

Torleif HÃ¸rd

List of Publications by Year in descending order

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97
papers

5,047
citations

94269

37
h-index

95083

68
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140
all docs

140
docs citations

140
times ranked

6075
citing authors

#	ARTICLE	IF	CITATIONS
1	Enhanced detection of ATTR amyloid using a nanofibril-based assay. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2021, 28, 158-167.	1.4	4
2	Coupled chemistry kinetics demonstrate the utility of functionalized Sup35 amyloid nanofibrils in biocatalytic cascades. <i>Journal of Biological Chemistry</i> , 2019, 294, 14966-14977.	1.6	4
3	Affibody-Mediated Sequestration of Amyloid β Demonstrates Preventive Efficacy in a Transgenic Alzheimer's Disease Mouse Model. <i>Frontiers in Aging Neuroscience</i> , 2019, 11, 64.	1.7	16
4	Protofibrillar and Fibrillar Amyloid- β Binding Proteins in Cerebrospinal Fluid. <i>Journal of Alzheimer's Disease</i> , 2018, 66, 1053-1064.	1.2	7
5	The kinetics of TEM1 antibiotic degrading enzymes that are displayed on Ure2 protein nanofibrils in a flow reactor. <i>PLoS ONE</i> , 2018, 13, e0196250.	1.1	2
6	Production of Ready-To-Use Functionalized Sup35 Nanofibrils Secreted by <i>Komagataella pastoris</i> . <i>ACS Nano</i> , 2018, 12, 9363-9371.	7.3	7
7	A fine-tuned composition of protein nanofibrils yields an upgraded functionality of displayed antibody binding domains. <i>Biotechnology Journal</i> , 2017, 12, 1600672.	1.8	8
8	Identification of proteins that specifically recognize and bind protofibrillar aggregates of amyloid- β . <i>Scientific Reports</i> , 2017, 7, 5949.	1.6	17
9	Structural basis for Myf and Psa fimbriae-mediated tropism of pathogenic strains of <i>Yersinia</i> for host tissues. <i>Molecular Microbiology</i> , 2016, 102, 593-610.	1.2	14
10	Combined Solution- and Magic Angle Spinning NMR Reveals Regions of Distinct Dynamics in Amyloid β Protofibrils. <i>ChemistrySelect</i> , 2016, 1, 5850-5853.	0.7	4
11	Contact between the β 1 and β 2 Segments of β -Synuclein that Inhibits Amyloid Formation. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 8837-8840.	7.2	25
12	A truncated and dimeric format of an Affibody library on bacteria enables FACS-mediated isolation of amyloid- β aggregation inhibitors with subnanomolar affinity. <i>Biotechnology Journal</i> , 2015, 10, 1707-1718.	1.8	35
13	A β -Hairpin-Binding Protein for Three Different Disease-Related Amyloidogenic Proteins. <i>ChemBioChem</i> , 2015, 16, 411-414.	1.3	24
14	Binding of Human Proteins to Amyloid- β Protofibrils. <i>ACS Chemical Biology</i> , 2015, 10, 766-774.	1.6	26
15	A Hexameric Peptide Barrel as Building Block of Amyloid- β Protofibrils. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 12756-12760.	7.2	128
16	Amyloid Fibrils: Formation, Polymorphism, and Inhibition. <i>Journal of Physical Chemistry Letters</i> , 2014, 5, 607-614.	2.1	42
17	A Hexameric Peptide Barrel as Building Block of Amyloid- β Protofibrils. <i>Angewandte Chemie</i> , 2014, 126, 12970-12974.	1.6	8
18	Staphylococcal display for combinatorial protein engineering of a head-to-tail affibody dimer binding the Alzheimer amyloid- β peptide. <i>Biotechnology Journal</i> , 2013, 8, 139-145.	1.8	14

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19	High-affinity binding to staphylococcal protein A by an engineered dimeric Affibody molecule. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 635-644.	1.0	25
20	Self-Cleaving Mucins. , 2013, , 3632-3635.		0
21	Amyloid- β Protofibrils: Size, Morphology and Synaptotoxicity of an Engineered Mimic. <i>PLoS ONE</i> , 2013, 8, e66101.	1.1	46
22	Folding-Reaction Coupling in a Self-Cleaving Protein. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3871-3879.	2.3	12
23	Inhibition of Amyloid Formation. <i>Journal of Molecular Biology</i> , 2012, 421, 441-465.	2.0	238
24	Monte Carlo Study of the Formation and Conformational Properties of Dimers of A β 242 Variants. <i>Journal of Molecular Biology</i> , 2011, 410, 357-367.	2.0	50
25	Protein engineering to stabilize soluble amyloid β protein aggregates for structural and functional studies. <i>FEBS Journal</i> , 2011, 278, 3884-3892.	2.2	35
26	Comparing the folding free energy landscapes of A β 242 variants with different aggregation properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2600-2608.	1.5	45
27	Structural basis for high-affinity HER2 receptor binding by an engineered protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15039-15044.	3.3	171
28	Stabilization of neurotoxic Alzheimer amyloid- β oligomers by protein engineering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15595-15600.	3.3	304
29	Sequestration of the A β 2 Peptide Prevents Toxicity and Promotes Degradation In Vivo. <i>PLoS Biology</i> , 2010, 8, e1000334.	2.6	70
30	Conserved Hydrophobic Clusters on the Surface of the Caf1A Usher C-Terminal Domain Are Important for F1 Antigen Assembly. <i>Journal of Molecular Biology</i> , 2010, 403, 243-259.	2.0	11
31	Rapid screening for improved solubility of small human proteins produced as fusion proteins in <i>Escherichia coli</i> . <i>Protein Science</i> , 2009, 11, 313-321.	3.1	277
32	Protein Autoproteolysis: Conformational Strain Linked to the Rate of Peptide Cleavage by the pH Dependence of the N \rightarrow O Acyl Shift Reaction. <i>Journal of the American Chemical Society</i> , 2009, 131, 9475-9477.	6.6	56
33	Recombinant amyloid beta-peptide production by coexpression with an affibody ligand. <i>BMC Biotechnology</i> , 2008, 8, 82.	1.7	37
34	SEA Domain Autoproteolysis Accelerated by Conformational Strain: Mechanistic Aspects. <i>Journal of Molecular Biology</i> , 2008, 377, 1130-1143.	2.0	34
35	SEA Domain Autoproteolysis Accelerated by Conformational Strain: Energetic Aspects. <i>Journal of Molecular Biology</i> , 2008, 377, 1117-1129.	2.0	25
36	Interaction of Alzheimer's A β 2 Peptide with an Engineered Binding Protein—Thermodynamics and Kinetics of Coupled Folding—Binding. <i>Journal of Molecular Biology</i> , 2008, 378, 398-411.	2.0	38

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37	New Insights into Multiple Coagulation Factor Deficiency from the Solution Structure of Human MCFD2. <i>Journal of Molecular Biology</i> , 2008, 381, 941-955.	2.0	37
38	A non-conservative polymorphism in the IL-6 signal transducer (IL6ST)/gp130 is associated with myocardial infarction in a hypertensive population. <i>Regulatory Peptides</i> , 2008, 146, 189-196.	1.9	23
39	Stabilization of a β -hairpin in monomeric Alzheimer's amyloid- β peptide inhibits amyloid formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5099-5104.	3.3	375
40	A Potential Role for <i>Drosophila</i> Mucins in Development and Physiology. <i>PLoS ONE</i> , 2008, 3, e3041.	1.1	93
41	Improved solubility of TEV protease by directed evolution. <i>Journal of Biotechnology</i> , 2006, 121, 291-298.	1.9	281
42	Conformational Stabilization of an Engineered Binding Protein. <i>Journal of the American Chemical Society</i> , 2006, 128, 7651-7660.	6.6	22
43	Thermodynamics of Folding and Binding in an Affibody:Affibody Complex. <i>Journal of Molecular Biology</i> , 2006, 359, 1305-1315.	2.0	14
44	Structural Basis for Molecular Recognition in an Affibody:Affibody Complex. <i>Journal of Molecular Biology</i> , 2006, 359, 1293-1304.	2.0	46
45	Autoproteolysis coupled to protein folding in the SEA domain of the membrane-bound MUC1 mucin. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 71-76.	3.6	233
46	NMR Assignments of the Free and Bound-state Protein Components of an Anti-idiotypic Affibody Complex. <i>Journal of Biomolecular NMR</i> , 2006, 36, 13-13.	1.6	3
47	Effect of N-terminal solubility enhancing fusion proteins on yield of purified target protein. <i>Journal of Structural and Functional Genomics</i> , 2006, 7, 1-14.	1.2	77
48	Dissecting the Thermodynamics of DNA-Protein Interactions. , 2005, , 81-91.		0
49	His tag effect on solubility of human proteins produced in <i>Escherichia coli</i> : a comparison between four expression vectors. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 217-229.	1.2	150
50	Thermodynamics of Folding, Stabilization, and Binding in an Engineered Protein-Protein Complex. <i>Journal of the American Chemical Society</i> , 2004, 126, 11220-11230.	6.6	26
51	Biophysical characterization of ZSPA-1-A phage-display selected binder to protein A. <i>Protein Science</i> , 2004, 13, 2078-2088.	3.1	23
52	NMR structure of the ribosomal protein L23 from <i>Thermus thermophilus</i> . <i>Journal of Biomolecular NMR</i> , 2003, 26, 131-137.	1.6	13
53	Screening methods to determine biophysical properties of proteins in structural genomics. <i>Analytical Biochemistry</i> , 2003, 318, 71-79.	1.1	22
54	An affibody in complex with a target protein: Structure and coupled folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3185-3190.	3.3	101

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55	The solution structure of ribosomal protein L18 from <i>Thermus thermophilus</i> reveals a conserved RNA-binding fold. <i>Biochemical Journal</i> , 2002, 363, 553.	1.7	12
56	The solution structure of ribosomal protein L18 from <i>Thermus thermophilus</i> reveals a conserved RNA-binding fold. <i>Biochemical Journal</i> , 2002, 363, 553-561.	1.7	14
57	The RUNX1 Runt Domain at 1.25Å... Resolution: A Structural Switch and Specifically Bound Chloride Ions Modulate DNA Binding. <i>Journal of Molecular Biology</i> , 2002, 322, 259-272.	2.0	52
58	¹ H, ¹³ C and ¹⁵ N resonance assignments of an affibody-target complex. <i>Journal of Biomolecular NMR</i> , 2002, 24, 271-272.	1.6	7
59	Chloride binding by the AML1/Runx1 transcription factor studied by NMR. <i>FEBS Letters</i> , 2001, 488, 81-84.	1.3	11
60	Intermolecular interactions between the SH3 domain and the proline-rich TH region of Bruton's tyrosine kinase. <i>FEBS Letters</i> , 2001, 489, 67-70.	1.3	35
61	Both proline-rich sequences in the TH region of Bruton's tyrosine kinase stabilize intermolecular interactions with the SH3 domain. <i>FEBS Letters</i> , 2001, 508, 11-15.	1.3	9
62	Structure and Backbone Dynamics of Apo-CBF ² in Solution. <i>Biochemistry</i> , 2001, 40, 11423-11432.	1.2	7
63	Crystallization and preliminary studies of the DNA-binding runt domain of AML1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 269-271.	2.5	4
64	A Complete Hermitian Operator Basis Set for any Spin Quantum Number. <i>Journal of Magnetic Resonance</i> , 2001, 153, 15-21.	1.2	19
65	The N-terminal Regions of Estrogen Receptor $\hat{1}$ and $\hat{2}$ Are Unstructured in Vitro and Show Different TBP Binding Properties. <i>Journal of Biological Chemistry</i> , 2001, 276, 45939-45944.	1.6	120
66	Another piece of the ribosome: solution structure of S16 and its location in the 30S subunit. <i>Structure</i> , 2000, 8, 875-882.	1.6	16
67	Simulations of NMR pulse sequences during equilibrium and non-equilibrium chemical exchange. <i>Journal of Biomolecular NMR</i> , 2000, 18, 49-63.	1.6	69
68	Letter to the editor: assignment and secondary structure identification of the ribosomal protein L18 from <i>Thermus thermophilus</i> . <i>Journal of Biomolecular NMR</i> , 2000, 17, 273-274.	1.6	4
69	Ansigt for Windows: an interactive computer program for semiautomatic assignment of protein NMR spectra. <i>Journal of Biomolecular NMR</i> , 2000, 18, 329-336.	1.6	84
70	The solution structure of ribosomal protein L36 from <i>Thermus thermophilus</i> reveals a zinc-ribbon-like fold 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 296, 169-180.	2.0	48
71	Sequence-Specific DNA Binding by the Glucocorticoid Receptor DNA-Binding Domain Is Linked to a Salt-Dependent Histidine Protonation. <i>Biochemistry</i> , 2000, 39, 8909-8916.	1.2	17
72	Solution properties of the free and DNA-bound Runt domain of AML1. <i>FEBS Journal</i> , 1999, 261, 251-260.	0.2	10

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73	Conformational Dynamics and Molecular Recognition: Backbone Dynamics of the Estrogen Receptor DNA-binding Domain. <i>Journal of Molecular Biology</i> , 1999, 289, 963-979.	2.0	33
74	Solution structure of the ribosomal protein S19 from <i>Thermus thermophilus</i> 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 292, 1071-1081.	2.0	11
75	NMR studies of protein-nucleic acid complexes: structures, solvation, dynamics and coupled protein folding. <i>Quarterly Reviews of Biophysics</i> , 1999, 32, 57-98.	2.4	16
76	Architecture of nonspecific protein-DNA interactions in the Sso7d-DNA complex. <i>Nature Structural Biology</i> , 1998, 5, 579-584.	9.7	80
77	The Complete Homogeneous Master Equation for a Heteronuclear Two-Spin System in the Basis of Cartesian Product Operators. <i>Journal of Magnetic Resonance</i> , 1998, 134, 7-16.	1.2	63
78	Solution Structure of the SH3 Domain from Bruton's Tyrosine Kinase. <i>Biochemistry</i> , 1998, 37, 2912-2924.	1.2	74
79	Thermodynamic characterization of non-sequence-specific DNA-binding by the Sso7d protein from <i>Sulfolobus solfataricus</i> . <i>Journal of Molecular Biology</i> , 1998, 276, 775-786.	2.0	88
80	Structure and Dynamics of the Glucocorticoid Receptor DNA-Binding Domain: Comparison of Wild Type and a Mutant with Altered Specificity. <i>Biochemistry</i> , 1997, 36, 11188-11197.	1.2	18
81	Preliminary NMR studies of <i>Thermus thermophilus</i> ribosomal protein S19 overproduced in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1997, 415, 155-159.	1.3	2
82	Solution structure of the ribosomal RNA binding protein S15 from <i>Thermus thermophilus</i> . <i>Nature Structural and Molecular Biology</i> , 1997, 4, 20-23.	3.6	67
83	NMR Relaxation Mechanisms for Backbone Carbonyl Carbons in a ¹³ C, ¹⁵ N-Labeled Protein. <i>Journal of Magnetic Resonance</i> , 1997, 126, 48-57.	1.2	31
84	A Method for Simulation of NOESY, ROESY, and Off-Resonance ROESY Spectra. <i>Journal of Magnetic Resonance</i> , 1997, 129, 19-29.	1.2	29
85	Thermodynamics of sequence-specific protein-DNA interactions. <i>Biophysical Chemistry</i> , 1996, 62, 121-139.	1.5	56
86	Salt Dependence of the Free Energy, Enthalpy, and Entropy of Nonsequence Specific DNA Binding. <i>The Journal of Physical Chemistry</i> , 1996, 100, 17690-17695.	2.9	42
87	Solution structure of a mammalian PCB-binding protein in complex with a PCB. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 983-989.	3.6	39
88	A method for production of double labelled RNA in <i>E. coli</i> , and subsequent in vitro synthesis of ribonucleotide 5' triphosphates. <i>Journal of Proteomics</i> , 1995, 30, 59-68.	2.4	4
89	DNA-binding Surface of the Sso7d Protein from <i>Sulfolobus solfataricus</i> . <i>Journal of Molecular Biology</i> , 1995, 247, 840-846.	2.0	47
90	Structural characterization of a minimal functional transactivation domain from the human glucocorticoid receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 1699-1703.	3.3	160

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91	Structural Characterization of a Short Peptide Fragment that Mediates Estrogen- α -Receptor Dimerization. FEBS Journal, 1995, 230, 879-885.	0.2	0
92	Structural Characterization of a Short Peptide Fragment that Mediates Estrogen-Receptor Dimerization. FEBS Journal, 1995, 230, 879-885.	0.2	4
93	Solution structure and DNA-binding properties of a thermostable protein from the archaeon <i>Sulfolobus solfataricus</i> . Nature Structural Biology, 1994, 1, 808-819.	9.7	162
94	Synthesis and NMR spectrum of [$^{13}\text{C}^{18}$]-meso-hexestrol, a fully carbon-13 substituted ligand for NMR studies of the estrogen receptor. Magnetic Resonance in Chemistry, 1993, 31, 977-986.	1.1	1
95	A comparison of ^{15}N NMR relaxation measurements with a molecular dynamics simulation: Backbone dynamics of the glucocorticoid receptor DNA-binding domain. Proteins: Structure, Function and Bioinformatics, 1993, 17, 375-390.	1.5	57
96	Association of short DNA fragments: Steady state fluorescence polarization study. Biopolymers, 1986, 25, 1519-1529.	1.2	16
97	Anisotropic overall and internal motions of short DNA fragments. Nucleic Acids Research, 1986, 14, 3945-3956.	6.5	6