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Forskning

I min forskning intresserar jag mig främst för proteiners dynamiska och strukturella egenskaper samt växelverkan med mindre molekyler, så som läkemedelsmolekyler och lösningsmedel.
Mina artiklar handlar exempelvis om förståelse av grundläggande principer för allosterisk bindning, enzymkatalys och bildning av sällsynta högenergetiska proteintillstånd som är viktiga för funktion.
Det främsta redskapet inom den forskningsgrupp jag tillhör är kärnmagnetisk resonans (NMR) och kemiska institutionen har idag ett laboratorium med utrustning av enastående hög kvalitet.

Kvalifikationer

Fysikalisk kemi, Filosofie doktor, Water and Protein Solutions Studied by Field-Dependent Magnetic Relaxation, Lunds Tekniska Högskola
1998 jan. 1 → 2003 okt. 23
Tilldelningsdatum: 2003 okt. 23

Fysikalisk kemi, Filosofie magisterexamen, A Nuclear Magnetic Relaxation Dispersion Study of Oxytocin Hydration, Naturvetenskapliga fakulteten
1993 aug. 30 → 1998 sep. 3
Tilldelningsdatum: 1998 sep. 3

2010 → … Excellent Teaching Practitioner, ETP

Anställning

Universitetslektor
Biofysikalisk kemi
Lunds universitet
Lund, Sverige
2010 nov. 1 → present

Vicerektor LTH
Lunds Tekniska Högskola
Lunds universitet
Lund, Sverige
2020 dec. 17 → present

Vikarierande lektor
Lund university: Department of Chemistry
Lund, Sverige
2007 jan. 7 → 2010 okt. 31

Vikarierande gymnasielärare i programmering
Polhemskolan, Lund
Lund, Sverige
2006 aug. 11 → 2007 jan. 12

Postdoc
University of Copenhagen
Copenhagen, Danmark
2003 nov. 1 → 2006 aug. 15

Forskningsoutput

Proton Transfer Kinetics in Histidine Side Chains Determined by pH-Dependent Multi-Nuclear NMR Relaxation
Raum, H. N., Modig, K., Akke, M. & Weininger, U., 2024 aug., I: Journal of the American Chemical Society. 146, 32, s. 22284-22294 11 s.

Ligand-induced protein transition state stabilization switches the binding pathway from conformational selection to induced fit
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Transition-State Compressibility and Activation Volume of Transient Protein Conformational Fluctuations
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Rotamer jumps, proton exchange, and amine inversion dynamics of dimethylated lysine residues in proteins resolved by ph-dependent ^{1}h and ^{13}c nmr relaxation dispersion
Weininger, U., Modig, K., Ishida, H., Vogel, H. J. & Akke, M., 2019 nov. 21, I: Journal of Physical Chemistry B. 123, 46, s. 9742−9750 9 s.

Dynamics of Aromatic Side Chains in the Active Site of FKBP12
Weininger, U., Modig, K., Geitner, A. J., Schmidpeter, P. A. M., Koch, J. R. & Akke, M., 2017 jan. 10, I: Biochemistry. 56, 1 , s. 334-343 10 s.

Molecular insights into substrate recognition and catalytic mechanism of the chaperone and FKBP peptidyl-prolyl isomerase SlyD
Quistgaard, E. M., Weininger, U., Ural-Blimke, Y., Modig, K., Nordlund, P., Akke, M. & Löw, C., 2016 sep. 23, I: BMC Biology. 14, 1, 82.

Off-resonance rotating-frame relaxation dispersion experiment for (13)C in aromatic side chains using L-optimized TROSY-selection.
Weininger, U., Brath, U., Modig, K., Teilum, K. & Akke, M., 2014, I: Journal of Biomolecular NMR. 59, 1, s. 23-29

Ring Flips Revisited: C-13 Relaxation Dispersion Measurements of Aromatic Side Chain Dynamics and Activation Barriers in Basic Pancreatic Trypsin Inhibitor
Weininger, U., Modig, K. & Akke, M., 2014, I: Biochemistry. 53, 28, s. 4519-4525

High water mobility on the ice-binding surface of a hyperactive antifreeze protein.
Modig, K., Qvist, J., Marshall, C. B., Davies, P. L. & Halle, B., 2010, I: Physical chemistry chemical physics : PCCP. 12, Online 29th July 2010, s. 10189-10197

Protein Flexibility and Conformational Entropy in Ligand Design Targeting the Carbohydrate Recognition Domain of Galectin-3.
Diehl, C., Engström, O., Delaine, T., Håkansson, M., Genheden, S., Modig, K., Leffler, H., Ryde, U., Nilsson, U. & Akke, M., 2010, I: Journal of the American Chemical Society. 132, s. 14577-14589

Structure and Dynamics of Ribosomal Protein L12: An Ensemble Model Based on SAXS and NMR Relaxation
Bernado, P., Modig, K., Grela, P., Svergun, D. I., Tchorzewski, M., Pons, M. & Akke, M., 2010, I: Biophysical Journal. 98, 10, s. 2374-2382

Conformational entropy changes upon lactose binding to the carbohydrate recognition domain of galectin-3.
Diehl, C., Genheden, S., Modig, K., Ryde, U. & Akke, M., 2009, I: Journal of Biomolecular NMR. 45, 1-2, s. 157-169

Kursutvärderingssystemet CEQ vid LTH: uppfylls avsedda syften?
Björnsson, L., Dahlbom, M., Modig, K. & Sjöberg, A., 2009, *Proceedings 2:a Utvecklingskonferensen för Sveriges ingenjörsutbildningar.* LTH

Students' micro cultures determine the quality of teaching!
Roxå, T. & Modig, K., 2009.

Model-independent interpretation of NMR relaxation data for unfolded proteins: the acid-denatured state of ACBP
Modig, K. & Poulsen, F. M., 2008, I: Journal of Biomolecular NMR. 42, 3, s. 163-177

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Halle, B., Denisov, V., Modig, K. & Davidovic, M., 2005, *Protein Folding Handbook.* Buchner, J. & Kiefhaber, T. (red.). John Wiley & Sons Inc., s. 201-246

Dynamics of protein and peptide hydration
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Temperature-dependent hydrogen-bond geometry in liquid water.
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Kumar, S., Modig, K. & Halle, B., 2003, I: Biochemistry. 42, 46, s. 13708-13716

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Modig, K., 2003, Biophysical Chemistry (LTH), Lund University. 248 s.

Water and urea interactions with the native and unfolded forms of a beta-barrel protein.
Modig, K., Kurian, E., Prendergast, F. G. & Halle, B., 2003, I: Protein Science. 12, 12, s. 2768-2781

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Modig, K., Rademacher, M., Lücke, C. & Halle, B., 2003, I: Journal of Molecular Biology. 332, 4, s. 965-977

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Modig, K. & Halle, B., 2002, I: Journal of the American Chemical Society. 124, 40, s. 12031-12041