

Matthew C Good

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

4,312
citations

304743

22
h-index

377865

34
g-index

37
all docs

37
docs citations

37
times ranked

6118
citing authors

#	ARTICLE	IF	CITATIONS
1	Co-assembly of liposomes, Dendrimersomes, and Polymersomes with amphiphilic Janus dendrimers conjugated to Mono- and Tris-Nitrilotriacetic Acid (NTA, TrisNTA) enhances protein recruitment. <i>Giant</i> , 2022, 9, 100089.	5.1	17
2	Peeking under the hood of early embryogenesis: Using tools and synthetic biology to understand native control systems and sculpt tissues. <i>Seminars in Cell and Developmental Biology</i> , 2022, , .	5.0	0
3	Patterning Microtubule Network Organization Reshapes Cell-Like Compartments. <i>ACS Synthetic Biology</i> , 2021, 10, 1338-1350.	3.8	4
4	Designer membraneless organelles sequester native factors for control of cell behavior. <i>Nature Chemical Biology</i> , 2021, 17, 998-1007.	8.0	60
5	OptoLRP6 Illuminates Wnt Signaling in Early Embryo Development. <i>Journal of Molecular Biology</i> , 2021, 433, 167053.	4.2	3
6	Incorporation and Assembly of a Light-Emitting Enzymatic Reaction into Model Protein Condensates. <i>Biochemistry</i> , 2021, 60, 3137-3151.	2.5	6
7	Nuclear sizER in Early Development. <i>Developmental Cell</i> , 2020, 54, 297-298.	7.0	1
8	Integrating cellular dimensions with cell differentiation during early development. <i>Current Opinion in Cell Biology</i> , 2020, 67, 109-117.	5.4	10
9	Direct Visualization of Vesicle Disassembly and Reassembly Using Photocleavable Dendrimers Elucidates Cargo Release Mechanisms. <i>ACS Nano</i> , 2020, 14, 7398-7411.	14.6	27
10	Identifying sequence perturbations to an intrinsically disordered protein that determine its phase-separation behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11421-11431.	7.1	202
11	SPLIT: Stable Protein Coacervation Using a Light Induced Transition. <i>ACS Synthetic Biology</i> , 2020, 9, 500-507.	3.8	44
12	Imaging nascent transcription in wholemount vertebrate embryos to characterize zygotic genome activation. <i>Methods in Enzymology</i> , 2020, 638, 139-165.	1.0	2
13	A <i>C. elegans</i> Zona Pellucida domain protein functions via its ZPc domain. <i>PLoS Genetics</i> , 2020, 16, e1009188.	3.5	8
14	Encapsulation of hydrophobic components in dendrimersomes and decoration of their surface with proteins and nucleic acids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15378-15385.	7.1	41
15	Spatiotemporal Patterning of Zygotic Genome Activation in a Model Vertebrate Embryo. <i>Developmental Cell</i> , 2019, 49, 852-866.e7.	7.0	54
16	Encoding biological recognition in a bicomponent cell-membrane mimic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5376-5382.	7.1	51
17	Optochemical Control of Protein Localization and Activity within Cell-like Compartments. <i>Biochemistry</i> , 2018, 57, 2590-2596.	2.5	26
18	Cell parts to complex processes, from the bottom up. <i>Nature</i> , 2018, 563, 188-189.	27.8	18

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19	Preparation of Cellular Extracts from <i>Xenopus</i> Eggs and Embryos. Cold Spring Harbor Protocols, 2018, 2018, pdb.prot097055.	0.3	38
20	Controllable protein phase separation and modular recruitment to form responsive membraneless organelles. Nature Communications, 2018, 9, 2985.	12.8	274
21	Probing the biology of cell boundary conditions through confinement of <i>Xenopus</i> cell-free cytoplasmic extracts. Genesis, 2017, 55, e23013.	1.6	8
22	Encapsulation of <i>Xenopus</i> Egg and Embryo Extract Spindle Assembly Reactions in Synthetic Cell-Like Compartments with Tunable Size. Methods in Molecular Biology, 2016, 1413, 87-108.	0.9	8
23	Size Regulation: Big Insights from Little Cells. Developmental Cell, 2016, 37, 392-394.	7.0	0
24	A Comparative Analysis of Spindle Morphometrics across Metazoans. Current Biology, 2015, 25, 1542-1550.	3.9	98
25	Turn Up the Volume: Uncovering Nucleus Size Control Mechanisms. Developmental Cell, 2015, 33, 496-497.	7.0	3
26	Cytoplasmic Volume Modulates Spindle Size During Embryogenesis. Science, 2013, 342, 856-860.	12.6	234
27	Scaffold Proteins: Hubs for Controlling the Flow of Cellular Information. Science, 2011, 332, 680-686.	12.6	756
28	Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. Science Signaling, 2010, 3, ra12.	3.6	341
29	Allosteric Activation Mechanism of the Mycobacterium tuberculosis Receptor Ser/Thr Protein Kinase, PknB. Structure, 2010, 18, 1667-1677.	3.3	50
30	The Ste5 Scaffold Directs Mating Signaling by Catalytically Unlocking the Fus3 MAP Kinase for Activation. Cell, 2009, 136, 1085-1097.	28.9	177
31	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. Nature, 2008, 451, 783-788.	27.8	1,006
32	The Ste5 Scaffold Allosterically Modulates Signaling Output of the Yeast Mating Pathway. Science, 2006, 311, 822-826.	12.6	266
33	Docking interactions in protein kinase and phosphatase networks. Current Opinion in Structural Biology, 2006, 16, 676-685.	5.7	168
34	The Role of Docking Interactions in Mediating Signaling Input, Output, and Discrimination in the Yeast MAPK Network. Molecular Cell, 2005, 20, 951-962.	9.7	145
35	An Alternate Conformation and a Third Metal in PstP/Ppp, the <i>M. tuberculosis</i> PP2C-Family Ser/Thr Protein Phosphatase. Structure, 2004, 12, 1947-1954.	3.3	96
36	Sensor Domain of the Mycobacterium tuberculosis Receptor Ser/Thr Protein Kinase, PknD, forms a Highly Symmetric \hat{I}^2 Propeller. Journal of Molecular Biology, 2004, 339, 459-469.	4.2	65