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List of Publications by Year
in descending order

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93 papers	4,562 citations	94433 37 h-index	110387 64 g-index
102 all docs	102 docs citations	102 times ranked	5556 citing authors

#	Article	IF	Citations
1	Structural Biology and Evolution of the TGF-Î² Family. Cold Spring Harbor Perspectives in Biology, 2016, 8, a022103.	5.5	267
2	Cooperative Assembly of TGF-Î² Superfamily Signaling Complexes Is Mediated by Two Disparate Mechanisms and Distinct Modes of Receptor Binding. Molecular Cell, 2008, 29, 157-168.	9.7	247
3	Structural Basis of J Cochaperone Binding and Regulation of Hsp70. Molecular Cell, 2007, 28, 422-433.	9.7	206
4	Structural studies of the TGFâ€Î²s and their receptors â€“ insights into evolution of the TGFâ€Î² superfamily. FEBS Letters, 2012, 586, 1860-1870.	2.8	185
5	Transforming Growth Factor Î²1:â€‰ Three-Dimensional Structure in Solution and Comparison with the X-ray Structure of Transforming Growth Factor Î²2,. Biochemistry, 1996, 35, 8517-8534.	2.5	175
6	A structurally distinct TGF-Î² mimic from an intestinal helminth parasite potently induces regulatory T cells. Nature Communications, 2017, 8, 1741.	12.8	159
7	Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. Nature Methods, 2017, 14, 399-402.	19.0	158
8	Effects of amino acid substitutions on the pressure denaturation of staphylococcal nuclease as monitored by fluorescence and nuclear magnetic resonance spectroscopy. Biochemistry, 1993, 32, 5222-5232.	2.5	141
9	Ternary Complex of Transforming Growth Factor-Î²1 Reveals Isoform-specific Ligand Recognition and Receptor Recruitment in the Superfamily. Journal of Biological Chemistry, 2010, 285, 14806-14814.	3.4	135
10	Multiple-Quantum Line Narrowing for Measurement of H.alpha.-H.beta. J Couplings in Isotopically Enriched Proteins. Journal of the American Chemical Society, 1995, 117, 5312-5315.	13.7	130
11	Crystal structure of the human TÎ²R2 ectodomainâ€“TGF-Î²3 complex. Nature Structural Biology, 2002, 9, 203-8.	9.7	130
12	TGF-Î² uses a novel mode of receptor activation to phosphorylate SMAD1/5 and induce epithelial-to-mesenchymal transition. ELife, 2018, 7, .	6.0	119
13	Solvent effects on the energetics of prolyl peptide bond isomerization. Journal of the American Chemical Society, 1992, 114, 5437-5439.	13.7	109
14	TGF-Î² signalling is mediated by two autonomously functioning TÎ²RI:TÎ²RII pairs. EMBO Journal, 2011, 30, 1263-1276.	7.8	98
15	High resolution solution structure of ribosomal protein L11-C76, a helical protein with a flexible loop that becomes structured upon binding to RNA. Nature Structural and Molecular Biology, 1997, 4, 70-77.	8.2	97
16	Structural basis for potency differences between GDF8 and GDF11. BMC Biology, 2017, 15, 19.	3.8	90
17	Polycomb Group Targeting through Different Binding Partners of RING1B C-Terminal Domain. Structure, 2010, 18, 966-975.	3.3	81
18	Schistosoma mansoni: TGF-Î² signaling pathways. Experimental Parasitology, 2007, 117, 304-317.	1.2	80

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19	Three Key Residues Underlie the Differential Affinity of the TGFÎ² Isoforms for the TGFÎ² Type II Receptor. Journal of Molecular Biology, 2006, 355, 47-62.	4.2	77
20	ALK1 signaling in development and disease: new paradigms. Cellular and Molecular Life Sciences, 2017, 74, 4539-4560.	5.4	76
21	Threeâ€dimensional solution structure of the HIVâ€1 protease complexed with DMP323, a novel cyclic ureaâ€type inhibitor, determined by nuclear magnetic resonance spectroscopy. Protein Science, 1996, 5, 495-506.	7.6	72
22	Assembly of TÎ²RI:TÎ²RII:TGFÎ² Ternary Complex in vitro with Receptor Extracellular Domains is Cooperative and Isoform-dependent. Journal of Molecular Biology, 2005, 354, 1052-1068.	4.2	71
23	D2HGDH regulates alpha-ketoglutarate levels and dioxygenase function by modulating IDH2. Nature Communications, 2015, 6, 7768.	12.8	64
24	Coupling between local structure and global stability of a protein: mutants of staphylococcal nuclease. Biochemistry, 1990, 29, 4516-4525.	2.5	58
25	The RNA binding domain of ribosomal protein L11: three-dimensional structure of the RNA-bound form of the protein and its interaction with 23 S rRNA. Journal of Molecular Biology, 1997, 274, 101-113.	4.2	57
26	Binding Affinity of Transforming Growth Factor-Î² for Its Type II Receptor Is Determined by the C-terminal Region of the Molecule. Journal of Biological Chemistry, 1996, 271, 30656-30662.	3.4	56
27	Two-dimensional NMR studies of staphylococcal nuclease. 2. Sequence-specific assignments of carbon-13 and nitrogen-15 signals from the nuclease H124L-thymidine 3',5'-bisphosphate-calcium ternary complex. Biochemistry, 1990, 29, 102-113.	2.5	55
28	The Growth-Suppressive Function of the Polycomb Group Protein Polyhomeotic Is Mediated by Polymerization of Its Sterile Alpha Motif (SAM) Domain. Journal of Biological Chemistry, 2012, 287, 8702-8713.	3.4	54
29	Biological Activity Differences between TGF-Î²1 and TGF-Î²3 Correlate with Differences in the Rigidity and Arrangement of Their Component Monomers. Biochemistry, 2014, 53, 5737-5749.	2.5	54
30	TÎ²R-II Discriminates the High- and Low-Affinity TGF-Î² Isoforms via Two Hydrogen-Bonded Ion Pairs. Biochemistry, 2009, 48, 2146-2155.	2.5	53
31	Solution studies of staphylococcal nuclease H124L. 2. Proton, carbon-13, and nitrogen-15 chemical shift assignments for the unligated enzyme and analysis of chemical shift changes that accompany formation of the nuclease-thymidine 3',5'-bisphosphate-calcium ternary complex. Biochemistry, 1992, 31, 921-936.	2.5	51
32	The Solution Structure of the Regulatory Domain of Tyrosine Hydroxylase. Journal of Molecular Biology, 2014, 426, 1483-1497.	4.2	47
33	Dynamic Interactions between Clathrin and Locally Structured Elements in a Disordered Protein Mediate Clathrin Lattice Assembly. Journal of Molecular Biology, 2010, 404, 274-290.	4.2	46
34	Structural characterization of an activin class ternary receptor complex reveals a third paradigm for receptor specificity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15505-15513.	7.1	46
35	A Novel TGFÎ² Trap Blocks Chemotherapeutics-Induced TGFÎ²1 Signaling and Enhances Their Anticancer Activity in Gynecologic Cancers. Clinical Cancer Research, 2018, 24, 2780-2793.	7.0	45
36	Engineered Disulfide Bonds in Staphylococcal Nuclease:Â Effects on the Stability and Conformation of the Folded Proteinâ€. Biochemistry, 1996, 35, 10328-10338.	2.5	44

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37	Structural biology of betaglycan and endoglin, membrane-bound co-receptors of the TGF-beta family. Experimental Biology and Medicine, 2019, 244, 1547-1558.	2.4	43
38	Betaglycan has Two Independent Domains Required for High Affinity TGF-Î² Binding: Proteolytic Cleavage Separates the Domains and Inactivates the Neutralizing Activity of the Soluble Receptor. Biochemistry, 2009, 48, 11755-11765.	2.5	42
39	NMR strategy for determining Xaa-Pro peptide bond configurations in proteins: Mutants of staphylococcal nuclease with altered configuration at proline-117. Biochemistry, 1993, 32, 11810-11818.	2.5	40
40	Blockade of Autocrine TGF-Î² Signaling Inhibits Stem Cell Phenotype, Survival, and Metastasis of Murine Breast Cancer Cells. Journal of Stem Cell Research & Therapy, 2012, 02, 1-8.	0.3	38
41	Direct evidence for a phenylalanine site in the regulatory domain of phenylalanine hydroxylase. Archives of Biochemistry and Biophysics, 2011, 505, 250-255.	3.0	37
42	Structure of the Alk1 Extracellular Domain and Characterization of Its Bone Morphogenetic Protein (BMP) Binding Properties. Biochemistry, 2012, 51, 6328-6341.	2.5	35
43	Structure and Dynamics of the Homodimeric Dynein Light Chain km23. Journal of Molecular Biology, 2005, 352, 338-354.	4.2	34
44	An engineered transforming growth factor Î² (TGF-Î²) monomer that functions as a dominant negative to block TGF-Î² signaling. Journal of Biological Chemistry, 2017, 292, 7173-7188.	3.4	34
45	Binding Properties of the Transforming Growth Factor-Î² Coreceptor Betaglycan: Proposed Mechanism for Potentiation of Receptor Complex Assembly and Signaling. Biochemistry, 2016, 55, 6880-6896.	2.5	33
46	A novel highly potent trivalent TGF-Î² receptor trap inhibits early-stage tumorigenesis and tumor cell invasion in murine Pten-deficient prostate glands. Oncotarget, 2016, 7, 86087-86102.	1.8	32
47	Solution Structure and Backbone Dynamics of the TGFÎ² Type II Receptor Extracellular Domainâ€,â€¡. Biochemistry, 2003, 42, 10126-10139.	2.5	28
48	Peptide ligands that use a novel binding site to target both TGF-Î² receptors. Molecular BioSystems, 2010, 6, 2392.	2.9	25
49	Production, Isolation, and Structural Analysis of Ligands and Receptors of the TGF-Î² Superfamily. Methods in Molecular Biology, 2016, 1344, 63-92.	0.9	25
50	Two-dimensional NMR studies of staphylococcal nuclease: evidence for conformational heterogeneity from hydrogen-1, carbon-13, and nitrogen-15 spin system assignments of the aromatic amino acids in the nuclease H124L-thymidine 3',5'-bisphosphate-calcium(2+) ternary complex. Biochemistry, 1990, 29, 4242-4253.	2.5	24
51	Sequential resonance assignments of the extracellular ligand binding domain of the human TGF-beta type II receptor. Journal of Biomolecular NMR, 2000, 18, 369-370.	2.8	24
52	Characterization of Ligand-Binding Properties of the Human BMP Type II Receptor Extracellular Domain. Journal of Molecular Biology, 2008, 378, 191-203.	4.2	23
53	Nuclear Magnetic Resonance Mapping and Functional Confirmation of the Collagen Binding Sites of Matrix Metalloproteinase-2. Biochemistry, 2009, 48, 5822-5831.	2.5	23
54	Structural Transitions of the RING1B C-Terminal Region upon Binding the Polycomb cbox Domain. Biochemistry, 2008, 47, 8007-8015.	2.5	21

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55	TGFBR3L is an inhibin B co-receptor that regulates female fertility. Science Advances, 2021, 7, eabl4391.	10.3	21
56	The TÎ²R-I Pre-Helix Extension Is Structurally Ordered in the Unbound Form and Its Flanking Prolines Are Essential for Binding. Journal of Molecular Biology, 2011, 412, 601-618.	4.2	20
57	Solution structure of protein SRP19 of Archaeoglobus fulgidus signal recognition particle. Journal of Molecular Biology, 2002, 317, 145-158.	4.2	19
58	Nuclear Magnetic Resonance Structural Mapping Reveals Promiscuous Interactions between Clathrin-Box Motif Sequences and the N-Terminal Domain of the Clathrin Heavy Chain. Biochemistry, 2015, 54, 2571-2580.	2.5	19
59	Structures of TGF-β Receptor Complexes: Implications for Function and Therapeutic Intervention Using Ligand Traps. Current Pharmaceutical Biotechnology, 2011, 12, 2081-2098.	1.6	18
60	Overexpression and purification of avian ovomucoid third domains in Escherichia coli. Protein Engineering, Design and Selection, 1993, 6, 221-227.	2.1	17
61	Expression, purification and characterization of BGERII: a novel pan-TGFÂ inhibitor. Protein Engineering, Design and Selection, 2008, 21, 463-473.	2.1	17
62	TGF-Î²2 uses the concave surface of its extended finger region to bind betaglycanâ€™s ZP domain via three residues specific to TGF-Î² and inhibin-Î±. Journal of Biological Chemistry, 2019, 294, 3065-3080.	3.4	15
63	The Amino Acid Specificity for Activation of Phenylalanine Hydroxylase Matches the Specificity for Stabilization of Regulatory Domain Dimers. Biochemistry, 2015, 54, 5167-5174.	2.5	14
64	Evaluation of competing J domain:Hsp70 complex models in light of existing mutational and NMR data. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E734; author reply E735.	7.1	13
65	Divergence(s) in nodal signaling between aggressive melanoma and embryonic stem cells. International Journal of Cancer, 2015, 136, E242-51.	5.1	13
66	Structural Adaptation in Its Orphan Domain Engenders Betaglycan with an Alternate Mode of Growth Factor Binding Relative to Endoglin. Structure, 2019, 27, 1427-1442.e4.	3.3	12
67	Structure and Role of BCOR PUFD in Noncanonical PRC1 Assembly and Disease. Biochemistry, 2020, 59, 2718-2728.	2.5	12
68	Convergent evolution of a parasite-encoded complement control protein-scaffold to mimic binding of mammalian TGF-Î² to its receptors, TÎ²RI and TÎ²RII. Journal of Biological Chemistry, 2022, 298, 101994.	3.4	12
69	Algorithm-assisted elucidation of disulfide structure: application of the negative signature mass algorithm to mass-mapping the disulfide structure of the 12-cysteine transforming growth factor Î² type II receptor extracellular domain. Analytical Biochemistry, 2004, 329, 91-103.	2.4	11
70	Characterization of the SRP68/72 interface of human signal recognition particle by systematic siteâ€directed mutagenesis. Protein Science, 2009, 18, 2183-2195.	7.6	11
71	Identification of Nucleic Acid Binding Residues in the FCS Domain of the Polycomb Group Protein Polyhomeotic. Biochemistry, 2011, 50, 4998-5007.	2.5	11
72	Novel TGFÎ² Inhibitors Ameliorate Oral Squamous Cell Carcinoma Progression and Improve the Antitumor Immune Response of Antiâ€“PD-L1 Immunotherapy. Molecular Cancer Therapeutics, 2021, 20, 1102-1111.	4.1	11

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73	The conserved adenosine in helix 6 ofArchaeoglobus fulgidussignal recognition particle RNA initiates SRP assembly. Archaea, 2004, 1, 269-275.	2.3	10
74	Human Polyhomeotic Homolog 3 (PHC3) Sterile Alpha Motif (SAM) Linker Allows Open-Ended Polymerization of PHC3 SAM. Biochemistry, 2012, 51, 5379-5386.	2.5	10
75	Histidine-121 of staphylococcal nuclease. Correction of the H.delta.2 1H NMR assignment and reinterpretation of the role this residue plays in conformational heterogeneity of the protein. Journal of the American Chemical Society, 1990, 112, 9031-9034.	13.7	8
76	Characterization of Hydride Transfer to Flavin Adenine Dinucleotide in Neuronal Nitric Oxide Synthase Reductase Domain: Geometric Relationship between the Nicotinamide and Isoalloxazine Rings. Archives of Biochemistry and Biophysics, 2001, 395, 129-135.	3.0	7
77	Letter to the Editor: Sequential resonance assignments of the extracellular domain of the human TGFÎ² typeÂII receptor in complex with monomeric TGFÎ²3. Journal of Biomolecular NMR, 2004, 29, 103-104.	2.8	7
78	TGF-Î² Antagonists: Same Knot, but Different Hold. Structure, 2013, 21, 1269-1270.	3.3	7
79	Complexes with truncated RNAs from the large domain ofArchaeoglobus fulgidussignal recognition particle. FEMS Microbiology Letters, 2001, 198, 105-110.	1.8	6
80	Structure-guided engineering of TGF-Î²s for the development of novel inhibitors and probing mechanism. Bioorganic and Medicinal Chemistry, 2018, 26, 5239-5246.	3.0	6
81	In Search of â€œHepatic Factorâ€• Lack of Evidence for ALK1 Ligands BMP9 and BMP10. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 249-251.	5.6	6
82	A.Âfulgidus SRP54ÂM-domain. Journal of Biomolecular NMR, 2008, 41, 241-8.	2.8	5
83	Distinct intramolecular interactions regulate autoinhibition of vinculin binding in Î±T-catenin and Î±E-catenin. Journal of Biological Chemistry, 2021, 296, 100582.	3.4	5
84	Sequence-specific 1H, 13C and 15N signal assignments and secondary structure of archaeoglobusfulgidus SRP19. Journal of Biomolecular NMR, 2001, 20, 187-188.	2.8	4
85	Model-free analysis for large proteins at high magnetic field strengths. Journal of Biomolecular NMR, 2007, 38, 315-324.	2.8	4
86	Case study of protein structure, stability, and function: NMR investigations of the proline residues in staphylococcal nuclease. Pure and Applied Chemistry, 1994, 66, 65-69.	1.9	4
87	Kinetic, Dynamic, Ligand Binding Properties, and Structural Models of a Dual-Substrate Specific Nudix Hydrolase from Schizosaccharomyces pombe. Biochemistry, 2009, 48, 6224-6239.	2.5	3
88	Backbone sequential resonance assignments of yeast iso-2 cytochrome c, reduced and oxidized forms. Journal of Biomolecular NMR, 2002, 22, 93-94.	2.8	2
89	Sequential Resonance Assignment of the Human BMP Type II Receptor Extracellular Domain. Journal of Biomolecular NMR, 2005, 32, 336-336.	2.8	2
90	Class II Cytokine Common Receptors: Something Old, Something New. Structure, 2010, 18, 551-552.	3.3	0

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91	Methyl-Labeling Assisted NMR Structure Determination of a 66 KDA Growth Factor-Receptor Complex. Biophysical Journal, 2017, 112, 487a-488a.	0.5	0
92	An introduction to the special issue on biomolecular NMR. Archives of Biochemistry and Biophysics, 2017, 628, 1-2.	3.0	0
93	Probing biomolecular structure, dynamics, and function using hydrogen exchange. Archives of Biochemistry and Biophysics, 2022, , 109185.	3.0	0