

# Nicholas G Brown

## List of Publications by Year in descending order

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41  
papers

2,024  
citations

279701

23  
h-index

302012

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44  
all docs

44  
docs citations

44  
times ranked

2641  
citing authors

#	ARTICLE	IF	CITATIONS
1	APC7 mediates ubiquitin signaling in constitutive heterochromatin in the developing mammalian brain. <i>Molecular Cell</i> , 2022, 82, 90-105.e13.	4.5	4
2	Cryo-EM structure of the plant 26S proteasome. <i>Plant Communications</i> , 2022, 3, 100310.	3.6	7
3	Functional conservation and divergence of the helix-helix motif of E2 ubiquitin-conjugating enzymes. <i>EMBO Journal</i> , 2022, 41, e108823.	3.5	8
4	Examining the mechanistic relationship of APC/C and its interphase inhibitor EMI1. <i>Protein Science</i> , 2022, 31, .	3.1	4
5	Intricate Regulatory Mechanisms of the Anaphase-Promoting Complex/Cyclosome and Its Role in Chromatin Regulation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 687515.	1.8	13
6	Cyclin F drives proliferation through SCF-dependent degradation of the retinoblastoma-like tumor suppressor p130/RBL2. <i>ELife</i> , 2021, 10, .	2.8	9
7	USP15 suppresses tumor immunity via deubiquitylation and inactivation of TET2. <i>Science Advances</i> , 2020, 6, .	4.7	28
8	Ubiquitin chain-elongating enzyme UBE2S activates the RING E3 ligase APC/C for substrate priming. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 550-560.	3.6	26
9	Paradoxical mitotic exit induced by a small molecule inhibitor of APC/CCdc20. <i>Nature Chemical Biology</i> , 2020, 16, 546-555.	3.9	16
10	Comprehensive nucleosome interactome screen establishes fundamental principles of nucleosome binding. <i>Nucleic Acids Research</i> , 2020, 48, 9415-9432.	6.5	67
11	Quantifying the heterogeneity of macromolecular machines by mass photometry. <i>Nature Communications</i> , 2020, 11, 1772.	5.8	146
12	In silico APC/C substrate discovery reveals cell cycle-dependent degradation of UHRF1 and other chromatin regulators. <i>PLoS Biology</i> , 2020, 18, e3000975.	2.6	7
13	UBE2S Learns Self-Control. <i>Structure</i> , 2019, 27, 1185-1187.	1.6	0
14	Protein engineering of a ubiquitin-variant inhibitor of APC/C identifies a cryptic K48 ubiquitin chain binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17280-17289.	3.3	22
15	Posing the APC/C E3 Ubiquitin Ligase to Orchestrate Cell Division. <i>Trends in Cell Biology</i> , 2019, 29, 117-134.	3.6	101
16	Cezanne/OTUD 7B is a cell cycle-regulated deubiquitinase that antagonizes the degradation of APC/C substrates. <i>EMBO Journal</i> , 2018, 37, .	3.5	60
17	Mechanism of APC/C CDC20 activation by mitotic phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2570-8.	3.3	112
18	biGBac enables rapid gene assembly for the expression of large multisubunit protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2564-9.	3.3	263

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19	Cryo-EM of Mitotic Checkpoint Complex-Bound APC/C Reveals Reciprocal and Conformational Regulation of Ubiquitin Ligation. <i>Molecular Cell</i> , 2016, 63, 593-607.	4.5	123
20	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. <i>Cell</i> , 2016, 165, 1440-1453.	13.5	126
21	Measuring APC/C-Dependent Ubiquitylation In Vitro. <i>Methods in Molecular Biology</i> , 2016, 1342, 287-303.	0.4	12
22	Molecular Basis for the Catalytic Specificity of the CTX-M Extended-Spectrum $\beta$ -Lactamases. <i>Biochemistry</i> , 2015, 54, 447-457.	1.2	50
23	RING E3 mechanism for ubiquitin ligation to a disordered substrate visualized for human anaphase-promoting complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5272-5279.	3.3	80
24	Structure of an APC3-APC16 Complex: Insights into Assembly of the Anaphase-Promoting Complex/Cyclosome. <i>Journal of Molecular Biology</i> , 2015, 427, 1748-1764.	2.0	35
25	Role of $\beta$ -Lactamase residues in a common interface for binding the structurally unrelated inhibitory proteins BLIP and BLIP-II. <i>Protein Science</i> , 2014, 23, 1235-1246.	3.1	13
26	Probing the Sites of Interactions of Rotaviral Proteins Involved in Replication. <i>Journal of Virology</i> , 2014, 88, 12866-12881.	1.5	29
27	Mechanism of Polyubiquitination by Human Anaphase-Promoting Complex: RING Repurposing for Ubiquitin Chain Assembly. <i>Molecular Cell</i> , 2014, 56, 246-260.	4.5	98
28	Electron microscopy structure of human APC/CCDH1-EMI1 reveals multimodal mechanism of E3 ligase shutdown. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 827-835.	3.6	82
29	BLIP-II Is a Highly Potent Inhibitor of <i>Klebsiella pneumoniae</i> Carbapenemase (KPC-2). <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3398-3401.	1.4	13
30	Identification of the $\beta$ -Lactamase Inhibitor Protein-II (BLIP-II) Interface Residues Essential for Binding Affinity and Specificity for Class A $\beta$ -Lactamases. <i>Journal of Biological Chemistry</i> , 2013, 288, 17156-17166.	1.6	15
31	Characterization of a novel interaction between BLIP-II and <i>Staphylococcus aureus</i> PBP2a. <i>FASEB Journal</i> , 2013, 27, 1013.2.	0.2	0
32	Mutagenesis of Zinc Ligand Residue Cys221 Reveals Plasticity in the IMP-1 Metallo- $\beta$ -Lactamase Active Site. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 5667-5677.	1.4	22
33	APC15 mediates CDC20 autoubiquitylation by APC/CMCC and disassembly of the mitotic checkpoint complex. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1116-1123.	3.6	118
34	Deep Sequencing of Systematic Combinatorial Libraries Reveals $\beta$ -Lactamase Sequence Constraints at High Resolution. <i>Journal of Molecular Biology</i> , 2012, 424, 150-167.	2.0	76
35	Analysis of the Functional Contributions of Asn233 in Metallo- $\beta$ -Lactamase IMP-1. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 5696-5702.	1.4	30
36	An amino-terminal signal peptide of Vfr protein negatively influences RopB-dependent SpeB expression and attenuates virulence in <i>Streptococcus pyogenes</i> . <i>Molecular Microbiology</i> , 2011, 82, 1481-1495.	1.2	32

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37	Use of periplasmic target protein capture for phage display engineering of tight-binding protein-protein interactions. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 819-828.	1.0	4
38	Analysis of the Binding Forces Driving the Tight Interactions between $\beta$ -Lactamase Inhibitory Protein-II (BLIP-II) and Class A $\beta$ -Lactamases. <i>Journal of Biological Chemistry</i> , 2011, 286, 32723-32735.	1.6	18
39	Multiple Global Suppressors of Protein Stability Defects Facilitate the Evolution of Extended-Spectrum TEM $\beta$ -Lactamases. <i>Journal of Molecular Biology</i> , 2010, 404, 832-846.	2.0	71
40	Structural and Biochemical Evidence That a TEM-1 $\beta$ -Lactamase N170G Active Site Mutant Acts via Substrate-assisted Catalysis. <i>Journal of Biological Chemistry</i> , 2009, 284, 33703-33712.	1.6	45
41	Analysis of the plasticity of location of the Arg244 positive charge within the active site of the TEM $\beta$ -Lactamase. <i>Protein Science</i> , 2009, 18, 2080-2089.	3.1	35