

# Mats Wikström

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6215207/publications.pdf>

Version: 2024-02-01

37  
papers

1,456  
citations

331670

21  
h-index

345221

36  
g-index

37  
all docs

37  
docs citations

37  
times ranked

1731  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNF111/Arkadia is a SUMO-targeted ubiquitin ligase that facilitates the DNA damage response. <i>Journal of Cell Biology</i> , 2013, 201, 797-807.	5.2	129
2	Crystal Structure and Biological Implications of a Bacterial Albumin Binding Module in Complex with Human Serum Albumin. <i>Journal of Biological Chemistry</i> , 2004, 279, 42924-42928.	3.4	111
3	DNA damage-induced inducible SUMOylation of HERC2 promotes RNF8 binding via a novel SUMO-binding Zinc finger. <i>Journal of Cell Biology</i> , 2012, 197, 179-187.	5.2	109
4	Structure, Specificity, and Mode of Interaction for Bacterial Albumin-binding Modules. <i>Journal of Biological Chemistry</i> , 2002, 277, 8114-8120.	3.4	83
5	Solution structure of the albumin-binding GA module: a versatile bacterial protein domain. <i>Journal of Molecular Biology</i> , 1997, 266, 859-865.	4.2	78
6	Solution Structure of the DNA Binding Domain of the Human Forkhead Transcription Factor AFX (FOXO4). <i>Biochemistry</i> , 2001, 40, 5861-5869.	2.5	73
7	Structure-based screening and design in drug discovery. <i>Drug Discovery Today</i> , 2002, 7, 471-478.	6.4	72
8	Enabling adoption of 2D-NMR for the higher order structure assessment of monoclonal antibody therapeutics. <i>MAbs</i> , 2019, 11, 94-105.	5.2	67
9	The solution structure of a fungal AREA protein-DNA complex: an alternative binding mode for the basic carboxyl tail of GATA factors 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 277, 605-620.	4.2	66
10	Site-Selective Screening by NMR Spectroscopy with Labeled Amino Acid Pairs. <i>Journal of the American Chemical Society</i> , 2002, 124, 2446-2447.	13.7	65
11	Mapping of the Immunoglobulin Light Chain-binding Site of Protein L. <i>Journal of Molecular Biology</i> , 1995, 250, 128-133.	4.2	58
12	Solution structure and dynamics of the DNA-binding domain of the adipocyte-transcription factor FREAC-11 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 296, 351-359.	4.2	53
13	Structure-Based Screening As Applied to Human FABP4: A Highly Efficient Alternative to HTS for Hit Generation. <i>Journal of the American Chemical Society</i> , 2002, 124, 11874-11880.	13.7	52
14	The solution structure of the Leu22 → Val mutant AREA DNA binding domain complexed with a TGATAG core element defines a role for hydrophobic packing in the determination of specificity 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 277, 621-634.	4.2	40
15	Molecular Characterization of a Saline-Soluble Lectin from a Parasitic Fungus. Extensive Sequence Similarities Between Fungal Lectins. <i>FEBS Journal</i> , 1996, 238, 822-829.	0.2	39
16	The cis/trans interconversion of the calcium regulating hormone calcitonin is catalyzed by cyclophilin. <i>FEBS Letters</i> , 1993, 323, 198-202.	2.8	38
17	A quantitative Streptococcus pyogenes-human protein-protein interaction map reveals localization of opsonizing antibodies. <i>Nature Communications</i> , 2019, 10, 2727.	12.8	36
18	NMR analysis of the interaction between protein L and Ig light chains. <i>Journal of Molecular Biology</i> , 1997, 270, 8-13.	4.2	34

#	ARTICLE	IF	CITATIONS
19	Nano differential scanning fluorimetry for comparability studies of therapeutic proteins. <i>Analytical Biochemistry</i> , 2020, 593, 113581.	2.4	34
20	A Comparison Between Emerging and Current Biophysical Methods for the Assessment of Higher-Order Structure of Biopharmaceuticals. <i>Journal of Pharmaceutical Sciences</i> , 2020, 109, 247-253.	3.3	27
21	The GA module, a mobile albumin-binding bacterial domain, adopts a three-helix-bundle structure. <i>FEBS Letters</i> , 1995, 374, 257-261.	2.8	24
22	Structural Analysis of a Complex between Small Ubiquitin-like Modifier 1 (SUMO1) and the ZZ Domain of CREB-binding Protein (CBP/p300) Reveals a New Interaction Surface on SUMO. <i>Journal of Biological Chemistry</i> , 2016, 291, 12658-12672.	3.4	23
23	Differences in backbone dynamics of two homologous bacterial albumin-binding modules: implications for binding specificity and bacterial adaptation. <i>Journal of Molecular Biology</i> , 2002, 316, 1083-1099.	4.2	16
24	Backbone Dynamics of a Domain of Protein L Which Binds to Immunoglobulin Light Chains. <i>FEBS Journal</i> , 1996, 235, 543-548.	0.2	14
25	Analytical and functional similarity of biosimilar ABP 798 with rituximab reference product. <i>Biologicals</i> , 2020, 68, 79-91.	1.4	14
26	Analytical and Functional Similarity Assessment of ABP 710, a Biosimilar to Infliximab Reference Product. <i>Pharmaceutical Research</i> , 2020, 37, 114.	3.5	13
27	Comparative Analysis of One-Dimensional Protein Fingerprint by Line Shape Enhancement and Two-Dimensional <sup>1</sup> H, <sup>13</sup> C Methyl NMR Methods for Characterization of the Higher Order Structure of IgG1 Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2020, 92, 6366-6373.	6.5	12
28	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments of the DNA binding domain of the human forkhead transcription factor AFX. <i>Journal of Biomolecular NMR</i> , 2000, 17, 181-182.	2.8	11
29	Principal Component Analysis of 1D <sup>1</sup> H Diffusion Edited NMR Spectra of Protein Therapeutics. <i>Journal of Pharmaceutical Sciences</i> , 2021, 110, 3385-3394.	3.3	11
30	Use of the 2D <sup>1</sup> H- <sup>13</sup> C HSQC NMR Methyl Region to Evaluate the Higher Order Structural Integrity of Biopharmaceuticals. <i>Molecules</i> , 2021, 26, 2714.	3.8	10
31	A Mass Spectrometric Characterization of Light-Induced Modifications in Therapeutic Proteins. <i>Journal of Pharmaceutical Sciences</i> , 2022, 111, 1556-1564.	3.3	10
32	In Situ Quantification of Polysorbate in Pharmaceutical Samples of Therapeutic Proteins by Hydrodynamic Profiling by NMR Spectroscopy. <i>Analytical Chemistry</i> , 2019, 91, 7807-7811.	6.5	9
33	Advancing secondary structure characterization of monoclonal antibodies using Microfluidic Modulation Spectroscopy. <i>Analytical Biochemistry</i> , 2022, 646, 114629.	2.4	9
34	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 18175-18188.	3.4	6
35	Analytical Similarity Assessment of ABP 959 in Comparison with Eculizumab Reference Product. <i>BioDrugs</i> , 2021, 35, 563-577.	4.6	6
36	Determination of the experimental extinction coefficient of therapeutic proteins using the Edelhoch method. <i>Biologicals</i> , 2021, 71, 42-47.	1.4	4

#	ARTICLE	IF	CITATIONS
37	Structure and Interactions of a Dimeric Variant of sHIP, a Novel Virulence Determinant of <i>Streptococcus pyogenes</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 95.	3.5	0