

Documents

- 1) Murzenko, O., Olszewski, S., Boskin, O., Lurie, I., Savina, N., Voronenko, M., Lytvynenko, V.
Application of a combined approach for predicting a peptide-protein binding affinity using methods with advance reduction of features
(2019) *Proceedings of the 2019 10th IEEE International Conference on Intelligent Data Acquisition and Computing Systems: Technology and Applications, IDAACS 2019*, 1, art. no. 8924244, pp. 43-47.
- 2) Lurie, I., Lytvynenko, V., Osypenko, V., Voronenko, M.
The use of inductive methods for determination of the binding affinity of interacting biomolecules
(2018) *International Scientific and Technical Conference on Computer Sciences and Informatics*, 1, art. no. 8526753, pp. 483-487.
- 3) Kar, P., Ruiz-Perez, L., Arooj, M., Mancera, R.L.
Current methods for the prediction of T-cell epitopes
(2018) *Peptide Science*, 110 (2), art. no. e24046, .
- 4) Davies, M.N., Flower, D.R.
Computational epitope mapping
(2010) *Infectious Disease Informatics*, pp. 187-202.
- 5) Bordner, A.J.
Towards universal structure-based prediction of class II MHC epitopes for diverse allotypes
(2010) *PLoS ONE*, 5 (12), art. no. e14383, .
- 6) Bordner, A.J., Mittelman, H.D.
MultiRTA: A simple yet reliable method for predicting peptide binding affinities for multiple MHC alleles
(2010) *BMC Bioinformatics*, 11, art. no. 482, .

7) Bordner, A.J., Mittelman, H.D.

Prediction of the binding affinities of peptides to class II MHC using a regularized the
(2010) *BMC Bioinformatics*, 11, art. no. 41, .

8) Ivanciuc, O.

**Machine learning quantitative structure-activity relationships (QSAR) for peptides bind
amphiphysin-1 SH3 domain**
(2009) *Current Proteomics*, 6 (4), pp. 289-302.

9) Tian, F., Yang, L., Lv, F., Yang, Q., Zhou, P.

**In silico quantitative prediction of peptides binding affinity to human MHC molecule: A
structure-activity relationship approach**
(2009) *Amino Acids*, 36 (3), pp. 535-554.

10) Wiwanitkit, V.

**Predicted epitopes of malarial merozoite surface protein 1 by bioinformatics method:
development**
(2009) *Journal of Microbiology, Immunology and Infection*, 42 (1), pp. 19-21.

11) Mizutori, Y., Nagayama, Y., Flower, D., Misharin, A., Aliesky, H.A., Rapoport, B., McLachlan,

**Role of the transgenic human thyrotropin receptor A-subunit in thyroiditis induced by
regulatory T cell depletion**
(2008) *Clinical and Experimental Immunology*, 154 (3), pp. 305-315.

12) Zhou, P., Tian, F., Wu, Y., Li, Z., Shang, Z.

**Quantitative sequence-activity model (QSAM): Applying QSAR strategy to model and
function of peptides, proteins and nucleic acids**
(2008) *Current Computer-Aided Drug Design*, 4 (4), pp. 311-321.

13) Karpenko, O., Huang, L., Dai, Y.

A probabilistic meta-predictor for the MHC class II binding peptides
(2008) *Immunogenetics*, 60 (1), pp. 25-36.

14) Ivanciuc, O., Braun, W.

Robust quantitative modeling of peptide binding affinities for MHC molecules using p
(2007) *Protein and Peptide Letters*, 14 (9), pp. 903-916.

15) Lu, Y., Bulka, B., DesJardins, M., Freeland, S.J.

Amino acid quantitative structure property relationship database: A web-based platfo
investigations of amino acids
(2007) *Protein Engineering, Design and Selection*, 20 (7), pp. 347-351.

16) Holm, L., Frech, K., Dzhambazov, B., Holmdahl, R., Kihlberg, J., Linusson, A.

Quantitative structure-activity relationship of peptides binding to the class II major hi
molecule Aq associated with autoimmune arthritis
(2007) *Journal of Medicinal Chemistry*, 50 (9), pp. 2049-2059.

17) Salomon, J., Flower, D.R.

Predicting Class II MHC-Peptide binding: A kernel based approach using similarity sc
(2006) *BMC Bioinformatics*, 7, art. no. 501, .