

Prediction of MHC Class II binding peptides incorporating bayesian transfer hierarchies

Ravikiran Janardhana
Department of Computer Science
University of North Carolina at Chapel Hill
Email: ravikirn@cs.unc.edu

Abstract—T-cells are key players in regulating a specific immune response. Activation of cytotoxic T-cells requires recognition of specific peptides bound to Major Histocompatibility Complex (MHC) class II molecules. MHC-peptide complexes are potential tools for diagnosis and treatment of pathogens and cancer, as well as for the development of peptide vaccines. Only one in 100 to 200 potential binders actually binds to a certain MHC molecule, therefore a good prediction method for MHC class II binding peptides can reduce the number of candidate binders that need to be synthesized and tested for successful design of peptide and protein based vaccines.

I. INTRODUCTION

This demo file is intended to serve as a “starter file” for IEEE conference papers produced under \LaTeX using IEEE-tran.cls version 1.7 and later. I wish you the best of success.

mds

January 11, 2007

A. Subsection Heading Here

Subsection text here.

1) Subsubsection Heading Here: Subsubsection text here.

II. CONCLUSION

The conclusion goes here.

ACKNOWLEDGMENT

The authors would like to thank...

REFERENCES

- [1] H. Kopka and P. W. Daly, *A Guide to \LaTeX* , 3rd ed. Harlow, England: Addison-Wesley, 1999.