Thomas B Thompson

List of Publications by Year
in descending order

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80 papers	3,636 citations	136950 32 h-index	144013 57 g-index
88 all docs	88 docs citations	88 times ranked	4335 citing authors

#	Article	IF	Citations
1	Visceral adipose tissue remodeling in pancreatic ductal adenocarcinoma cachexia: the role of activin A signaling. Scientific Reports, 2022, 12, 1659.	3.3	8
2	Structures of activin ligand traps using natural sets of type I and type II TGFÎ² receptors. IScience, 2022, 25, 103590.	4.1	7
3	Heparin-mediated dimerization of follistatin. Experimental Biology and Medicine, 2021, 246, 467-482.	2.4	3
4	FSTL3-Neutralizing Antibodies Enhance Glucose-Responsive Insulin Secretion in Dysfunctional Male Mouse and Human Islets. Endocrinology, 2021, 162, .	2.8	2
5	Characterization of tolloid-mediated cleavage of the GDF8 procomplex. Biochemical Journal, 2021, 478, 1733-1747.	3.7	4
6	Structure of AMH bound to AMHR2 provides insight into a unique signaling pair in the TGF-Î² family. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	26
7	Deletion of Gremlin-2 alters estrous cyclicity and disrupts female fertility in mice. Biology of Reproduction, 2021, 105, 1205-1220.	2.7	6
8	Functional recombinant apolipoprotein A5 that is stable at high concentrations at physiological pH. Journal of Lipid Research, 2020, 61, 244-251.	4.2	4
9	Structural perspective of BMP ligands and signaling. Bone, 2020, 140, 115549.	2.9	35
10	Mutational Analysis of the Putative Anti-MÃ¼llerian Hormone (AMH) Binding Interface on its Type II Receptor, AMHR2. Endocrinology, 2020, 161, .	2.8	12
11	Activin A forms a non-signaling complex with ACVR1 and type II Activin/BMP receptors via its finger 2 tip loop. ELife, 2020, 9, .	6.0	45
12	Characterization of the different oligomeric states of the DAN family antagonists SOSTDC1 and SOST. Biochemical Journal, 2020, 477, 3167-3182.	3.7	7
13	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
14	Structural biology of the TGFÎ² family. Experimental Biology and Medicine, 2019, 244, 1530-1546.	2.4	26
15	Mutations in GDF11 and the extracellular antagonist, Follistatin, as a likely cause of Mendelian forms of orofacial clefting in humans. Human Mutation, 2019, 40, 1813-1825.	2.5	26
16	The anti-sigma factor MucA of Pseudomonas aeruginosa: Dramatic differences of a mucA22 vs. a Î”mucA mutant in anaerobic acidified nitrite sensitivity of planktonic and biofilm bacteria in vitro and during chronic murine lung infection. PLoS ONE, 2019, 14, e0216401.	2.5	10
17	Myostatin regulates pituitary development and hepatic IGF1. American Journal of Physiology - Endocrinology and Metabolism, 2019, 316, E1036-E1049.	3.5	12
18	Crystal structure of the WFIKKN2 follistatin domain reveals insight into how it inhibits growth differentiation factor 8 (GDF8) and GDF11. Journal of Biological Chemistry, 2019, 294, 6333-6343.	3.4	13

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19	Structural biology: Gaining atomic level insight into the biological function of macromolecules. Experimental Biology and Medicine, 2019, 244, 1507-1509.	2.4	1
20	Front Cover, Volume 40, Issue 10. Human Mutation, 2019, 40, i.	2.5	0
21	Structure of the human myostatin precursor and determinants of growth factor latency. EMBO Journal, 2018, 37, 367-383.	7.8	58
22	Molecular characterization of latent GDF8 reveals mechanisms of activation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E866-E875.	7.1	30
23	A thumbwheel mechanism for APOA1 activation of LCAT activity in HDL[S]. Journal of Lipid Research, 2018, 59, 1244-1255.	4.2	59
24	Activins and Inhibins in Female Reproduction. , 2018, , 202-210.		0
25	New Insight Into Hyperemesis Gravidarum and a Potential Role for GDF15. Endocrinology, 2018, 159, 2698-2700.	2.8	2
26	Analysis and identification of the Grem2 heparin/heparan sulfate-binding motif. Biochemical Journal, 2017, 474, 1093-1107.	3.7	10
27	Coordinated Proliferation and Differentiation of Human-Induced Pluripotent Stem Cell-Derived Cardiac Progenitor Cells Depend on Bone Morphogenetic Protein Signaling Regulation by GREMLIN 2. Stem Cells and Development, 2017, 26, 678-693.	2.1	17
28	Structural basis for potency differences between GDF8 and GDF11. BMC Biology, 2017, 15, 19.	3.8	90
29	BMP and BMP Regulation: Structure and Function. , 2017, , 73-111.		1
30	A consensus model of human apolipoprotein A-I in its monomeric and lipid-free state. Nature Structural and Molecular Biology, 2017, 24, 1093-1099.	8.2	54
31	Biochemistry and Biology of GDF11 and Myostatin. Circulation Research, 2016, 118, 1125-1142.	4.5	155
32	Structure of Gremlin-2 in Complex with GDF5 Gives Insight into DAN-Family-Mediated BMP Antagonism. Cell Reports, 2016, 16, 2077-2086.	6.4	37
33	MuSK is a BMP co-receptor that shapes BMP responses and calcium signaling in muscle cells. Science Signaling, 2016, 9, ra87.	3.6	26
34	BMP Antagonist Gremlin 2 Limits Inflammation After Myocardial Infarction. Circulation Research, 2016, 119, 434-449.	4.5	40
35	An Evaluation of the Crystal Structure of C-terminal Truncated Apolipoprotein A-I in Solution Reveals Structural Dynamics Related to Lipid Binding. Journal of Biological Chemistry, 2016, 291, 5439-5451.	3.4	16
36	Myostatin Attenuation In Vivo Reduces Adiposity, but Activates Adipogenesis. Endocrinology, 2016, 157, 282-291.	2.8	17

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37	Circulating Growth Differentiation Factor 11/8 Levels Decline With Age. Circulation Research, 2016, 118, 29-37.	4.5	161
38	Fibronectin-based scaffold domain proteins that bind myostatin: a patent evaluation of WO2014043344. Expert Opinion on Therapeutic Patents, 2015, 25, 619-624.	5.0	7
39	Alternative Binding Modes Identified for Growth and Differentiation Factor-associated Serum Protein (GASP) Family Antagonism of Myostatin. Journal of Biological Chemistry, 2015, 290, 7506-7516.	3.4	35
40	Role of Conserved Proline Residues in Human Apolipoprotein A-IV Structure and Function. Journal of Biological Chemistry, 2015, 290, 10689-10702.	3.4	11
41	Structure of Neuroblastoma Suppressor of Tumorigenicity 1 (NBL1). Journal of Biological Chemistry, 2015, 290, 4759-4771.	3.4	32
42	Amino Acid 72 of Mouse and Human GDF9 Mature Domain Is Responsible for Altered Homodimer Bioactivities but Has Subtle Effects on GDF9:BMP15 Heterodimer Activities1. Biology of Reproduction, 2014, 91, 142.	2.7	4
43	The Structure of Human Apolipoprotein A-IV as Revealed by Stable Isotope-assisted Cross-linking, Molecular Dynamics, and Small Angle X-ray Scattering. Journal of Biological Chemistry, 2014, 289, 5596-5608.	3.4	26
44	The DAN family: Modulators of TGFâ€Î² signaling and beyond. Protein Science, 2014, 23, 999-1012.	7.6	62
45	Myostatin Stimulates, Not Inhibits, C2C12 Myoblast Proliferation. Endocrinology, 2014, 155, 670-675.	2.8	35
46	Activins bind and signal via bone morphogenetic protein receptor type II (BMPR2) in immortalized gonadotrope-like cells. Cellular Signalling, 2013, 25, 2717-2726.	3.6	30
47	Growth differentiation factor 9:bone morphogenetic protein 15 heterodimers are potent regulators of ovarian functions. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E776-85.	7.1	251
48	Structure of Protein Related to Dan and Cerberus: Insights into the Mechanism of Bone Morphogenetic Protein Antagonism. Structure, 2013, 21, 1417-1429.	3.3	54
49	Reply to Mottershead et al.: GDF9:BMP15 heterodimers are potent regulators of ovarian functions. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2258-E2258.	7.1	6
50	Development of a Small-Molecule Screening Method for Inhibitors of Cellular Response to Myostatin and Activin A. Journal of Biomolecular Screening, 2013, 18, 837-844.	2.6	20
51	Small-angle X-ray Scattering of Apolipoprotein A-IV Reveals the Importance of Its Termini for Structural Stability. Journal of Biological Chemistry, 2013, 288, 4854-4866.	3.4	10
52	Members of the DAN Family Are BMP Antagonists That Form Highly Stable Noncovalent Dimers. Journal of Molecular Biology, 2012, 424, 313-327.	4.2	54
53	Structure of MyostatinÂ·Follistatin-like 3. Journal of Biological Chemistry, 2012, 287, 1043-1053.	3.4	76
54	Expression and purification of recombinant protein related to DAN and cerberus (PRDC). Protein Expression and Purification, 2012, 82, 389-395.	1.3	10

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55	Characterization of Follistatin-Type Domains and Their Contribution to Myostatin and Activin A Antagonism. Molecular Endocrinology, 2012, 26, 1167-1178.	3.7	28
56	Analysis of the Interaction between Heparin and Follistatin and Heparin and Follistatinâ€“Ligand Complexes Using Surface Plasmon Resonance. Biochemistry, 2012, 51, 6797-6803.	2.5	12
57	Improving the diffraction of apoA-IV crystals through extreme dehydration. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 105-110.	0.7	10
58	The Structure of Dimeric Apolipoprotein A-IV and Its Mechanism of Self-Association. Structure, 2012, 20, 767-779.	3.3	39
59	Cytochrome b5 reductaseâ€“cytochrome b5 as an active P450 redox enzyme system in Phanerochaete chrysosporium: Atypical properties and in vivo evidence of electron transfer capability to CYP63A2. Archives of Biochemistry and Biophysics, 2011, 509, 26-32.	3.0	40
60	Structure of dimeric apoAâ€‰IV: basis for HDL model. FASEB Journal, 2011, 25, 938.1.	0.5	0
61	The structure of myostatin:follistatin 288: insights into receptor utilization and heparin binding. EMBO Journal, 2009, 28, 2662-2676.	7.8	148
62	The Structure of FSTL3Â·Activin A Complex. Journal of Biological Chemistry, 2008, 283, 32831-32838.	3.4	63
63	The Structure of Apolipoprotein A-I in High Density Lipoproteins. Journal of Biological Chemistry, 2007, 282, 22249-22253.	3.4	176
64	Structural Studies of the Parainfluenza Virus 5 Hemagglutinin-Neuraminidase Tetramer in Complex with Its Receptor, Sialyllactose. Structure, 2005, 13, 803-815.	3.3	187
65	Structural Basis for a Functional Antagonist in the Transforming Growth Factor Î² Superfamily. Journal of Biological Chemistry, 2005, 280, 40177-40186.	3.4	16
66	The Structure of the Follistatin:Activin Complex Reveals Antagonism of Both Type I and Type II Receptor Binding. Developmental Cell, 2005, 9, 535-543.	7.0	247
67	Structural and Functional Analysis of Tetracenomycin F2 Cyclase from Streptomyces glaucescens. Journal of Biological Chemistry, 2004, 279, 37956-37963.	3.4	54
68	Molecular Biology of Inhibin Action. Seminars in Reproductive Medicine, 2004, 22, 269-276.	1.1	66
69	Beta A versus beta B: is it merely a matter of expression?. Molecular and Cellular Endocrinology, 2004, 225, 9-17.	3.2	70
70	Structures of an ActRIIB:activin A complex reveal a novel binding mode for TGF-beta ligand:receptor interactions. EMBO Journal, 2003, 22, 1555-1566.	7.8	188
71	Three-Dimensional Structure of ATP:Corrinoid Adenosyltransferase fromSalmonella typhimuriumin Its Free State, Complexed with MgATP, or Complexed with Hydroxycobalamin and MgATPâ€‚â€¡. Biochemistry, 2001, 40, 361-374.	2.5	72
72	Analysis of the Adenosylcobinamide Kinase/Adenosylcobinamide-phosphate Guanylyltransferase (CobU) Enzyme of Salmonella typhimurium LT2. Journal of Biological Chemistry, 2000, 275, 27576-27586.	3.4	26

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73	Evolution of Enzymatic Activity in the Enolase Superfamily:â€‰ Structure of o-Succinylbenzoate Synthase from Escherichia coli in Complex with Mg2+ and o-Succinylbenzoate,. Biochemistry, 2000, 39, 10662-10676.	2.5	71
74	Three-Dimensional Structure of Adenosylcobinamide Kinase/Adenosylcobinamide Phosphate Guanylyltransferase (CobU) Complexed with GMP:Â Evidence for a Substrate-Induced Transferase Active Siteâ€,â€¡. Biochemistry, 1999, 38, 12995-13005.	2.5	33
75	Three-Dimensional Structure of Adenosylcobinamide Kinase/Adenosylcobinamide Phosphate Guanylyltransferase fromSalmonella typhimuriumDetermined to 2.3 Ã… Resolutionâ€,â€¡. Biochemistry, 1998, 37, 7686-7695.	2.5	46
76	The 1.5-Ã… Resolution Crystal Structure of Bacterial Luciferase in Low Salt Conditions. Journal of Biological Chemistry, 1996, 271, 21956-21968.	3.4	122
77	Neural Network Prediction of the HIV-1 Protease Cleavage Sites. Journal of Theoretical Biology, 1995, 177, 369-379.	1.7	88
78	Analysis of the loop-helix interaction in bundle motif protein structures. The Protein Journal, 1995, 14, 559-566.	1.1	6
79	The orphan ligand, activin C, signals through activin receptor-like kinase 7. ELife, 0, 11, .	6.0	21
80	Molecular Mechanisms of AMH Signaling. Frontiers in Endocrinology, 0, 13, .	3.5	10