

## EPSVR and EPMeta: Prediction of discontinuous B-cell epitopes using support vector regression and multiple server results

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Accurate prediction of antigenic epitopes is important for immunologic research and medical applications, but it is still an open problem in bioinformatics. The case for discontinuous epitopes is even worse – currently there are only a few discontinuous epitope prediction servers available, though discontinuous peptides constitute the majority of all B-cell antigenic epitopes. The small number of structures for antigen-antibody complexes limits the development of reliable discontinuous epitope prediction methods and an unbiased benchmark to evaluate developed methods. In this work, we present two novel server applications for discontinuous epitope prediction: EPSVR and EPMeta. EPSVR uses a Support Vector Regression (SVR) method to integrate six scoring terms. Furthermore, we combined EPSVR with five existing epitope prediction servers to construct EPMeta. All methods were benchmarked by our curated independent test set, in which all antigens had no complex structures with the antibody, and their epitopes were identified by various biochemical experiments. The AUCs of EPSVR and EPMeta are 0.597 and 0.638, respectively, which are higher than that of any other existing single server.

### Biography

Chi Zhang obtained his Ph.D. in 2002, from University of Kentucky and had been postdoctoral fellow in the State University of New York at Buffalo from 2002 to 2007. Now, he is an Assistant Professor in School of Biological Sciences, University of Nebraska, Lincoln, NE. He has published more than 30 papers in peer-reviewed journals.

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