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### Keywords

Protein – peptide – aggregation – chaperone – prediction – proteome – genome – structure  
– toxicity – database

### Science

Accurate prediction of molecular chaperone binding sites is an essential prerequisite to understand the precise function of chaperones and the properties of its substrate proteins. We use an integrated method of experimental data and homology protein modeling to unravel the substrate-binding residue preferences of molecular chaperones.

### Selected publications

Almeida-Souza, L., Goethals, S., de Winter, V., Dierick, I., Gallardo, R., **Van Durme, J.**, Irobi, J., Gettemans, J., Rousseau, F., Schymkowitz, J., Timmerman, V. & Janssens, S. (2010). Increased monomerization of mutant HSPB1 leads to protein hyperactivity in Charcot-Marie-Tooth neuropathy. *J Biol Chem*.

**Van Durme, J.**, Maurer-Stroh, S., Gallardo, R., Wilkinson, H., Rousseau, F. & Schymkowitz, J. (2009). Accurate Prediction of DnaK-Peptide Binding via Homology Modelling and Experimental Data. *Plos Computational Biology* 5.

Van Damme, P., Maurer-Stroh, S., Plasman, K., **Van Durme, J.**, Colaert, N., Timmerman, E., De Bock, P. J., Goethals, M., Rousseau, F., Schymkowitz, J., Vandekerckhove, J. & Gevaert, K. (2009). Analysis of protein processing by N-terminal proteomics reveals novel species-specific substrate determinants of granzyme B orthologs. *Mol Cell Proteomics* 8, 258-72.

Spaepen, S., **Van Durme, J.**, Das, F., Maurer-Stroh, S., Rousseau, F., Schymkowitz, J. & Vanderleyden, J. (2009). Brominated phenols as auxin-like molecules. *European Journal of Soil Biology* 45, 81-87.

Demon, D., Van Damme, P., Vanden Berghe, T., Deceuninck, A., **Van Durme, J.**, Verspurten, J., Helsens, K., Impens, F., Wejda, M., Schymkowitz, J., Rousseau, F., Madder, A., Vandekerckhove, J., Declercq, W., Gevaert, K. & Vandenabeele, P. (2009). Proteome-wide substrate analysis indicates substrate exclusion as a mechanism to generate caspase-7 versus caspase-3 specificity. *Mol Cell Proteomics*.

Saverwyns, H., Visser, A., **Van Durme, J.**, Power, D., Morgado, I., Kennedy, M. W., Knox, D. P., Schymkowitz, J., Rousseau, F., Gevaert, K., Vercruysse, J., Claerebout, E. & Geldhof,

P. (2008). Analysis of the transthyretin-like (TTL) gene family in *Ostertagia ostertagi* - Comparison with other strongylid nematodes and *Caenorhabditis elegans*. *Int J Parasitol*.

Reumers, J., Conde, L., Medina, I., Maurer-Stroh, S., **Van Durme, J.**, Dopazo, J., Rousseau, F. & Schymkowitz, J. (2008). Joint annotation of coding and non-coding single nucleotide polymorphisms and mutations in the SNPeffect and PupaSuite databases. *Nucleic Acids Res* 36, D825-9.

Meyvis, Y., Callewaert, N., Gevaert, K., Timmerman, E., **Van Durme, J.**, Schymkowitz, J., Rousseau, F., Vercruyse, J., Claerebout, E. & Geldhof, P. (2008). Hybrid N-glycans on the host protective activation-associated secreted proteins of *Ostertagia ostertagi* and their importance in immunogenicity. *Mol Biochem Parasitol* 161, 67-71.