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Keywords

protein – peptide – mutant – gatekeeper – aggregation – amyloid – chaperone – prediction – docking – algorithm – proteome – genome – structure – toxicity – database -p53 – Alzheimer - Sod1 - ApoE

Science:

Joost is a group leader at the Flanders Institute for Biotechnology (VIB) at the Catholic University of Leuven, (Belgium) where he conducts research on mechanisms of protein misfolding and aggregation. The research of the Switch Lab endeavors to advance biological science via a combined approach of computational modeling and biophysical and cell biological experimentation. Model systems are selected from disease cases, with a focus on neurodegeneration and cancer.

Selected publications:

Siekierska, A., De Baets, G., Reumers, J., Gallardo, R., Rudyak, S., Broersen, K., Couceiro, J., Van Durme, J., **Schymkowitz, J.** & Rousseau, F. (2012). alpha-Galactosidase aggregation is a determinant of pharmacological chaperone efficacy on Fabry disease mutants. *J Biol Chem* 287, 28386-97.

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Maurer-Stroh, S., Debulpaep, M., Kuemmerer, N., de la Paz, M. L., Martins, I. C., Reumers, J., Morris, K. L., Copland, A., Serpell, L., Serrano, L., **Schymkowitz, J. W.** & Rousseau, F. (2010). Exploring the sequence determinants of amyloid structure using position-specific scoring matrices. *Nat Methods* 7, 237-42.

Kuperstein, I., Broersen, K., Benilova, I., Rozenski, J., Jonckheere, W., Debulpaep, M., Vandersteen, A., Segers-Nolten, I., Van Der Werf, K., Subramaniam, V., Braeken, D.,

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Fernandez-Escamilla, A. M., Rousseau, F., **Schymkowitz, J.** & Serrano, L. (2004). Prediction of sequence-dependent and mutational effects on the aggregation of peptides and proteins. *Nat Biotechnol* 22, 1302-6.

[All publications](#)