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	DnaK response to expression of protein mutants is dependent on translation rate and stability. Communications Biology, 2022, 5, .	4.4	5
2	ZEAL: protein structure alignment based on shape similarity. Bioinformatics, 2021, 37, 2874-2881.	4.1	5
3	Orientational Ambiguity in Septin Coiled Coils and its Structural Basis. Journal of Molecular Biology, 2021, 433, 166889.	4.2	18
4	An ultraâ€high affinity proteinâ€“protein interface displaying sequenceâ€robustness. Protein Science, 2021, 30, 1144-1156.	7.6	2
5	A thermodynamic model of protein structure evolution explains empirical amino acid substitution matrices. Protein Science, 2021, 30, 2057-2068.	7.6	13
6	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
7	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
8	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
9	Computational assessment of folding energy landscapes in heterodimeric coiled coils. Proteins: Structure, Function and Bioinformatics, 2018, 86, 790-801.	2.6	3
10	Modeling the Structure of Helical Assemblies with Experimental Constraints in Rosetta. Methods in Molecular Biology, 2018, 1764, 475-489.	0.9	3
11	Bayesian inference of protein conformational ensembles from limited structural data. PLoS Computational Biology, 2018, 14, e1006641.	3.2	32
12	Cover Image, Volume 86, Issue 7. Proteins: Structure, Function and Bioinformatics, 2018, 86, C4-C4.	2.6	0
13	A Proteinâ€Based Encapsulation System with Calciumâ€Controlled Cargo Loading and Detachment. Angewandte Chemie - International Edition, 2018, 57, 11334-11338.	13.8	14
14	A Proteinâ€Based Encapsulation System with Calciumâ€Controlled Cargo Loading and Detachment. Angewandte Chemie, 2018, 130, 11504-11508.	2.0	3
15	Thermal stability and structural changes in bacterial toxins responsible for food poisoning. PLoS ONE, 2017, 12, e0172445.	2.5	16
16	Computational design of protein self-assembly. Current Opinion in Structural Biology, 2016, 39, 39-45.	5.7	48
17	A De Novo Designed Coiled-Coil Peptide with a Reversible pH-Induced Oligomerization Switch. Structure, 2016, 24, 946-955.	3.3	36
18	Mapping the Ca2+ induced structural change in calreticulin. Journal of Proteomics, 2016, 142, 138-148.	2.4	32

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19	Automatedde novophasing and model building of coiled-coil proteins. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 606-614.	2.5	14
20	Automated determination of fibrillar structures by simultaneous model building and fiber diffraction refinement. Nature Methods, 2015, 12, 679-684.	19.0	6
21	Computational De Novo Design of a Self-Assembling Peptide with Predefined Structure. Journal of Molecular Biology, 2015, 427, 550-562.	4.2	20
22	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
23	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
24	The RosettaCon 2012 Special Collection: Code Writ on Water, Documentation Writ in Stone. PLoS ONE, 2013, 8, e73775.	2.5	1
25	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
26	Computational Design of Self-Assembling Protein Nanomaterials with Atomic Level Accuracy. Science, 2012, 336, 1171-1174.	12.6	588
27	Energy Fluctuations Shape Free Energy of Nonspecific Biomolecular Interactions. Journal of Statistical Physics, 2012, 146, 870-877.	1.2	5
28	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
29	Alternate States of Proteins Revealed by Detailed Energy Landscape Mapping. Journal of Molecular Biology, 2011, 405, 607-618.	4.2	324
30	Modeling Symmetric Macromolecular Structures in Rosetta3. PLoS ONE, 2011, 6, e20450.	2.5	197
31	RosettaRemodel: A Generalized Framework for Flexible Backbone Protein Design. PLoS ONE, 2011, 6, e24109.	2.5	310
32	Rosetta in CAPRI rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3212-3218.	2.6	20
33	Interactions of the Transmembrane Polymeric Rings of the Salmonella enterica Serovar Typhimurium Type III Secretion System. MBio, 2010, 1, .	4.1	37
34	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
35	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
36	A Double S Shape Provides the Structural Basis for the Extraordinary Binding Specificity of Dscam Isoforms. Cell, 2008, 134, 1007-1018.	28.9	109

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37	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
38	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
39	A Vast Repertoire of Dscam Binding Specificities Arises from Modular Interactions of Variable Ig Domains. Cell, 2007, 130, 1134-1145.	28.9	210
40	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
41	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
42	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
43	RosettaDock in CAPRI rounds 6â€“12. Proteins: Structure, Function and Bioinformatics, 2007, 69, 758-763.	2.6	26
44	Salt Enhances Calmodulin-Target Interaction. Biophysical Journal, 2006, 90, 2903-2910.	0.5	27
45	Streptococcal M Protein:â€‰ Structural Studies of the Hypervariable Region, Free and Bound to Human C4BP. Biochemistry, 2006, 45, 4559-4568.	2.5	34
46	Electrostatic Contributions to Residue-Specific Protonation Equilibria and Proton Binding Capacitance for a Small Protein. Biochemistry, 2006, 45, 13993-14002.	2.5	31
47	Calbindin D28k EF-Hand Ligand Binding and Oligomerization:â€‰ Four High-Affinity SitesThree Modes of Action. Biochemistry, 2005, 44, 13522-13532.	2.5	8
48	The Role of Electrostatic Interactions in Calmodulin-Peptide Complex Formation. Biophysical Journal, 2004, 87, 1929-1938.	0.5	57
49	Measurement of Ca2+-Binding Constants of Proteins and Presentation of the CaLigator Software. Analytical Biochemistry, 2002, 305, 195-205.	2.4	91