

Thomas B Thompson

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

79
papers

2,800
citations

28
h-index

52
g-index

88
ext. papers

3,262
ext. citations

6.2
avg, IF

4.88
L-index

#	Paper	IF	Citations
79	Visceral adipose tissue remodeling in pancreatic ductal adenocarcinoma cachexia: the role of activin A signaling.. <i>Scientific Reports</i> , 2022 , 12, 1659	4.9	0
78	Structures of activin ligand traps using natural sets of type I and type II TGF β receptors.. <i>iScience</i> , 2022 , 25, 103590	6.1	1
77	Characterization of tolloid-mediated cleavage of the GDF8 procomplex. <i>Biochemical Journal</i> , 2021 , 478, 1733-1747	3.8	1
76	Structure of AMH bound to AMHR2 provides insight into a unique signaling pair in the TGF β family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	8
75	Heparin-mediated dimerization of follistatin. <i>Experimental Biology and Medicine</i> , 2021 , 246, 467-482	3.7	2
74	Deletion of Gremlin-2 alters estrous cyclicity and disrupts female fertility in mice <i>Biology of Reproduction</i> , 2021 , 105, 1205-1220	3.9	1
73	Mutational Analysis of the Putative Anti-Müllerian Hormone (AMH) Binding Interface on its Type II Receptor, AMHR2. <i>Endocrinology</i> , 2020 , 161,	4.8	5
72	Characterization of the different oligomeric states of the DAN family antagonists SOSTDC1 and SOST. <i>Biochemical Journal</i> , 2020 , 477, 3167-3182	3.8	1
71	Activin A forms a non-signaling complex with ACVR1 and type II Activin/BMP receptors via its finger 2 tip loop. <i>ELife</i> , 2020 , 9,	8.9	13
70	Functional recombinant apolipoprotein A5 that is stable at high concentrations at physiological pH. <i>Journal of Lipid Research</i> , 2020 , 61, 244-251	6.3	2
69	Structural perspective of BMP ligands and signaling. <i>Bone</i> , 2020 , 140, 115549	4.7	12
68	Mutations in GDF11 and the extracellular antagonist, Follistatin, as a likely cause of Mendelian forms of orofacial clefting in humans. <i>Human Mutation</i> , 2019 , 40, 1813-1825	4.7	14
67	The anti-sigma factor MucA of <i>Pseudomonas aeruginosa</i> : Dramatic differences of a mucA22 vs. a MucA mutant in anaerobic acidified nitrite sensitivity of planktonic and biofilm bacteria in vitro and during chronic murine lung infection. <i>PLoS ONE</i> , 2019 , 14, e0216401	3.7	6
66	Myostatin regulates pituitary development and hepatic IGF1. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019 , 316, E1036-E1049	6	8
65	Structural characterization of an activin class ternary receptor complex reveals a third paradigm for receptor specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 15505-15513	11.5	28
64	Structural biology of the TGF β family. <i>Experimental Biology and Medicine</i> , 2019 , 244, 1530-1546	3.7	15
63	Crystal structure of the WFIKKN2 follistatin domain reveals insight into how it inhibits growth differentiation factor 8 (GDF8) and GDF11. <i>Journal of Biological Chemistry</i> , 2019 , 294, 6333-6343	5.4	6

62	Structural biology: Gaining atomic level insight into the biological function of macromolecules. <i>Experimental Biology and Medicine</i> , 2019 , 244, 1507-1509	3.7	1
61	Structure of the human myostatin precursor and determinants of growth factor latency. <i>EMBO Journal</i> , 2018 , 37, 367-383	13	30
60	Molecular characterization of latent GDF8 reveals mechanisms of activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E866-E875	11.5	23
59	Activins and Inhibins in Female Reproduction 2018 , 202-210		
58	New Insight Into Hyperemesis Gravidarum and a Potential Role for GDF15. <i>Endocrinology</i> , 2018 , 159, 2698-2700	4.8	0
57	A thumbwheel mechanism for APOA1 activation of LCAT activity in HDL. <i>Journal of Lipid Research</i> , 2018 , 59, 1244-1255	6.3	32
56	Analysis and identification of the Grem2 heparin/heparan sulfate-binding motif. <i>Biochemical Journal</i> , 2017 , 474, 1093-1107	3.8	6
55	Coordinated Proliferation and Differentiation of Human-Induced Pluripotent Stem Cell-Derived Cardiac Progenitor Cells Depend on Bone Morphogenetic Protein Signaling Regulation by GREMLIN 2. <i>Stem Cells and Development</i> , 2017 , 26, 678-693	4.4	12
54	Structural basis for potency differences between GDF8 and GDF11. <i>BMC Biology</i> , 2017 , 15, 19	7.3	63
53	BMP and BMP Regulation: Structure and Function 2017 , 73-111		1
52	A consensus model of human apolipoprotein A-I in its monomeric and lipid-free state. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 1093-1099	17.6	36
51	Circulating Growth Differentiation Factor 11/8 Levels Decline With Age. <i>Circulation Research</i> , 2016 , 118, 29-37	15.7	122
50	MuSK is a BMP co-receptor that shapes BMP responses and calcium signaling in muscle cells. <i>Science Signaling</i> , 2016 , 9, ra87	8.8	17
49	BMP Antagonist Gremlin 2 Limits Inflammation After Myocardial Infarction. <i>Circulation Research</i> , 2016 , 119, 434-49	15.7	30
48	An Evaluation of the Crystal Structure of C-terminal Truncated Apolipoprotein A-I in Solution Reveals Structural Dynamics Related to Lipid Binding. <i>Journal of Biological Chemistry</i> , 2016 , 291, 5439-5454	5.4	13
47	Myostatin Attenuation In Vivo Reduces Adiposity, but Activates Adipogenesis. <i>Endocrinology</i> , 2016 , 157, 282-91	4.8	15
46	Biochemistry and Biology of GDF11 and Myostatin: Similarities, Differences, and Questions for Future Investigation. <i>Circulation Research</i> , 2016 , 118, 1125-41; discussion 1142	15.7	116
45	Structure of Gremlin-2 in Complex with GDF5 Gives Insight into DAN-Family-Mediated BMP Antagonism. <i>Cell Reports</i> , 2016 , 16, 2077-2086	10.6	22

44	Alternative binding modes identified for growth and differentiation factor-associated serum protein (GASP) family antagonism of myostatin. <i>Journal of Biological Chemistry</i> , 2015 , 290, 7506-16	5.4	22
43	Role of Conserved Proline Residues in Human Apolipoprotein A-IV Structure and Function. <i>Journal of Biological Chemistry</i> , 2015 , 290, 10689-702	5.4	10
42	Structure of neuroblastoma suppressor of tumorigenicity 1 (NBL1): insights for the functional variability across bone morphogenetic protein (BMP) antagonists. <i>Journal of Biological Chemistry</i> , 2015 , 290, 4759-4771	5.4	20
41	Fibronectin-based scaffold domain proteins that bind myostatin: a patent evaluation of WO2014043344. <i>Expert Opinion on Therapeutic Patents</i> , 2015 , 25, 619-24	6.8	4
40	The structure of human apolipoprotein A-IV as revealed by stable isotope-assisted cross-linking, molecular dynamics, and small angle x-ray scattering. <i>Journal of Biological Chemistry</i> , 2014 , 289, 5596-6084	5.4	22
39	The DAN family: modulators of TGF- β signaling and beyond. <i>Protein Science</i> , 2014 , 23, 999-1012	6.3	53
38	Myostatin stimulates, not inhibits, C2C12 myoblast proliferation. <i>Endocrinology</i> , 2014 , 155, 670-5	4.8	28
37	Amino acid 72 of mouse and human GDF9 mature domain is responsible for altered homodimer bioactivities but has subtle effects on GDF9:BMP15 heterodimer activities. <i>Biology of Reproduction</i> , 2014 , 91, 142	3.9	3
36	Activins bind and signal via bone morphogenetic protein receptor type II (BMPRII) in immortalized gonadotrope-like cells. <i>Cellular Signalling</i> , 2013 , 25, 2717-26	4.9	27
35	Growth differentiation factor 9:bone morphogenetic protein 15 heterodimers are potent regulators of ovarian functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E776-85	11.5	194
34	Structure of protein related to Dan and Cerberus: insights into the mechanism of bone morphogenetic protein antagonism. <i>Structure</i> , 2013 , 21, 1417-29	5.2	46
33	Reply to Mottershead et al.: GDF9:BMP15 heterodimers are potent regulators of ovarian functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E2258	11.5	3
32	Development of a small-molecule screening method for inhibitors of cellular response to myostatin and activin A. <i>Journal of Biomolecular Screening</i> , 2013 , 18, 837-44		19
31	Small-angle X-ray scattering of apolipoprotein A-IV reveals the importance of its termini for structural stability. <i>Journal of Biological Chemistry</i> , 2013 , 288, 4854-66	5.4	10
30	The structure of dimeric apolipoprotein A-IV and its mechanism of self-association. <i>Structure</i> , 2012 , 20, 767-79	5.2	34
29	Members of the DAN family are BMP antagonists that form highly stable noncovalent dimers. <i>Journal of Molecular Biology</i> , 2012 , 424, 313-27	6.5	46
28	Structure of myostatin/follistatin-like 3: N-terminal domains of follistatin-type molecules exhibit alternate modes of binding. <i>Journal of Biological Chemistry</i> , 2012 , 287, 1043-53	5.4	59
27	Expression and purification of recombinant protein related to DAN and cerberus (PRDC). <i>Protein Expression and Purification</i> , 2012 , 82, 389-95	2	8

26	Characterization of follistatin-type domains and their contribution to myostatin and activin A antagonism. <i>Molecular Endocrinology</i> , 2012 , 26, 1167-78		22
25	Analysis of the interaction between heparin and follistatin and heparin and follistatin-ligand complexes using surface plasmon resonance. <i>Biochemistry</i> , 2012 , 51, 6797-803	3.2	11
24	Improving the diffraction of apoA-IV crystals through extreme dehydration. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 105-10		10
23	Cytochrome b ₅ reductase-cytochrome b ₅ as an active P450 redox enzyme system in <i>Phanerochaete chrysosporium</i> : atypical properties and in vivo evidence of electron transfer capability to CYP63A2. <i>Archives of Biochemistry and Biophysics</i> , 2011 , 509, 26-32	4.1	36
22	Structure of dimeric apoA-IV: basis for HDL model. <i>FASEB Journal</i> , 2011 , 25, 938.1		0.9
21	The structure of myostatin:follistatin 288: insights into receptor utilization and heparin binding. <i>EMBO Journal</i> , 2009 , 28, 2662-76	13	117
20	The structure of FSTL3:activin A complex. Differential binding of N-terminal domains influences follistatin-type antagonist specificity. <i>Journal of Biological Chemistry</i> , 2008 , 283, 32831-8	5.4	52
19	The structure of apolipoprotein A-I in high density lipoproteins. <i>Journal of Biological Chemistry</i> , 2007 , 282, 22249-53	5.4	159
18	The structure of the follistatin:activin complex reveals antagonism of both type I and type II receptor binding. <i>Developmental Cell</i> , 2005 , 9, 535-43	10.2	205
17	Structural studies of the parainfluenza virus 5 hemagglutinin-neuraminidase tetramer in complex with its receptor, sialyllactose. <i>Structure</i> , 2005 , 13, 803-15	5.2	161
16	Structural basis for a functional antagonist in the transforming growth factor beta superfamily. <i>Journal of Biological Chemistry</i> , 2005 , 280, 40177-86	5.4	12
15	Structural and functional analysis of tetracenomycin F2 cyclase from <i>Streptomyces glaucescens</i> . A type II polyketide cyclase. <i>Journal of Biological Chemistry</i> , 2004 , 279, 37956-63	5.4	42
14	Molecular biology of inhibin action. <i>Seminars in Reproductive Medicine</i> , 2004 , 22, 269-76	1.4	59
13	Beta A versus beta B: is it merely a matter of expression?. <i>Molecular and Cellular Endocrinology</i> , 2004 , 225, 9-17	4.4	64
12	Structures of an ActRIIB:activin A complex reveal a novel binding mode for TGF-beta ligand:receptor interactions. <i>EMBO Journal</i> , 2003 , 22, 1555-66	13	172
11	Three-dimensional structure of ATP:corrinoid adenosyltransferase from <i>Salmonella typhimurium</i> in its free state, complexed with MgATP, or complexed with hydroxycobalamin and MgATP. <i>Biochemistry</i> , 2001 , 40, 361-74	3.2	63
10	Analysis of the adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase (CobU) enzyme of <i>Salmonella typhimurium</i> LT2. Identification of residue His-46 as the site of guanylylation. <i>Journal of Biological Chemistry</i> , 2000 , 275, 27576-86	5.4	24
9	Evolution of enzymatic activity in the enolase superfamily: structure of o-succinylbenzoate synthase from <i>Escherichia coli</i> in complex with Mg ²⁺ and o-succinylbenzoate. <i>Biochemistry</i> , 2000 , 39, 10662-76	3.2	66

8	Three-dimensional structure of adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase (CobU) complexed with GMP: evidence for a substrate-induced transferase active site. <i>Biochemistry</i> , 1999 , 38, 12995-3005	3.2	27
7	Three-dimensional structure of adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase from <i>Salmonella typhimurium</i> determined to 2.3 Å resolution. <i>Biochemistry</i> , 1998 , 37, 7686-95	3.2	36
6	The 1.5-Å resolution crystal structure of bacterial luciferase in low salt conditions. <i>Journal of Biological Chemistry</i> , 1996 , 271, 21956-68	5.4	99
5	Analysis of the loop-helix interaction in bundle motif protein structures. <i>The Protein Journal</i> , 1995 , 14, 559-66		6
4	Neural network prediction of the HIV-1 protease cleavage sites. <i>Journal of Theoretical Biology</i> , 1995 , 177, 369-79	2.3	79
3	Structure of the human pro-myostatin precursor and determinants of growth factor latency		4
2	The finger 2 tip loop of Activin A is required for the formation of its non-signaling complex with ACVR1 and type II Bone Morphogenetic Protein receptors		1
1	Molecular characterization of latent GDF8 reveals mechanisms of activation		2