

Andrew P Hinck

List of Publications by Year in descending order

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93
papers

4,562
citations

94433

37
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110387

64
g-index

102
all docs

102
docs citations

102
times ranked

5556
citing authors

#	ARTICLE	IF	CITATIONS
1	Probing biomolecular structure, dynamics, and function using hydrogen exchange. Archives of Biochemistry and Biophysics, 2022, , 109185.	3.0	0
2	Convergent evolution of a parasite-encoded complement control protein-scaffold to mimic binding of mammalian TGF- β 2 to its receptors, T β RI and T β RII. Journal of Biological Chemistry, 2022, 298, 101994.	3.4	12
3	In Search of "Hepatic Factor" Lack of Evidence for ALK1 Ligands BMP9 and BMP10. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 249-251.	5.6	6
4	Distinct intramolecular interactions regulate autoinhibition of vinculin binding in β -catenin and γ -catenin. Journal of Biological Chemistry, 2021, 296, 100582.	3.4	5
5	Novel TGF β 2 Inhibitors Ameliorate Oral Squamous Cell Carcinoma Progression and Improve the Antitumor Immune Response of Anti-PD-L1 Immunotherapy. Molecular Cancer Therapeutics, 2021, 20, 1102-1111.	4.1	11
6	TGFBR3L is an inhibin B co-receptor that regulates female fertility. Science Advances, 2021, 7, eabl4391.	10.3	21
7	Structure and Role of BCOR PUF in Noncanonical PRC1 Assembly and Disease. Biochemistry, 2020, 59, 2718-2728.	2.5	12
8	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
9	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
10	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
11	TGF- β 2 uses the concave surface of its extended finger region to bind betaglycan's ZP domain via three residues specific to TGF- β 2 and inhibin- β 1. Journal of Biological Chemistry, 2019, 294, 3065-3080.	3.4	15
12	A Novel TGF β 2 Trap Blocks Chemotherapeutics-Induced TGF β 21 Signaling and Enhances Their Anticancer Activity in Gynecologic Cancers. Clinical Cancer Research, 2018, 24, 2780-2793.	7.0	45
13	TGF- β 2 uses a novel mode of receptor activation to phosphorylate SMAD1/5 and induce epithelial-to-mesenchymal transition. ELife, 2018, 7, .	6.0	119
14	Structure-guided engineering of TGF- β 2s for the development of novel inhibitors and probing mechanism. Bioorganic and Medicinal Chemistry, 2018, 26, 5239-5246.	3.0	6
15	An engineered transforming growth factor β 2 (TGF- β 2) monomer that functions as a dominant negative to block TGF- β 2 signaling. Journal of Biological Chemistry, 2017, 292, 7173-7188.	3.4	34
16	Structural basis for potency differences between GDF8 and GDF11. BMC Biology, 2017, 15, 19.	3.8	90
17	Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. Nature Methods, 2017, 14, 399-402.	19.0	158
18	Methyl-Labeling Assisted NMR Structure Determination of a 66 KDA Growth Factor-Receptor Complex. Biophysical Journal, 2017, 112, 487a-488a.	0.5	0

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19	ALK1 signaling in development and disease: new paradigms. Cellular and Molecular Life Sciences, 2017, 74, 4539-4560.	5.4	76
20	A structurally distinct TGF- β 2 mimic from an intestinal helminth parasite potently induces regulatory T cells. Nature Communications, 2017, 8, 1741.	12.8	159
21	An introduction to the special issue on biomolecular NMR. Archives of Biochemistry and Biophysics, 2017, 628, 1-2.	3.0	0
22	A novel highly potent trivalent TGF- β 2 receptor trap inhibits early-stage tumorigenesis and tumor cell invasion in murine Pten-deficient prostate glands. Oncotarget, 2016, 7, 86087-86102.	1.8	32
23	Binding Properties of the Transforming Growth Factor- β 2 Coreceptor Betaglycan: Proposed Mechanism for Potentiation of Receptor Complex Assembly and Signaling. Biochemistry, 2016, 55, 6880-6896.	2.5	33
24	Structural Biology and Evolution of the TGF- β 2 Family. Cold Spring Harbor Perspectives in Biology, 2016, 8, a022103.	5.5	267
25	Production, Isolation, and Structural Analysis of Ligands and Receptors of the TGF- β 2 Superfamily. Methods in Molecular Biology, 2016, 1344, 63-92.	0.9	25
26	D2HGDH regulates alpha-ketoglutarate levels and dioxygenase function by modulating IDH2. Nature Communications, 2015, 6, 7768.	12.8	64
27	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
28	Divergence(s) in nodal signaling between aggressive melanoma and embryonic stem cells. International Journal of Cancer, 2015, 136, E242-51.	5.1	13
29	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
30	Biological Activity Differences between TGF- β 21 and TGF- β 23 Correlate with Differences in the Rigidity and Arrangement of Their Component Monomers. Biochemistry, 2014, 53, 5737-5749.	2.5	54
31	The Solution Structure of the Regulatory Domain of Tyrosine Hydroxylase. Journal of Molecular Biology, 2014, 426, 1483-1497.	4.2	47
32	TGF- β 2 Antagonists: Same Knot, but Different Hold. Structure, 2013, 21, 1269-1270.	3.3	7
33	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
34	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
35	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
36	Structure of the Alk1 Extracellular Domain and Characterization of Its Bone Morphogenetic Protein (BMP) Binding Properties. Biochemistry, 2012, 51, 6328-6341.	2.5	35

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37	Structural studies of the TGF β 2s and their receptors – insights into evolution of the TGF β 2 superfamily. <i>FEBS Letters</i> , 2012, 586, 1860-1870.	2.8	185
38	Blockade of Autocrine TGF β 2 Signaling Inhibits Stem Cell Phenotype, Survival, and Metastasis of Murine Breast Cancer Cells. <i>Journal of Stem Cell Research & Therapy</i> , 2012, 02, 1-8.	0.3	38
39	Identification of Nucleic Acid Binding Residues in the FCS Domain of the Polycomb Group Protein Polyhomeotic. <i>Biochemistry</i> , 2011, 50, 4998-5007.	2.5	11
40	Direct evidence for a phenylalanine site in the regulatory domain of phenylalanine hydroxylase. <i>Archives of Biochemistry and Biophysics</i> , 2011, 505, 250-255.	3.0	37
41	The T β RI Pre-Helix Extension Is Structurally Ordered in the Unbound Form and Its Flanking Prolines Are Essential for Binding. <i>Journal of Molecular Biology</i> , 2011, 412, 601-618.	4.2	20
42	Structures of TGF β Receptor Complexes: Implications for Function and Therapeutic Intervention Using Ligand Traps. <i>Current Pharmaceutical Biotechnology</i> , 2011, 12, 2081-2098.	1.6	18
43	TGF β 2 signalling is mediated by two autonomously functioning T β RI:T β RII pairs. <i>EMBO Journal</i> , 2011, 30, 1263-1276.	7.8	98
44	Class II Cytokine Common Receptors: Something Old, Something New. <i>Structure</i> , 2010, 18, 551-552.	3.3	0
45	Polycomb Group Targeting through Different Binding Partners of RING1B C-Terminal Domain. <i>Structure</i> , 2010, 18, 966-975.	3.3	81
46	Ternary Complex of Transforming Growth Factor β 1 Reveals Isoform-specific Ligand Recognition and Receptor Recruitment in the Superfamily. <i>Journal of Biological Chemistry</i> , 2010, 285, 14806-14814.	3.4	135
47	Dynamic Interactions between Clathrin and Locally Structured Elements in a Disordered Protein Mediate Clathrin Lattice Assembly. <i>Journal of Molecular Biology</i> , 2010, 404, 274-290.	4.2	46
48	Peptide ligands that use a novel binding site to target both TGF β 2 receptors. <i>Molecular BioSystems</i> , 2010, 6, 2392.	2.9	25
49	Betaglycan has Two Independent Domains Required for High Affinity TGF β 2 Binding: Proteolytic Cleavage Separates the Domains and Inactivates the Neutralizing Activity of the Soluble Receptor. <i>Biochemistry</i> , 2009, 48, 11755-11765.	2.5	42
50	Characterization of the SRP68/72 interface of human signal recognition particle by systematic site-directed mutagenesis. <i>Protein Science</i> , 2009, 18, 2183-2195.	7.6	11
51	T β RII Discriminates the High- and Low-Affinity TGF β 2 Isoforms via Two Hydrogen-Bonded Ion Pairs. <i>Biochemistry</i> , 2009, 48, 2146-2155.	2.5	53
52	Nuclear Magnetic Resonance Mapping and Functional Confirmation of the Collagen Binding Sites of Matrix Metalloproteinase-2. <i>Biochemistry</i> , 2009, 48, 5822-5831.	2.5	23
53	Kinetic, Dynamic, Ligand Binding Properties, and Structural Models of a Dual-Substrate Specific Nudix Hydrolase from <i>Schizosaccharomyces pombe</i> . <i>Biochemistry</i> , 2009, 48, 6224-6239.	2.5	3
54	A.Âfulgidus SRP54ÂM-domain. <i>Journal of Biomolecular NMR</i> , 2008, 41, 241-8.	2.8	5

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55	Characterization of Ligand-Binding Properties of the Human BMP Type II Receptor Extracellular Domain. <i>Journal of Molecular Biology</i> , 2008, 378, 191-203.	4.2	23
56	Cooperative Assembly of TGF- β Superfamily Signaling Complexes Is Mediated by Two Disparate Mechanisms and Distinct Modes of Receptor Binding. <i>Molecular Cell</i> , 2008, 29, 157-168.	9.7	247
57	Expression, purification and characterization of BGERII: a novel pan-TGF β inhibitor. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 463-473.	2.1	17
58	Structural Transitions of the RING1B C-Terminal Region upon Binding the Polycomb cbox Domain. <i>Biochemistry</i> , 2008, 47, 8007-8015.	2.5	21
59	Structural Basis of J Co-chaperone Binding and Regulation of Hsp70. <i>Molecular Cell</i> , 2007, 28, 422-433.	9.7	206
60	<i>Schistosoma mansoni</i> : TGF- β signaling pathways. <i>Experimental Parasitology</i> , 2007, 117, 304-317.	1.2	80
61	Model-free analysis for large proteins at high magnetic field strengths. <i>Journal of Biomolecular NMR</i> , 2007, 38, 315-324.	2.8	4
62	Three Key Residues Underlie the Differential Affinity of the TGF β Isoforms for the TGF β Type II Receptor. <i>Journal of Molecular Biology</i> , 2006, 355, 47-62.	4.2	77
63	Sequential Resonance Assignment of the Human BMP Type II Receptor Extracellular Domain. <i>Journal of Biomolecular NMR</i> , 2005, 32, 336-336.	2.8	2
64	Structure and Dynamics of the Homodimeric Dynein Light Chain km23. <i>Journal of Molecular Biology</i> , 2005, 352, 338-354.	4.2	34
65	Assembly of T β RI:T β RII:TGF β Ternary Complex in vitro with Receptor Extracellular Domains is Cooperative and Isoform-dependent. <i>Journal of Molecular Biology</i> , 2005, 354, 1052-1068.	4.2	71
66	The conserved adenosine in helix 6 of <i>Archaeoglobus fulgidus</i> signal recognition particle RNA initiates SRP assembly. <i>Archaea</i> , 2004, 1, 269-275.	2.3	10
67	Letter to the Editor: Sequential resonance assignments of the extracellular domain of the human TGF β type II receptor in complex with monomeric TGF β 3. <i>Journal of Biomolecular NMR</i> , 2004, 29, 103-104.	2.8	7
68	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 β type II receptor extracellular domain. <i>Analytical Biochemistry</i> , 2004, 329, 91-103.	2.4	11
69	Solution Structure and Backbone Dynamics of the TGF β Type II Receptor Extracellular Domain. <i>Biochemistry</i> , 2003, 42, 10126-10139.	2.5	28
70	Solution structure of protein SRP19 of <i>Archaeoglobus fulgidus</i> signal recognition particle. <i>Journal of Molecular Biology</i> , 2002, 317, 145-158.	4.2	19
71	Crystal structure of the human T β R2 ectodomain-TGF β 3 complex. <i>Nature Structural Biology</i> , 2002, 9, 203-8.	9.7	130
72	Backbone sequential resonance assignments of yeast iso-2 cytochrome c, reduced and oxidized forms. <i>Journal of Biomolecular NMR</i> , 2002, 22, 93-94.	2.8	2

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73	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
74	Sequence-specific ¹ H, ¹³ C and ¹⁵ N signal assignments and secondary structure of archaeoglobusfulgidus SRP19. Journal of Biomolecular NMR, 2001, 20, 187-188.	2.8	4
75	Complexes with truncated RNAs from the large domain of Archaeoglobus fulgidus signal recognition particle. FEMS Microbiology Letters, 2001, 198, 105-110.	1.8	6
76	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
77	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
78	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
79	Transforming Growth Factor β 1: Three-Dimensional Structure in Solution and Comparison with the X-ray Structure of Transforming Growth Factor β 2. Biochemistry, 1996, 35, 8517-8534.	2.5	175
80	Engineered Disulfide Bonds in Staphylococcal Nuclease: Effects on the Stability and Conformation of the Folded Protein. Biochemistry, 1996, 35, 10328-10338.	2.5	44
81	Three-dimensional solution structure of the HIV-1 protease complexed with DMP323, a novel cyclic urea-type inhibitor, determined by nuclear magnetic resonance spectroscopy. Protein Science, 1996, 5, 495-506.	7.6	72
82	Binding Affinity of Transforming Growth Factor- β 2 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
83	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
84	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
85	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
86	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
87	Overexpression and purification of avian ovomucoid third domains in Escherichia coli. Protein Engineering, Design and Selection, 1993, 6, 221-227.	2.1	17
88	Solvent effects on the energetics of prolyl peptide bond isomerization. Journal of the American Chemical Society, 1992, 114, 5437-5439.	13.7	109
89	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
90	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

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91	Histidine-121 of staphylococcal nuclease. Correction of the H _{δ2} 1H NMR assignment and reinterpretation of the role this residue plays in conformational heterogeneity of the protein. <i>Journal of the American Chemical Society</i> , 1990, 112, 9031-9034.	13.7	8
92	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. <i>Biochemistry</i> , 1990, 29, 4242-4253.	2.5	24
93	Coupling between local structure and global stability of a protein: mutants of staphylococcal nuclease. <i>Biochemistry</i> , 1990, 29, 4516-4525.	2.5	58