Ingemar AndrÃ©

List of Publications by Year
in descending order

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49 papers	3,580 citations	218677 26 h-index	197818 49 g-index
56 all docs	56 docs citations	56 times ranked	5295 citing authors

#	Article	IF	Citations
1	Computational Design of Self-Assembling Protein Nanomaterials with Atomic Level Accuracy. Science, 2012, 336, 1171-1174.	12.6	588
2	Alternate States of Proteins Revealed by Detailed Energy Landscape Mapping. Journal of Molecular Biology, 2011, 405, 607-618.	4.2	324
3	RosettaRemodel: A Generalized Framework for Flexible Backbone Protein Design. PLoS ONE, 2011, 6, e24109.	2.5	310
4	A Vast Repertoire of Dscam Binding Specificities Arises from Modular Interactions of Variable Ig Domains. Cell, 2007, 130, 1134-1145.	28.9	210
5	Modeling Symmetric Macromolecular Structures in Rosetta3. PLoS ONE, 2011, 6, e20450.	2.5	197
6	Structure prediction for CASP7 targets using extensive all-atom refinement with Rosetta@home. Proteins: Structure, Function and Bioinformatics, 2007, 69, 118-128.	2.6	178
7	A conserved structural motif mediates formation of the periplasmic rings in the type III secretion system. Nature Structural and Molecular Biology, 2009, 16, 468-476.	8.2	170
8	Prediction of the structure of symmetrical protein assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17656-17661.	7.1	164
9	Emergence of symmetry in homooligomeric biological assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16148-16152.	7.1	153
10	Simultaneous prediction of protein folding and docking at high resolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18978-18983.	7.1	145
11	A Double S Shape Provides the Structural Basis for the Extraordinary Binding Specificity of Dscam Isoforms. Cell, 2008, 134, 1007-1018.	28.9	109
12	Residue-Specific pK_a Determination of Lysine and Arginine Side Chains by Indirect ¹⁵N and ¹³C NMR Spectroscopy:â€‰ Application to apo Calmodulin. Journal of the American Chemical Society, 2007, 129, 15805-15813.	13.7	99
13	Measurement of Ca2+-Binding Constants of Proteins and Presentation of the CaLigator Software. Analytical Biochemistry, 2002, 305, 195-205.	2.4	91
14	Determination of the Structures of Symmetric Protein Oligomers from NMR Chemical Shifts and Residual Dipolar Couplings. Journal of the American Chemical Society, 2011, 133, 6288-6298.	13.7	65
15	The Role of Electrostatic Interactions in Calmodulin-Peptide Complex Formation. Biophysical Journal, 2004, 87, 1929-1938.	0.5	57
16	Computational design of a leucine-rich repeat protein with a predefined geometry. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17875-17880.	7.1	53
17	Structure of the basal components of a bacterial transporter. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5446-5451.	7.1	49
18	Computational design of protein self-assembly. Current Opinion in Structural Biology, 2016, 39, 39-45.	5.7	48

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19	Crystal Structure of Non-Structural Protein 10 from Severe Acute Respiratory Syndrome Coronavirus-2. International Journal of Molecular Sciences, 2020, 21, 7375.	4.1	48
20	pKa Values for Side-Chain Carboxyl Groups of a PGB1 Variant Explain Salt and pH-Dependent Stability. Biophysical Journal, 2007, 92, 257-266.	0.5	46
21	Interactions of the Transmembrane Polymeric Rings of the Salmonella enterica Serovar Typhimurium Type III Secretion System. MBio, 2010, 1, .	4.1	37
22	A De Novo Designed Coiled-Coil Peptide with a Reversible pH-Induced Oligomerization Switch. Structure, 2016, 24, 946-955.	3.3	36
23	Streptococcal M Protein:â€‰ Structural Studies of the Hypervariable Region, Free and Bound to Human C4BP. Biochemistry, 2006, 45, 4559-4568.	2.5	34
24	Mapping the Ca2+ induced structural change in calreticulin. Journal of Proteomics, 2016, 142, 138-148.	2.4	32
25	Bayesian inference of protein conformational ensembles from limited structural data. PLoS Computational Biology, 2018, 14, e1006641.	3.2	32
26	Electrostatic Contributions to Residue-Specific Protonation Equilibria and Proton Binding Capacitance for a Small Protein. Biochemistry, 2006, 45, 13993-14002.	2.5	31
27	Salt Enhances Calmodulin-Target Interaction. Biophysical Journal, 2006, 90, 2903-2910.	0.5	27
28	RosettaDock in CAPRI rounds 6â€“12. Proteins: Structure, Function and Bioinformatics, 2007, 69, 758-763.	2.6	26
29	Amyloid Î² 42 fibril structure based on small-angle scattering. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	23
30	Exploring alternate states and oligomerization preferences of coiledâ€coils by de novo structure modeling. Proteins: Structure, Function and Bioinformatics, 2015, 83, 235-247.	2.6	22
31	Rosetta in CAPRI rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3212-3218.	2.6	20
32	Computational De Novo Design of a Self-Assembling Peptide with Predefined Structure. Journal of Molecular Biology, 2015, 427, 550-562.	4.2	20
33	Orientational Ambiguity in Septin Coiled Coils and its Structural Basis. Journal of Molecular Biology, 2021, 433, 166889.	4.2	18
34	Thermal stability and structural changes in bacterial toxins responsible for food poisoning. PLoS ONE, 2017, 12, e0172445.	2.5	16
35	Assembly of Capsids from Hepatitis B Virus Core Protein Progresses through Highly Populated Intermediates in the Presence and Absence of RNA. ACS Nano, 2020, 14, 10226-10238.	14.6	16
36	Automatedde novophasing and model building of coiled-coil proteins. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 606-614.	2.5	14

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37	A Proteinâ€Based Encapsulation System with Calciumâ€Controlled Cargo Loading and Detachment. Angewandte Chemie - International Edition, 2018, 57, 11334-11338.	13.8	14
38	A thermodynamic model of protein structure evolution explains empirical amino acid substitution matrices. Protein Science, 2021, 30, 2057-2068.	7.6	13
39	Calbindin D28k EF-Hand Ligand Binding and Oligomerization:â€‰ Four High-Affinity SitesThree Modes of Action. Biochemistry, 2005, 44, 13522-13532.	2.5	8
40	Automated determination of fibrillar structures by simultaneous model building and fiber diffraction refinement. Nature Methods, 2015, 12, 679-684.	19.0	6
41	Energy Fluctuations Shape Free Energy of Nonspecific Biomolecular Interactions. Journal of Statistical Physics, 2012, 146, 870-877.	1.2	5
42	ZEAL: protein structure alignment based on shape similarity. Bioinformatics, 2021, 37, 2874-2881.	4.1	5
43	DnaK response to expression of protein mutants is dependent on translation rate and stability. Communications Biology, 2022, 5, .	4.4	5
44	Computational assessment of folding energy landscapes in heterodimeric coiled coils. Proteins: Structure, Function and Bioinformatics, 2018, 86, 790-801.	2.6	3
45	Modeling the Structure of Helical Assemblies with Experimental Constraints in Rosetta. Methods in Molecular Biology, 2018, 1764, 475-489.	0.9	3
46	A Proteinâ€Based Encapsulation System with Calciumâ€Controlled Cargo Loading and Detachment. Angewandte Chemie, 2018, 130, 11504-11508.	2.0	3
47	An ultraâ€high affinity proteinâ€“protein interface displaying sequenceâ€robustness. Protein Science, 2021, 30, 1144-1156.	7.6	2
48	The RosettaCon 2012 Special Collection: Code Writ on Water, Documentation Writ in Stone. PLoS ONE, 2013, 8, e73775.	2.5	1
49	Cover Image, Volume 86, Issue 7. Proteins: Structure, Function and Bioinformatics, 2018, 86, C4-C4.	2.6	0