

# Torleif HÃ¸rd

## List of Publications by Year in descending order

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97  
papers

5,047  
citations

94433

37  
h-index

95266

68  
g-index

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. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2021, 28, 158-167.	3.0	4
2	Coupled chemistry kinetics demonstrate the utility of functionalized Sup35 amyloid nanofibrils in biocatalytic cascades. Journal of Biological Chemistry, 2019, 294, 14966-14977.	3.4	4
3	Affibody-Mediated Sequestration of Amyloid $\beta$ Demonstrates Preventive Efficacy in a Transgenic Alzheimer's Disease Mouse Model. Frontiers in Aging Neuroscience, 2019, 11, 64.	3.4	16
4	Protofibrillar and Fibrillar Amyloid- $\beta$ Binding Proteins in Cerebrospinal Fluid. Journal of Alzheimer's Disease, 2018, 66, 1053-1064.	2.6	7
5	The kinetics of TEM1 antibiotic degrading enzymes that are displayed on Ure2 protein nanofibrils in a flow reactor. PLoS ONE, 2018, 13, e0196250.	2.5	2
6	Production of Ready-To-Use Functionalized Sup35 Nanofibrils Secreted by <i>Komagataella pastoris</i> . ACS Nano, 2018, 12, 9363-9371.	14.6	7
7	A fine-tuned composition of protein nanofibrils yields an upgraded functionality of displayed antibody binding domains. Biotechnology Journal, 2017, 12, 1600672.	3.5	8
8	Identification of proteins that specifically recognize and bind protofibrillar aggregates of amyloid- $\beta$ . Scientific Reports, 2017, 7, 5949.	3.3	17
9	Structural basis for Myf and Psa fimbriae-mediated tropism of pathogenic strains of <i>Yersinia</i> for host tissues. Molecular Microbiology, 2016, 102, 593-610.	2.5	14
10	Combined Solution- and Magic Angle Spinning NMR Reveals Regions of Distinct Dynamics in Amyloid $\beta$ Protofibrils. ChemistrySelect, 2016, 1, 5850-5853.	1.5	4
11	Contact between the $\beta$ 1 and $\beta$ 2 Segments of $\beta$ -Synuclein that Inhibits Amyloid Formation. Angewandte Chemie - International Edition, 2015, 54, 8837-8840.	13.8	25
12	A truncated and dimeric format of an Affibody library on bacteria enables FACS-mediated isolation of amyloid- $\beta$ aggregation inhibitors with subnanomolar affinity. Biotechnology Journal, 2015, 10, 1707-1718.	3.5	35
13	A $\beta$ -Hairpin-Binding Protein for Three Different Disease-Related Amyloidogenic Proteins. ChemBioChem, 2015, 16, 411-414.	2.6	24
14	Binding of Human Proteins to Amyloid- $\beta$ Protofibrils. ACS Chemical Biology, 2015, 10, 766-774.	3.4	26
15	A Hexameric Peptide Barrel as Building Block of Amyloid- $\beta$ Protofibrils. Angewandte Chemie - International Edition, 2014, 53, 12756-12760.	13.8	128
16	Amyloid Fibrils: Formation, Polymorphism, and Inhibition. Journal of Physical Chemistry Letters, 2014, 5, 607-614.	4.6	42
17	A Hexameric Peptide Barrel as Building Block of Amyloid- $\beta$ Protofibrils. Angewandte Chemie, 2014, 126, 12970-12974.	2.0	8
18	Staphylococcal display for combinatorial protein engineering of a head-to-tail affibody dimer binding the Alzheimer amyloid- $\beta$ peptide. Biotechnology Journal, 2013, 8, 139-145.	3.5	14

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19	High-affinity binding to staphylococcal protein A by an engineered dimeric Affibody molecule. Protein Engineering, Design and Selection, 2013, 26, 635-644.	2.1	25
20	Self-Cleaving Mucins. , 2013, , 3632-3635.		0
21	Amyloid-Î² Protofibrils: Size, Morphology and Synaptotoxicity of an Engineered Mimic. PLoS ONE, 2013, 8, e66101.	2.5	46
22	Folding-Reaction Coupling in a Self-Cleaving Protein. Journal of Chemical Theory and Computation, 2012, 8, 3871-3879.	5.3	12
23	Inhibition of Amyloid Formation. Journal of Molecular Biology, 2012, 421, 441-465.	4.2	238
24	Monte Carlo Study of the Formation and Conformational Properties of Dimers of AÎ²42 Variants. Journal of Molecular Biology, 2011, 410, 357-367.	4.2	50
25	Protein engineering to stabilize soluble amyloid Î²â€protein aggregates for structural and functional studies. FEBS Journal, 2011, 278, 3884-3892.	4.7	35
26	Comparing the folding freeâ€energy landscapes of AÎ²42 variants with different aggregation properties. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2600-2608.	2.6	45
27	Structural basis for high-affinity HER2 receptor binding by an engineered protein. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15039-15044.	7.1	171
28	Stabilization of neurotoxic Alzheimer amyloid-Î² oligomers by protein engineering. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15595-15600.	7.1	304
29	Sequestration of the AÎ² Peptide Prevents Toxicity and Promotes Degradation In Vivo. PLoS Biology, 2010, 8, e1000334.	5.6	70
30	Conserved Hydrophobic Clusters on the Surface of the Caf1A Usher C-Terminal Domain Are Important for F1 Antigen Assembly. Journal of Molecular Biology, 2010, 403, 243-259.	4.2	11
31	Rapid screening for improved solubility of small human proteins produced as fusion proteins in Escherichia coli. Protein Science, 2009, 11, 313-321.	7.6	277
32	Protein Autoproteolysis: Conformational Strain Linked to the Rate of Peptide Cleavage by the pH Dependence of the N â† O Acyl Shift Reaction. Journal of the American Chemical Society, 2009, 131, 9475-9477.	13.7	56
33	Recombinant amyloid beta-peptide production by coexpression with an affibody ligand. BMC Biotechnology, 2008, 8, 82.	3.3	37
34	SEA Domain Autoproteolysis Accelerated by Conformational Strain: Mechanistic Aspects. Journal of Molecular Biology, 2008, 377, 1130-1143.	4.2	34
35	SEA Domain Autoproteolysis Accelerated by Conformational Strain: Energetic Aspects. Journal of Molecular Biology, 2008, 377, 1117-1129.	4.2	25
36	Interaction of Alzheimerâ€™s AÎ² Peptide with an Engineered Binding Proteinâ€Thermodynamics and Kinetics of Coupled Foldingâ€Binding. Journal of Molecular Biology, 2008, 378, 398-411.	4.2	38

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37	New Insights into Multiple Coagulation Factor Deficiency from the Solution Structure of Human MCFD2. Journal of Molecular Biology, 2008, 381, 941-955.	4.2	37
38	A non-conservative polymorphism in the IL-6 signal transducer (IL6ST)/gp130 is associated with myocardial infarction in a hypertensive population. Regulatory Peptides, 2008, 146, 189-196.	1.9	23
39	Stabilization of a $\beta^2$ -hairpin in monomeric Alzheimer's amyloid- $\beta^2$ peptide inhibits amyloid formation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5099-5104.	7.1	375
40	A Potential Role for Drosophila Mucins in Development and Physiology. PLoS ONE, 2008, 3, e3041.	2.5	93
41	Improved solubility of TEV protease by directed evolution. Journal of Biotechnology, 2006, 121, 291-298.	3.8	281
42	Conformational Stabilization of an Engineered Binding Protein. Journal of the American Chemical Society, 2006, 128, 7651-7660.	13.7	22
43	Thermodynamics of Folding and Binding in an Affibody:Affibody Complex. Journal of Molecular Biology, 2006, 359, 1305-1315.	4.2	14
44	Structural Basis for Molecular Recognition in an Affibody:Affibody Complex. Journal of Molecular Biology, 2006, 359, 1293-1304.	4.2	46
45	Autoproteolysis coupled to protein folding in the SEA domain of the membrane-bound MUC1 mucin. Nature Structural and Molecular Biology, 2006, 13, 71-76.	8.2	233
46	NMR Assignments of the Free and Bound-state Protein Components of an Anti-idiotypic Affibody Complex. Journal of Biomolecular NMR, 2006, 36, 13-13.	2.8	3
47	Effect of N-terminal solubility enhancing fusion proteins on yield of purified target protein. Journal of Structural and Functional Genomics, 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 Escherichia coli: a comparison between four expression vectors. Journal of Structural and Functional Genomics, 2004, 5, 217-229.	1.2	150
50	Thermodynamics of Folding, Stabilization, and Binding in an Engineered Protein~Protein Complex. Journal of the American Chemical Society, 2004, 126, 11220-11230.	13.7	26
51	Biophysical characterization of ZSPA-1-A phage-display selected binder to protein A. Protein Science, 2004, 13, 2078-2088.	7.6	23
52	NMR structure of the ribosomal protein L23 from Thermus thermophilus. Journal of Biomolecular NMR, 2003, 26, 131-137.	2.8	13
53	Screening methods to determine biophysical properties of proteins in structural genomics. Analytical Biochemistry, 2003, 318, 71-79.	2.4	22
54	An affibody in complex with a target protein: Structure and coupled folding. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3185-3190.	7.1	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.	3.7	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.	3.7	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.	4.2	52
58	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments of an affibody-target complex. <i>Journal of Biomolecular NMR</i> , 2002, 24, 271-272.	2.8	7
59	Chloride binding by the AML1/Runx1 transcription factor studied by NMR. <i>FEBS Letters</i> , 2001, 488, 81-84.	2.8	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.	2.8	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.	2.8	9
62	Structure and Backbone Dynamics of Apo-CBF $\hat{1}^2$ in Solution. <i>Biochemistry</i> , 2001, 40, 11423-11432.	2.5	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.	2.1	19
65	The N-terminal Regions of Estrogen Receptor $\hat{1}^{\pm}$ and $\hat{1}^2$ Are Unstructured in Vitro and Show Different TBP Binding Properties. <i>Journal of Biological Chemistry</i> , 2001, 276, 45939-45944.	3.4	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.	3.3	16
67	Simulations of NMR pulse sequences during equilibrium and non-equilibrium chemical exchange. <i>Journal of Biomolecular NMR</i> , 2000, 18, 49-63.	2.8	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.	2.8	4
69	Ansig for Windows: an interactive computer program for semiautomatic assignment of protein NMR spectra. <i>Journal of Biomolecular NMR</i> , 2000, 18, 329-336.	2.8	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.	4.2	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.	2.5	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.	4.2	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.	4.2	11
75	NMR studies of proteinâ€“nucleic acid complexes: structures, solvation, dynamics and coupled protein folding. <i>Quarterly Reviews of Biophysics</i> , 1999, 32, 57-98.	5.7	16
76	Architecture of nonspecific proteinâ€“DNA interactions in the Sso7dâ€“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.	2.1	63
78	Solution Structure of the SH3 Domain from Bruton's Tyrosine Kinaseâ€“,â€“. <i>Biochemistry</i> , 1998, 37, 2912-2924.	2.5	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.	4.2	88
80	Structure and Dynamics of the Glucocorticoid Receptor DNA-Binding Domain:â€“ Comparison of Wild Type and a Mutant with Altered Specificity. <i>Biochemistry</i> , 1997, 36, 11188-11197.	2.5	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.	2.8	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.	8.2	67
83	NMR Relaxation Mechanisms for Backbone Carbonyl Carbons in a <sup>13</sup> C, <sup>15</sup> N-Labeled Protein. <i>Journal of Magnetic Resonance</i> , 1997, 126, 48-57.	2.1	31
84	A Method for Simulation of NOESY, ROESY, and Off-Resonance ROESY Spectra. <i>Journal of Magnetic Resonance</i> , 1997, 129, 19-29.	2.1	29
85	Thermodynamics of sequence-specific protein-DNA interactions. <i>Biophysical Chemistry</i> , 1996, 62, 121-139.	2.8	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.	8.2	39
88	A method for production of double labelled RNA in <i>E. coli</i> , and subsequent in vitro synthesis of ribonucleotide 5â€“ 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.	4.2	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.	7.1	160

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91	Structural Characterization of a Short Peptide Fragment that Mediates Estrogen-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 Sulfolobus solfataricus. Nature Structural Biology, 1994, 1, 808-819.	9.7	162
94	Synthesis and NMR spectrum of [13C18]-meso-hexestrol, a fully carbon-13 substituted ligand for NMR studies of the estrogen receptor. Magnetic Resonance in Chemistry, 1993, 31, 977-986.	1.9	1
95	A comparison of 15N 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.	2.6	57
96	Association of short DNA fragments: Steady state fluorescence polarization study. Biopolymers, 1986, 25, 1519-1529.	2.4	16
97	Anisotropic overall and internal motions of short DNA fragments. Nucleic Acids Research, 1986, 14, 3945-3956.	14.5	6