38
15	VGAIQAFIF	222	4.8000	41.38
16	FVFILISNW	94	4.7000	40.52
17	FVGAIQAFI	221	4.6000	39.66
18	FVCYHTAGI	139	4.5200	38.97
19	VLSTAIAGL	29	4.5000	38.79
20	VTLLAPINL	164	4.5000	38.79
21	IAGLIVIAL	34	4.3000	37.07
22	LRLFGNIFA	184	4.2000	36.21
23	WLAVLPVQY	102	4.1000	35.34
24	FILISNWLA	96	4.0000	34.48
25	VAKPISLSL	176	4.0000	34.48

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	FYLRAKVTS	44	5.1000	59.30
2	FVCYHTAGI	139	5.0000	58.14
3	LRAKVSTSD	46	4.0000	46.51
4	WLGMTVNTD	19	3.5000	40.70
5	IQMRNQVES	68	3.2000	37.21
6	IWRRGIVGH	147	2.8000	32.56
7	LAFYLRAKV	42	2.6000	30.23
8	FVFILISNW	94	2.5000	29.07
9	YVLALALFV	130	2.4000	27.91
10	ILYFSQAME	235	2.3000	26.74
11	FALLTILYF	230	2.0000	23.26
12	FVGAIQAFI	221	1.9000	22.09
13	IVIALAFYL	38	1.7000	19.77
14	VQYTDKHHG	108	1.7000	19.77
15	WRRGIVGHP	148	1.7000	19.77

16	IGMRIAPFV	78	1.6000	18.60
17	YIMWAPNAI	206	1.6000	18.60
18	LRLFGNIFA	184	1.3000	15.12
19	LIVIALAFY	37	1.2000	13.95
20	WKAFDLFVG	215	1.2000	13.95
21	ILVALIALF	195	1.1000	12.79
22	FVLPLAVTI	85	0.9000	10.47
23	FVFVCYHTA	137	0.9000	10.47
24	IFVFILISN	93	0.8000	9.30
25	WLAVLPVQY	102	0.8000	9.30

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	FYLRAKVTS	44	5.1000	63.75
2	FVCYHTAGI	139	4.8000	60.00
3	IQMRNQVES	68	3.2000	40.00
4	LAFYLRAKV	42	2.3000	28.75
5	YVLALALFV	130	2.1000	26.25
6	FVGAIQAFI	221	1.7000	21.25
7	FVFILISNW	94	1.6000	20.00
8	IWRRGIVGH	147	1.5800	19.75
9	YIMWAPNAI	206	1.4000	17.50
10	LRAKVSTSD	46	1.3000	16.25
11	IGMRIAPFV	78	1.3000	16.25
12	WRRGIVGHP	148	1.3000	16.25
13	LRLFGNIFA	184	1.3000	16.25
14	FALLTILYF	230	1.1000	13.75
15	FVFVCYHTA	137	0.9000	11.25
16	WLGMTVNTD	19	0.8000	10.00
17	IVIALAFYL	38	0.7000	8.75
18	FVLPLAVTI	85	0.7000	8.75
19	FILISNWLA	96	0.6000	7.50
20	FGNIFAGGI	187	0.5000	6.25
21	VQYTDKHHG	108	0.4800	6.00
22	ILVALIALF	195	0.2000	2.50
23	LVALIALFP	196	0.2000	2.50

24	LIVIALAFY	37	0.1000	1.25
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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	IQMRNQVES	68	4.2000	52.50
2	FYLRAKVTS	44	4.1000	51.25
3	FVCYHTAGI	139	3.8000	47.50
4	LAFYLRAKV	42	3.3000	41.25
5	IWRRGIVGH	147	2.5800	32.25
6	LRAKVTSTD	46	2.3000	28.75
7	IGMRIAPFV	78	2.3000	28.75
8	LRLFGNIFA	184	2.3000	28.75
9	IVIALAFYL	38	1.7000	21.25
10	VQYTDKHGH	108	1.4800	18.50
11	ILVALIALF	195	1.2000	15.00
12	LVALIALFP	196	1.2000	15.00
13	LIVIALAFY	37	1.1000	13.75
14	YVLALALFV	130	1.1000	13.75
15	LKGHVTLA	160	0.8000	10.00
16	LSLRLFGNI	182	0.8000	10.00
17	LIALFPPYI	199	0.8000	10.00
18	FVGAIQAFI	221	0.7000	8.75
19	FVFILISNW	94	0.6000	7.50
20	VFILISNWL	95	0.6000	7.50
21	INYVLALAL	128	0.6000	7.50
22	LISNWLAVL	98	0.5000	6.25
23	IALFPPYIM	200	0.5000	6.25
24	LFPPYIMWA	202	0.5000	6.25
25	IFALLTILY	229	0.5000	6.25

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
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1	LRAKVTSTD	46	5.0000	58.14
2	IQMRNQVES	68	4.2000	48.84
3	FYLRAKVTS	44	4.1000	47.67
4	FVCYHTAGI	139	4.0000	46.51
5	IWRRGIVGH	147	3.8000	44.19
6	LAFYLRAKV	42	3.6000	41.86
7	ILYFSQAME	235	3.3000	38.37
8	IVIALAFYL	38	2.7000	31.40
9	VQYTDKHGH	108	2.7000	31.40
10	IGMRIAPFV	78	2.6000	30.23
11	WLGMTVNTD	19	2.5000	29.07
12	LRLFGNIFA	184	2.3000	26.74
13	LIVIALAFY	37	2.2000	25.58
14	ILVALIALF	195	2.1000	24.42
15	IFVFILISN	93	1.8000	20.93
16	VFILISNWL	95	1.6000	18.60
17	INYVLALAL	128	1.6000	18.60
18	LVALIALFP	196	1.6000	18.60
19	IALFPPYIM	200	1.6000	18.60
20	IFALLTILY	229	1.6000	18.60
21	FVFILISNW	94	1.5000	17.44
22	LISNWLAVL	98	1.5000	17.44
23	YVLALALFV	130	1.4000	16.28
24	VTL LAPINL	164	1.4000	16.28
25	IAGLIVIAL	34	1.3000	15.12

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	FYLRAKVTS	44	6.1000	70.11
2	FVCYHTAGI	139	4.8000	55.17
3	IQMRNQVES	68	4.2000	48.28
4	FVFILISNW	94	3.4000	39.08
5	YIMWAPNAI	206	3.4000	39.08
6	LRAKVTSTD	46	3.1000	35.63
7	WLGMTVNTD	19	2.8000	32.18
8	YVLALALFV	130	2.7000	31.03

9	IWRRGIVGH	147	2.5800	29.66
10	LAFYLRAKV	42	2.3000	26.44
11	LRLFGNIFA	184	2.1800	25.06
12	YLRAKVTST	45	2.1000	24.14
13	FVLPLAVTI	85	1.7000	19.54
14	FVGAIQAFI	221	1.7000	19.54
15	FALLTILYF	230	1.7000	19.54
16	VLPLAVTIF	86	1.6000	18.39
17	VFILISNWL	95	1.6000	18.39
18	IVIALAFYL	38	1.5500	17.82
19	IGMRIAPFV	78	1.5000	17.24
20	FIFALLTIL	228	1.5000	17.24
21	FVFVCYHTA	137	1.4000	16.09
22	LFFEAITIQ	61	1.2000	13.79
23	FILISNWL	96	1.1000	12.64
24	VQYTDKHHG	108	0.9800	11.26
25	LVALIALFP	196	0.8000	9.20

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	FYLRAKVTS	44	5.6000	55.45
2	FVCYHTAGI	139	5.0000	49.50
3	YVLALALFV	130	4.2000	41.58
4	LRAKVSTSD	46	4.0000	39.60
5	WLGMTVNTD	19	3.8000	37.62
6	FALLTILYF	230	3.8000	37.62
7	IQMRNQVES	68	3.7000	36.63
8	IWRRGIVGH	147	3.3000	32.67
9	LRLFGNIFA	184	2.9000	28.71
10	IGMRIAPFV	78	2.7500	27.23
11	LAFYLRAKV	42	2.6000	25.74
12	FVFILISNW	94	2.5000	24.75
13	IFVFILISN	93	2.4000	23.76
14	VQYTDKHHG	108	2.4000	23.76
15	INYVLALAL	128	2.4000	23.76
16	LVALIALFP	196	2.4000	23.76

17	ILYFSQAME	235	2.3000	22.77
18	IVIALAFYL	38	2.2000	21.78
19	IFALLTILY	229	2.2000	21.78
20	VTLLAPINL	164	2.0000	19.80
21	IAGLIVIAL	34	1.9000	18.81
22	FFEAITIQM	62	1.9000	18.81
23	YIMWAPNAI	206	1.9000	18.81
24	FVGAIQAFI	221	1.9000	18.81
25	WRRGIVGHP	148	1.8000	17.82

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	YVLALALFV	130	3.9000	46.99
2	FALLTILYF	230	3.3000	39.76
3	LRLFGNIFA	184	2.8000	33.73
4	FYLRAKVTS	44	2.6000	31.33
5	LVALIALFP	196	2.4000	28.92
6	FVFILISNW	94	2.2000	26.51
7	FILISNWLA	96	2.0000	24.10
8	LKGHVTLA	160	2.0000	24.10
9	FVCYHTAGI	139	1.9000	22.89
10	FVFVCYHTA	137	1.7000	20.48
11	FVGAIQAFI	221	1.7000	20.48
12	YIMWAPNAI	206	1.6000	19.28
13	VQYTDKHHG	108	1.5800	19.04
14	INYVLALAL	128	1.5000	18.07
15	IFALLTILY	229	1.5000	18.07
16	VTLLAPINL	164	1.4000	16.87
17	LIALFPPYI	199	1.3500	16.27
18	IAGLIVIAL	34	1.3000	15.66
19	IVIALAFYL	38	1.2000	14.46
20	FGNIFAGGI	187	1.2000	14.46
21	FFEAITIQM	62	0.8000	9.64
22	WLGMTVNTD	19	0.7000	8.43
23	LIVIALAFY	37	0.7000	8.43
24	IQMRNQVES	68	0.7000	8.43

25	WRRGIVGHP	148	0.7000	8.43
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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	LKGHVTLA	160	4.0000	47.62
2	IVGHPIKLL	152	3.5000	41.67
3	IVIALAFYL	38	3.2000	38.10
4	IQMRNQVES	68	3.1000	36.90
5	FYLRAKVTS	44	3.0000	35.71
6	LRLFGNIFA	184	2.9000	34.52
7	VQYTDKHHG	108	2.5800	30.71
8	ITIQMRNQV	66	2.5000	29.76
9	YIMWAPNAI	206	2.5000	29.76
10	FVCYHTAGI	139	2.0000	23.81
11	YVLALALFV	130	1.8000	21.43
12	VFILISNWL	95	1.7000	20.24
13	IALFPPYIM	200	1.7000	20.24
14	LVALIALFP	196	1.6000	19.05
15	LAFYLRAKV	42	1.5000	17.86
16	IWRRGIVGH	147	1.4800	17.62
17	LRAKVTSTD	46	1.2000	14.29
18	VLALALFVF	131	1.2000	14.29
19	ILVALIALF	195	1.2000	14.29
20	LIALFPPYI	199	1.2000	14.29
21	VLPLAVTIF	86	1.0000	11.90
22	IGMRIAPFV	78	0.9000	10.71
23	MRIAPFVLP	80	0.9000	10.71
24	IKLLKGHVT	157	0.9000	10.71
25	LFFEAITIQ	61	0.8000	9.52

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
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1	LRLFGNIFA	184	3.8000	45.78
2	LVALIALFP	196	3.4000	40.96
3	LKGHVTLA	160	3.0000	36.14
4	YVLALALFV	130	2.9000	34.94
5	VQYTDKHGH	108	2.5800	31.08
6	INYVLALAL	128	2.5000	30.12
7	IFALLTILY	229	2.5000	30.12
8	VTLLAPINL	164	2.4000	28.92
9	LIALFPPYI	199	2.3500	28.31
10	IAGLIVIAL	34	2.3000	27.71
11	FALLTILYF	230	2.3000	27.71
12	IVIALAFYL	38	2.2000	26.51
13	LIVIALAFY	37	1.7000	20.48
14	IQMRNQVES	68	1.7000	20.48
15	FYLRAKVTS	44	1.6000	19.28
16	VGHPIKLLK	153	1.5000	18.07
17	ISLSLRLFG	180	1.5000	18.07
18	LPLAVTIFV	87	1.4000	16.87
19	LFPPYIMWA	202	1.4000	16.87
20	VLPLAVTIF	86	1.3000	15.66
21	IFVFILISN	93	1.3000	15.66
22	VFILISNWL	95	1.3000	15.66
23	IFAGGILVA	190	1.3000	15.66
24	LYFSQAMEL	236	1.3000	15.66
25	VEEVAKPIS	173	1.2500	15.06

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	LRLFGNIFA	184	3.8000	45.78
2	LVALIALFP	196	3.4000	40.96
3	LKGHVTLA	160	3.0000	36.14
4	YVLALALFV	130	2.9000	34.94
5	VQYTDKHGH	108	2.5800	31.08
6	INYVLALAL	128	2.5000	30.12
7	IFALLTILY	229	2.5000	30.12
8	VTLLAPINL	164	2.4000	28.92

9	LIALFPPYI	199	2.3500	28.31
10	IAGLIVIAL	34	2.3000	27.71
11	FALLTILYF	230	2.3000	27.71
12	IVIALAFYL	38	2.2000	26.51
13	LIVIALAFY	37	1.7000	20.48
14	IQMRNQVES	68	1.7000	20.48
15	FYLRAKVTS	44	1.6000	19.28
16	VGHPIKLLK	153	1.5000	18.07
17	ISLSLRLFG	180	1.5000	18.07
18	LPLAVTIFV	87	1.4000	16.87
19	LFPPYIMWA	202	1.4000	16.87
20	VLPLAVTIF	86	1.3000	15.66
21	IFVFILISN	93	1.3000	15.66
22	VFILISNWL	95	1.3000	15.66
23	IFAGGILVA	190	1.3000	15.66
24	LYFSQAMEL	236	1.3000	15.66
25	VEEVAKPIS	173	1.2500	15.06

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	VNTDTVLST	24	3.3000	36.26
2	IVIALAFYL	38	3.1000	34.07
3	LYFSQAMEL	236	2.5000	27.47
4	WRRGIVGHP	148	2.4000	26.37
5	LKGHVTLA	160	2.3000	25.27
6	IQMRNQVES	68	2.2000	24.18
7	IFAGGILVA	190	2.2000	24.18
8	FVFILISNW	94	2.1700	23.85
9	FYLRAKVTS	44	2.1000	23.08
10	LRLFGNIFA	184	2.0000	21.98
11	LIALFPPYI	199	2.0000	21.98
12	LFPPYIMWA	202	1.9000	20.88
13	ITIQMRNQV	66	1.7100	18.79
14	LFFEAITIQ	61	1.7000	18.68
15	YVLALALFV	130	1.6000	17.58
16	LLKGHVTLA	159	1.6000	17.58

17	VEEVAKPIS	173	1.6000	17.58
18	ISLSLRLFG	180	1.6000	17.58
19	VQYTDKHHG	108	1.5800	17.36
20	VLPLAVTIF	86	1.4000	15.38
21	LLKSAADI	120	1.4000	15.38
22	LFVGAIQAF	220	1.4000	15.38
23	LIVIALAFY	37	1.3000	14.29
24	ILISNWLAV	97	1.3000	14.29
25	MRIAPFVLP	80	1.2000	13.19

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	FYLRAKVTS	44	4.0000	47.62
2	YIMWAPNAI	206	3.5000	41.67
3	FVCYHTAGI	139	3.0000	35.71
4	LKGHVTLA	160	3.0000	35.71
5	YVLALALFV	130	2.8000	33.33
6	IVGHPIKLL	152	2.5000	29.76
7	IVIALAFYL	38	2.2000	26.19
8	IQMRNQVES	68	2.1000	25.00
9	LRLFGNIFA	184	1.9000	22.62
10	WKAFDLFVG	215	1.7000	20.24
11	FVGAIQAFI	221	1.7000	20.24
12	WLGMTVNTD	19	1.6000	19.05
13	VQYTDKHHG	108	1.5800	18.81
14	ITIQMRNQV	66	1.5000	17.86
15	WAPNAIWKA	209	1.5000	17.86
16	FALLTILYF	230	1.5000	17.86
17	FILISNWL	96	1.3000	15.48
18	FVLPLAVTI	85	1.2000	14.29
19	FVFILISNW	94	1.1000	13.10
20	FVFVCYHTA	137	0.9000	10.71
21	YHTAGIWR	142	0.9000	10.71
22	YLRAKVTS	45	0.8000	9.52
23	VFILISNWL	95	0.7000	8.33
24	IALFPPYIM	200	0.7000	8.33

25	LVALIALFP	196	0.6000	7.14
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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	FYLRAKVTS	44	4.4000	50.00
2	YIMWAPNAI	206	4.4000	50.00
3	FVCYHTAGI	139	3.9000	44.32
4	YVLALALFV	130	3.8000	43.18
5	IVGHPIKLL	152	3.4600	39.32
6	FALLTILYF	230	3.4000	38.64
7	IVIALAFYL	38	3.1600	35.91
8	WKAFDLFVG	215	3.1000	35.23
9	LKGHVTLA	160	3.0000	34.09
10	WLGMTVNTD	19	2.7000	30.68
11	FVGAIQAFI	221	2.6000	29.55
12	ITIQMRNQV	66	2.5000	28.41
13	IQMRNQVES	68	2.5000	28.41
14	YHTAGIWRR	142	2.4000	27.27
15	IALFPPYIM	200	2.2000	25.00
16	FVLPLAVTI	85	2.1000	23.86
17	VLALALFVF	131	2.1000	23.86
18	ILVALIALF	195	2.1000	23.86
19	VLPLAVTIF	86	1.9000	21.59
20	LRLFGNIFA	184	1.9000	21.59
21	VFILISNWL	95	1.6600	18.86
22	LVALIALFP	196	1.6000	18.18
23	LAFYLRAKV	42	1.5000	17.05
24	YLRKVSTST	45	1.5000	17.05
25	WAPNAIWKA	209	1.5000	17.05

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
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1	LKGHVTLA	160	4.0000	47.62
2	IVGHPIKLL	152	3.5000	41.67
3	IVIALAFYL	38	3.2000	38.10
4	IQMRNQVES	68	3.1000	36.90
5	FYLRAKVTS	44	3.0000	35.71
6	LRLFGNIFA	184	2.9000	34.52
7	VQYTDKHGH	108	2.5800	30.71
8	ITIQMRNQV	66	2.5000	29.76
9	YIMWAPNAI	206	2.5000	29.76
10	FVCYHTAGI	139	2.0000	23.81
11	YVLALALFV	130	1.8000	21.43
12	VFILISNWL	95	1.7000	20.24
13	IALFPPYIM	200	1.7000	20.24
14	LVALIALFP	196	1.6000	19.05
15	LAFYLRAKV	42	1.5000	17.86
16	IWRRGIVGH	147	1.4800	17.62
17	LRAKVSTSD	46	1.2000	14.29
18	VLALALFVF	131	1.2000	14.29
19	ILVALIALF	195	1.2000	14.29
20	LIALFPPYI	199	1.2000	14.29
21	VLPLAVTIF	86	1.0000	11.90
22	IGMRIAPFV	78	0.9000	10.71
23	MRIAPFVLP	80	0.9000	10.71
24	IKLLKGHVT	157	0.9000	10.71
25	LFFEAITIQ	61	0.8000	9.52

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	FALLTILYF	230	5.2000	59.77
2	YVLALALFV	130	4.9000	56.32
3	LVALIALFP	196	3.4000	39.08
4	FYLRAKVTS	44	3.0000	34.48
5	FVCYHTAGI	139	2.8000	32.18
6	LRLFGNIFA	184	2.8000	32.18
7	IFALLTILY	229	2.8000	32.18
8	FVGAIQAFI	221	2.6000	29.89

9	YIMWAPNAI	206	2.5000	28.74
10	INYVLALAL	128	2.4600	28.28
11	VTLLAPINL	164	2.3600	27.13
12	FFEAITIQM	62	2.3000	26.44
13	IAGLIVIAL	34	2.2600	25.98
14	LIALFPPYI	199	2.2500	25.86
15	VLPLAVTIF	86	2.2000	25.29
16	FVFILISNW	94	2.2000	25.29
17	IVIALAFYL	38	2.1600	24.83
18	FGNIFAGGI	187	2.1000	24.14
19	ILVALIALF	195	2.1000	24.14
20	LIVIALAFY	37	2.0000	22.99
21	FILISNWLA	96	2.0000	22.99
22	LKGHVTLA	160	2.0000	22.99
23	ISLSLRLFG	180	1.9000	21.84
24	WLGMTVNTD	19	1.8000	20.69
25	VLALALFVF	131	1.8000	20.69

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	IVGHPIKLL	152	4.4600	50.68
2	IVIALAFYL	38	4.1600	47.27
3	LKGHVTLA	160	4.0000	45.45
4	ITIQMRNQV	66	3.5000	39.77
5	IQMRNQVES	68	3.5000	39.77
6	FYLRAKVTS	44	3.4000	38.64
7	YIMWAPNAI	206	3.4000	38.64
8	IALFPPYIM	200	3.2000	36.36
9	VLALALFVF	131	3.1000	35.23
10	ILVALIALF	195	3.1000	35.23
11	VLPLAVTIF	86	2.9000	32.95
12	FVCYHTAGI	139	2.9000	32.95
13	LRLFGNIFA	184	2.9000	32.95
14	YVLALALFV	130	2.8000	31.82
15	VFILISNWL	95	2.6600	30.23
16	LVALIALFP	196	2.6000	29.55

17	LAFYLRAKV	42	2.5000	28.41
18	FALLTILYF	230	2.4000	27.27
19	LRAKVTSTD	46	2.3000	26.14
20	LIALFPPYI	199	2.1000	23.86
21	WKAFDLFVG	215	2.1000	23.86
22	VQYTDKHHG	108	2.0000	22.73
23	ILYFSQAME	235	2.0000	22.73
24	IGMRIAPFV	78	1.9000	21.59
25	MRIAPFVLP	80	1.9000	21.59

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	FYLRAKVTS	44	4.4000	50.00
2	YIMWAPNAI	206	4.4000	50.00
3	FVCYHTAGI	139	3.9000	44.32
4	YVLALALFV	130	3.8000	43.18
5	IVGHPIKLL	152	3.4600	39.32
6	FALLTILYF	230	3.4000	38.64
7	IVIALAFYL	38	3.1600	35.91
8	WKAFDLFVG	215	3.1000	35.23
9	LKGHVTLA	160	3.0000	34.09
10	WLGMTVNTD	19	2.7000	30.68
11	FVGAIQAFI	221	2.6000	29.55
12	ITIQMRNQV	66	2.5000	28.41
13	IQMRNQVES	68	2.5000	28.41
14	YHTAGIWRR	142	2.4000	27.27
15	IALFPPYIM	200	2.2000	25.00
16	FVLPLAVTI	85	2.1000	23.86
17	VLALALFVF	131	2.1000	23.86
18	ILVALIALF	195	2.1000	23.86
19	VLPLAVTIF	86	1.9000	21.59
20	LRLFGNIFA	184	1.9000	21.59
21	VFILISNWL	95	1.6600	18.86
22	LVALIALFP	196	1.6000	18.18
23	LAFYLRAKV	42	1.5000	17.05
24	YLRAKVTST	45	1.5000	17.05

25	WAPNAIWKA	209	1.5000	17.05
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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	IVGHPIKLL	152	4.5000	50.00
2	IVIALAFYL	38	4.2000	46.67
3	LKGHVTLA	160	4.0000	44.44
4	LRAKVTSTD	46	3.9000	43.33
5	VQYTDKHHG	108	3.8000	42.22
6	ILYFSQAME	235	3.6000	40.00
7	WLGMTVNTD	19	3.3000	36.67
8	IQMRNQVES	68	3.1000	34.44
9	FYLRAKVTS	44	3.0000	33.33
10	LRLFGNIFA	184	2.9000	32.22
11	ITIQMRNQV	66	2.8000	31.11
12	IALFPPYIM	200	2.8000	31.11
13	VFILISNWL	95	2.7000	30.00
14	IWRRGIVGH	147	2.7000	30.00
15	YIMWAPNAI	206	2.7000	30.00
16	IFVFILISN	93	2.4000	26.67
17	FVCYHTAGI	139	2.2000	24.44
18	YVLALALFV	130	2.1000	23.33
19	VLALALFVF	131	2.1000	23.33
20	ILVALIALF	195	2.1000	23.33
21	LVALIALFP	196	2.0000	22.22
22	WKAFDLFVG	215	2.0000	22.22
23	VLPLAVTIF	86	1.9000	21.11
24	LAFYLRAKV	42	1.8000	20.00
25	IKLLKGHVT	157	1.8000	20.00

ALLELE: DRB1_1305	Threshold for 3 % with score: 2.2	Highest Score achievable by any peptide: 8.7
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Rank	Sequence	At Position	Score	% of Highest Score
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1	FALLTILYF	230	5.2000	59.77
2	YVLALALFV	130	4.9000	56.32
3	LVALIALFP	196	3.4000	39.08
4	FYLRAKVTS	44	3.0000	34.48
5	FVCYHTAGI	139	2.8000	32.18
6	LRLFGNIFA	184	2.8000	32.18
7	IFALLTILY	229	2.8000	32.18
8	FVGAIQAFI	221	2.6000	29.89
9	YIMWAPNAI	206	2.5000	28.74
10	INYVLALAL	128	2.4600	28.28
11	VTLLAPINL	164	2.3600	27.13
12	FFEAITIQM	62	2.3000	26.44
13	IAGLIVIAL	34	2.2600	25.98
14	LIALFPPYI	199	2.2500	25.86
15	VLPLAVTIF	86	2.2000	25.29
16	FVFILISNW	94	2.2000	25.29
17	IVIALAFYL	38	2.1600	24.83
18	FGNIFAGGI	187	2.1000	24.14
19	ILVALIALF	195	2.1000	24.14
20	LIVIALAFY	37	2.0000	22.99
21	FILISNWLA	96	2.0000	22.99
22	LKGHVTLA	160	2.0000	22.99
23	ISLSLRLFG	180	1.9000	21.84
24	WLGMTVNTD	19	1.8000	20.69
25	VLALALFVF	131	1.8000	20.69

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	FVFILISNW	94	2.2000	32.35
2	FYLRAKVTS	44	2.1000	30.88
3	YVLALALFV	130	2.1000	30.88
4	FVCYHTAGI	139	1.9000	27.94
5	FVGAIQAFI	221	1.7000	25.00
6	FALLTILYF	230	1.5000	22.06
7	YIMWAPNAI	206	1.3000	19.12
8	FILISNWLA	96	1.2000	17.65

9	LRLFGNIFA	184	1.2000	17.65
10	FGNIFAGGI	187	1.1000	16.18
11	FVFVCYHTA	137	1.0000	14.71
12	VQYTDKHHG	108	0.8800	12.94
13	LIVIALAFY	37	0.7000	10.29
14	IVIALAFYL	38	0.7000	10.29
15	WRRGIVGHP	148	0.6000	8.82
16	LVALIALFP	196	0.6000	8.82
17	WLGMTVNTD	19	0.4000	5.88
18	IQMRNQVES	68	0.2000	2.94
19	LKGHVTLA	160	0.2000	2.94
20	ILVALIALF	195	0.2000	2.94
21	LIALFPPYI	199	0.2000	2.94
22	FDLFVGAIQ	218	-0.1000	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	LRLFGNIFA	184	3.8000	45.78
2	LVALIALFP	196	3.4000	40.96
3	LKGHVTLA	160	3.0000	36.14
4	YVLALALFV	130	2.9000	34.94
5	VQYTDKHHG	108	2.5800	31.08
6	INYVLALAL	128	2.5000	30.12
7	IFALLTILY	229	2.5000	30.12
8	VTLLAPINL	164	2.4000	28.92
9	LIALFPPYI	199	2.3500	28.31
10	IAGLIVIAL	34	2.3000	27.71
11	FALLTILYF	230	2.3000	27.71
12	IVIALAFYL	38	2.2000	26.51
13	LIVIALAFY	37	1.7000	20.48
14	IQMRNQVES	68	1.7000	20.48
15	FYLRKAVTS	44	1.6000	19.28
16	VGHPIKLLK	153	1.5000	18.07
17	ISLSLRLFG	180	1.5000	18.07
18	LPLAVTIFV	87	1.4000	16.87
19	LFPPYIMWA	202	1.4000	16.87

20	VLPLAVTIF	86	1.3000	15.66
21	IFVFILISN	93	1.3000	15.66
22	VFILISNWL	95	1.3000	15.66
23	IFAGGILVA	190	1.3000	15.66
24	LYFSQAMEL	236	1.3000	15.66
25	VEEVAKPIS	173	1.2500	15.06

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	YVLALALFV	130	4.2000	47.19
2	FALLTILYF	230	4.2000	47.19
3	WLGMTVNTD	19	3.4000	38.20
4	FVFILISNW	94	3.1000	34.83
5	VQYTDKHHG	108	2.8000	31.46
6	LRLFGNIFA	184	2.8000	31.46
7	LVALIALFP	196	2.8000	31.46
8	FYLRAKVTS	44	2.6000	29.21
9	IFALLTILY	229	2.6000	29.21
10	INYVLALAL	128	2.5000	28.09
11	VTLLAPINL	164	2.4000	26.97
12	IAGLIVIAL	34	2.3000	25.84
13	IFVFILISN	93	2.3000	25.84
14	IVIALAFYL	38	2.2000	24.72
15	ILYFSQAME	235	2.2000	24.72
16	FVCYHTAGI	139	2.1000	23.60
17	FILISNWLA	96	2.0000	22.47
18	LKGHVTLA	160	2.0000	22.47
19	FFEAITIQM	62	1.9000	21.35
20	FVGAIQAFI	221	1.9000	21.35
21	LIVIALAFY	37	1.8000	20.22
22	ISLSLRLFG	180	1.8000	20.22
23	YIMWAPNAI	206	1.8000	20.22
24	FVFVCYHTA	137	1.7000	19.10
25	WKAFDLFG	215	1.6000	17.98

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	LKGHVTLA	160	4.0000	47.62
2	IVGHPIKLL	152	3.5000	41.67
3	IVIALAFYL	38	3.2000	38.10
4	IQMRNQVES	68	3.1000	36.90
5	FYLRAKVTS	44	3.0000	35.71
6	LRLFGNIFA	184	2.9000	34.52
7	VQYTDKHGH	108	2.5800	30.71
8	ITIQMRNQV	66	2.5000	29.76
9	YIMWAPNAI	206	2.5000	29.76
10	FVCYHTAGI	139	2.0000	23.81
11	YVLALALFV	130	1.8000	21.43
12	VFILISNWL	95	1.7000	20.24
13	IALFPPYIM	200	1.7000	20.24
14	LVALIALFP	196	1.6000	19.05
15	LAFYLRKV	42	1.5000	17.86
16	IWRRGIVGH	147	1.4800	17.62
17	LRAKVSTD	46	1.2000	14.29
18	VLALALFVF	131	1.2000	14.29
19	ILVALIALF	195	1.2000	14.29
20	LIALFPPYI	199	1.2000	14.29
21	VLPLAVTIF	86	1.0000	11.90
22	IGMRIAPFV	78	0.9000	10.71
23	MRIAPFVLP	80	0.9000	10.71
24	IKLLKGHVT	157	0.9000	10.71
25	LFFEAITIQ	61	0.8000	9.52

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	FYLRAKVTS	44	4.0000	47.62
2	YIMWAPNAI	206	3.5000	41.67
3	FVCYHTAGI	139	3.0000	35.71
4	LKGHVTLA	160	3.0000	35.71

5	YVLALALFV	130	2.8000	33.33
6	IVGHPIKLL	152	2.5000	29.76
7	IVIALAFYL	38	2.2000	26.19
8	IQMRNQVES	68	2.1000	25.00
9	LRLFGNIFA	184	1.9000	22.62
10	WKAFDLFVG	215	1.7000	20.24
11	FVGAIQAFI	221	1.7000	20.24
12	WLGMTVNTD	19	1.6000	19.05
13	VQYTDKHHG	108	1.5800	18.81
14	ITIQMRNQV	66	1.5000	17.86
15	WAPNAIWKA	209	1.5000	17.86
16	FALLTILYF	230	1.5000	17.86
17	FILISNWL	96	1.3000	15.48
18	FVLPLAVTI	85	1.2000	14.29
19	FVFILISNW	94	1.1000	13.10
20	FVFVCYHTA	137	0.9000	10.71
21	YHTAGIWR	142	0.9000	10.71
22	YLRAKVTS	45	0.8000	9.52
23	VFILISNWL	95	0.7000	8.33
24	IALFPPYIM	200	0.7000	8.33
25	LVALIALFP	196	0.6000	7.14

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	IVGHPIKLL	152	4.4600	50.68
2	IVIALAFYL	38	4.1600	47.27
3	LKGHVTLA	160	4.0000	45.45
4	ITIQMRNQV	66	3.5000	39.77
5	IQMRNQVES	68	3.5000	39.77
6	FYLRAKVTS	44	3.4000	38.64
7	YIMWAPNAI	206	3.4000	38.64
8	IALFPPYIM	200	3.2000	36.36
9	VLALALFVF	131	3.1000	35.23
10	ILVALIALF	195	3.1000	35.23
11	VLPLAVTIF	86	2.9000	32.95
12	FVCYHTAGI	139	2.9000	32.95

13	LRLFGNIFA	184	2.9000	32.95
14	YVLALALFV	130	2.8000	31.82
15	VFILISNWL	95	2.6600	30.23
16	LVALIALFP	196	2.6000	29.55
17	LAFYLRAKV	42	2.5000	28.41
18	FALLTILYF	230	2.4000	27.27
19	LRAKVTSTD	46	2.3000	26.14
20	LIALFPPYI	199	2.1000	23.86
21	WKAFDLFVG	215	2.1000	23.86
22	VQYTDKHHG	108	2.0000	22.73
23	ILYFSQAME	235	2.0000	22.73
24	IGMRIAPFV	78	1.9000	21.59
25	MRIAPFVLP	80	1.9000	21.59

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	IVGHPKLL	152	4.4600	50.68
2	IVIALAFYL	38	4.1600	47.27
3	LKGHVTLA	160	4.0000	45.45
4	ITIQMRNQV	66	3.5000	39.77
5	IQMRNQVES	68	3.5000	39.77
6	FYLRAKVTS	44	3.4000	38.64
7	YIMWAPNAI	206	3.4000	38.64
8	IALFPPYIM	200	3.2000	36.36
9	VLALALFVF	131	3.1000	35.23
10	ILVALIALF	195	3.1000	35.23
11	VLPLAVTIF	86	2.9000	32.95
12	FVCYHTAGI	139	2.9000	32.95
13	LRLFGNIFA	184	2.9000	32.95
14	YVLALALFV	130	2.8000	31.82
15	VFILISNWL	95	2.6600	30.23
16	LVALIALFP	196	2.6000	29.55
17	LAFYLRAKV	42	2.5000	28.41
18	FALLTILYF	230	2.4000	27.27
19	LRAKVTSTD	46	2.3000	26.14
20	LIALFPPYI	199	2.1000	23.86

21	WKAFDLFVG	215	2.1000	23.86
22	VQYTDKHHG	108	2.0000	22.73
23	ILYFSQAME	235	2.0000	22.73
24	IGMRIAPFV	78	1.9000	21.59
25	MRIAPFVLP	80	1.9000	21.59

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	LRLFGNIFA	184	7.8000	79.59
2	VTIFVFILI	91	5.8000	59.18
3	IVIALAFYL	38	5.5000	56.12
4	LAFYLRAKV	42	4.6000	46.94
5	VFILISNWL	95	4.6000	46.94
6	YVLALALFV	130	4.3000	43.88
7	FVCYHTAGI	139	4.2600	43.47
8	LKGHVTLA	160	4.2600	43.47
9	IFVFILISN	93	4.2000	42.86
10	INYVLALAL	128	4.2000	42.86
11	LFVFVCYHT	136	4.2000	42.86
12	ILISNWLAV	97	4.0000	40.82
13	IALFPPYIM	200	3.9800	40.61
14	IQAFIFALL	225	3.8000	38.78
15	IVGHPIKLL	152	3.6500	37.24
16	LYFSQAMEL	236	3.6000	36.73
17	IKLLKGHVT	157	3.5000	35.71
18	VQLFFEAIT	59	3.4000	34.69
19	LVALIALFP	196	3.4000	34.69
20	IALAFYLRA	40	3.3000	33.67
21	VTLLAPINL	164	3.3000	33.67
22	WKAFDLFVG	215	3.3000	33.67
23	VESAIGMRI	74	3.2000	32.65
24	IAPFVLPLA	82	3.2000	32.65
25	FVFVCYHTA	137	3.1000	31.63

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	LRLFGNIFA	184	6.8000	69.39
2	YVLALALFV	130	5.3000	54.08
3	FVCYHTAGI	139	5.2600	53.67
4	VTIFVFILI	91	4.8000	48.98
5	IVIALAFYL	38	4.5000	45.92
6	WKAFDLFVG	215	4.3000	43.88
7	FVFVCYHTA	137	4.1000	41.84
8	YIMWAPNAI	206	4.1000	41.84
9	FILISNWL	96	4.0000	40.82
10	FVLPLAVTI	85	3.8000	38.78
11	LAFYLRAKV	42	3.6000	36.73
12	VFILISNWL	95	3.6000	36.73
13	LKGHVTLA	160	3.2600	33.27
14	IFVFILISN	93	3.2000	32.65
15	INYVLALAL	128	3.2000	32.65
16	LFVVCYHT	136	3.2000	32.65
17	FALLTILYF	230	3.0500	31.12
18	ILISNWLAV	97	3.0000	30.61
19	IALFPPYIM	200	2.9800	30.41
20	IQAFIFALL	225	2.8000	28.57
21	FIFALLTIL	228	2.8000	28.57
22	IVGHPIKLL	152	2.6500	27.04
23	LYFSQAMEL	236	2.6000	26.53
24	IKLLKGHVT	157	2.5000	25.51
25	FVFILISNW	94	2.4500	25.00

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	LRLFGNIFA	184	7.8000	79.59
2	VTIFVFILI	91	5.8000	59.18
3	IVIALAFYL	38	5.5000	56.12
4	LAFYLRAKV	42	4.6000	46.94

5	VFILISNWL	95	4.6000	46.94
6	YVLALALFV	130	4.3000	43.88
7	FVCYHTAGI	139	4.2600	43.47
8	LKGHVTLA	160	4.2600	43.47
9	IFVFILISN	93	4.2000	42.86
10	INYVLALAL	128	4.2000	42.86
11	LFVFCYHT	136	4.2000	42.86
12	ILISNWLAV	97	4.0000	40.82
13	IALFPPYIM	200	3.9800	40.61
14	IQAFIFALL	225	3.8000	38.78
15	IVGHPIKLL	152	3.6500	37.24
16	LYFSQAMEL	236	3.6000	36.73
17	IKLLKGHVT	157	3.5000	35.71
18	VQLFFEAIT	59	3.4000	34.69
19	LVALIALFP	196	3.4000	34.69
20	IALAFYLRA	40	3.3000	33.67
21	VTLLAPINL	164	3.3000	33.67
22	WKAFDLFVG	215	3.3000	33.67
23	VESAIGMRI	74	3.2000	32.65
24	IAPFVLPLA	82	3.2000	32.65
25	FVFCYHTA	137	3.1000	31.63

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	IVIALAFYL	38	5.4000	55.10
2	FVFCYHTA	137	4.2000	42.86
3	FGNIFAGGI	187	4.1000	41.84
4	INYVLALAL	128	3.6000	36.73
5	YVLALALFV	130	3.5000	35.71
6	VGAIQAFIF	222	3.5000	35.71
7	VLPVQYTDK	105	3.4000	34.69
8	WLAVLPVQY	102	3.3000	33.67
9	VTLLAPINL	164	3.3000	33.67
10	FEAITIQMR	63	3.2000	32.65
11	VFILISNWL	95	3.2000	32.65
12	YIMWAPNAI	206	3.0000	30.61

13	VIALAFYLR	39	2.7000	27.55
14	FVLPLAVTI	85	2.5000	25.51
15	FILISNWLA	96	2.5000	25.51
16	FIFALLTIL	228	2.5000	25.51
17	LLTILYFSQ	232	2.5000	25.51
18	IKLLKGHVT	157	2.4000	24.49
19	VLALALFVF	131	2.3000	23.47
20	YHTAGIWRR	142	2.3000	23.47
21	INLVEEVAK	170	2.3000	23.47
22	LIVIALAFY	37	2.2000	22.45
23	FVGAIQAFI	221	2.1000	21.43
24	IFALLTILY	229	2.1000	21.43
25	VQYTDKHHG	108	2.0000	20.41

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	IVIALAFYL	38	5.4000	55.10
2	FVFVCYHTA	137	4.2000	42.86
3	FGNIFAGGI	187	4.1000	41.84
4	INYVLALAL	128	3.6000	36.73
5	YVLALALFV	130	3.5000	35.71
6	VGAIQAFIF	222	3.5000	35.71
7	VLPVQYTDK	105	3.4000	34.69
8	WLAVLPVQY	102	3.3000	33.67
9	VTLLAPINL	164	3.3000	33.67
10	FEAITIQMR	63	3.2000	32.65
11	VFILISNWL	95	3.2000	32.65
12	YIMWAPNAI	206	3.0000	30.61
13	VIALAFYLR	39	2.7000	27.55
14	FVLPLAVTI	85	2.5000	25.51
15	FILISNWLA	96	2.5000	25.51
16	FIFALLTIL	228	2.5000	25.51
17	LLTILYFSQ	232	2.5000	25.51
18	IKLLKGHVT	157	2.4000	24.49
19	VLALALFVF	131	2.3000	23.47
20	YHTAGIWRR	142	2.3000	23.47

21	INLVEEVAK	170	2.3000	23.47
22	LIVIALAFY	37	2.2000	22.45
23	FVGAIQAFI	221	2.1000	21.43
24	IFALLTILY	229	2.1000	21.43
25	VQYTDKHH	108	2.0000	20.41