

MHC Class-II Binding Peptide Prediction Results

[HELP](#)
[HOME](#)
[MHC & Prediction Algorithm](#)

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Jan 27 11:35:15 2010
Length of input sequence	144 amino acids
Number of nanomers from input sequence	136
Number of nanomers with obligatory P1 anchor residue	41
Threshold setting	3
Number of alleles in query	3
Number of top scorers to be displayed	14

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	FVRTVSLPV	97	1.8000	30.00
2	LFAAFPSFA	20	-0.6000	0
3	FAGLRPTFD	27	-0.9100	0
4	FAAFPSFAG	21	-1.0200	0
5	YGSFVRTVS	94	-1.2300	0
6	FPSFAGLRP	24	-1.3200	0
7	MVRDGQLTI	68	-1.4000	0
8	ILTVSVAVS	120	-1.4500	0
9	FAYGSFVRT	92	-1.5000	0
10	VRTVSLPVG	98	-1.5800	0
11	LRPTFDTRL	30	-1.6100	0
12	FSELF AAFP	17	-1.7000	0
13	IMVRDGQLT	67	-1.8000	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6
----------------------	--------------------------------------	---

Rank	Sequence	At Position	Score	% of Highest Score
1	FVRTVSLPV	97	1.8000	30.00
2	LFAAFPSFA	20	0.4000	6.67
3	MVRDGQLTI	68	-0.4000	0
4	ILTVSVAVS	120	-0.4500	0
5	VRTVSLPVG	98	-0.5800	0
6	LRPTFDTRL	30	-0.6100	0
7	IMVRDGQLT	67	-0.8000	0
8	LFPEFSELF	13	-0.9000	0
9	VAVSEGKPT	125	-0.9000	0
10	FAGLRPTFD	27	-0.9100	0
11	FAAFPSFAG	21	-1.0200	0
12	VQRHPRSLF	6	-1.2000	0
13	FPSFAGLRP	24	-1.3200	0

ALLELE: DRB1_0301	Threshold for 3 % with score: 2.96	Highest Score achievable by any peptide: 9.5
----------------------	---------------------------------------	---

Rank	Sequence	At Position	Score	% of Highest Score
1	MVRDGQLTI	68	5.6000	58.95
2	VQRHPRSLF	6	3.8700	40.74
3	VRTVSLPVG	98	3.5000	36.84
4	ILTVSVAVS	120	3.3000	34.74
5	LPVQRHPRS	4	1.7000	17.89
6	MRLEDEMKE	39	1.6000	16.84
7	LFAAFPSFA	20	1.3700	14.42
8	VRDGQLTIK	69	1.3000	13.68
9	VRAELPGVD	52	1.2000	12.63
10	FVRTVSLPV	97	1.2000	12.63
11	LTVSVAVSE	121	1.1000	11.58
12	LFPEFSELF	13	0.7000	7.37
13	YGSFVRTVS	94	0.7000	7.37
14	IKAERTEQK	76	0.5000	5.26