Systematic investigation of protein-protein docking servers for auxin response related proteins

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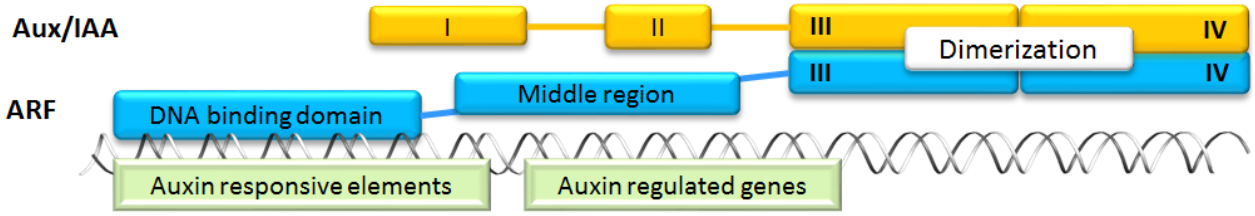
The control of plant growth and development is strongly regulated by and correlated to the response of the plant hormone auxin. In the hierarchical control of gene expression two plant protein families, Aux/IAAs (Auxin/Indol-3-Acetic Acid binding proteins) and ARFs (Auxin Response Factors), play an important role as transcription factors. The protein structures of both families consist of four domains, which contain a structurally similar protein-protein-interaction domain III/IV [1].



For these dimer domains there are no X-ray structures available. Therefore, insights into the most likely dimer arrangements should be derived from *in silico* homo- and heterodimerization (protein-protein docking) studies.

As a prerequisite for more detailed studies on the auxin related proteins, the most appropriate docking server programs should be identified. For this purpose two already known related heterodimer structures were used as test systems. The $p40^{phox}$-$p67^{phox}$-PB1 complex (PDB code: 1OEY [2]) and PKCι/λ-Par6α-PB1 complex (PDB code: 1WMH [3]) were split into monomers and used for protein-protein docking studies. ClusPro [4], GrammX [5], Hex [6], and ZDock [7] were tested with different parameters. All obtained dimer models were ranked and compared with interaction energies based on subsequent force field energy optimizations using Amber12:EHT. Finally, the RMSD (Cα) values between the dimer models and the X-ray structures were calculated.

As a result of these studies, Hex appeared as the most promising one. However, dimer arrangements with most negative interaction energies neither do correlate with those of the experimental structures nor with the best results from the server programs.

[1] S. Abel, *ACS Chem. Biol.*, **2007**, *2*, 380-384.
[2] M. I. Wilson, D. J. Gill, O. Perisic, M. T. Quinn, R. L. Williams, *Mol. Cell*, **2003**, *12*, 39-50.
[3] Y. Hirano, S. Yoshinaga, R. Takeya, N. N. Suzuki, M. Horiuchi, M. Kohjima, H. Sumimoto, F. Inagaki, *J. Biol. Chem.*, **2005**, *280*, 9653-9661.
[4] ClusPro version 2.0, http://cluspro.bu.edu, accessed 2013-07-25.
[5] GrammX version 1.2.0, http://vakser.bioinformatics.ku.edu/resources/gramm/grammx/, accessed 2013-07-25.
[6] Hex version 8.0.0, http://hexserver.loria.fr, accessed 2013-12-02.
[7] ZDock version 3.0.2/2.3.2, http://zdock.umassmed.edu, accessed 2013-07-26.