

David Barford

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

6,290
citations

159585

30
h-index

206112

48
g-index

68
all docs

68
docs citations

68
times ranked

8917
citing authors

#	ARTICLE	IF	CITATIONS
1	The APC/C targets the Cep152&Cep63 complex at the centrosome to regulate mitotic spindle assembly. <i>Journal of Cell Science</i> , 2022, 135, .	2.0	7
2	Dame Louise Napier Johnson. 26 September 1940&25 September 2012. <i>Biographical Memoirs of Fellows of the Royal Society</i> , 2022, 72, 221-250.	0.1	0
3	Structure of the human inner kinetochore bound to a centromeric CENP-A nucleosome. <i>Science</i> , 2022, 376, 844-852.	12.6	40
4	Structure of the SARS-CoV-2 RNA-dependent RNA polymerase in the presence of favipiravir-RTP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	144
5	Molecular mechanisms of APC/C release from spindle assembly checkpoint inhibition by APC/C SUMOylation. <i>Cell Reports</i> , 2021, 34, 108929.	6.4	12
6	Molecular mechanism of Mad1 kinetochore targeting by phosphorylated Bub1. <i>EMBO Reports</i> , 2021, 22, e52242.	4.5	26
7	Structural basis of human separase regulation by securin and CDK1&cyclin B1. <i>Nature</i> , 2021, 596, 138-142.	27.8	51
8	Structural interconversions of the anaphase-promoting complex/cyclosome (APC/C) regulate cell cycle transitions. <i>Current Opinion in Structural Biology</i> , 2020, 61, 86-97.	5.7	38
9	Structure of the DOCK2&ELMO1 complex provides insights into regulation of the auto-inhibited state. <i>Nature Communications</i> , 2020, 11, 3464.	12.8	34
10	Crystal structure of the Cenp-HIKHead-TW sub-module of the inner kinetochore CCAN complex. <i>Nucleic Acids Research</i> , 2020, 48, 11172-11184.	14.5	16
11	A unique binding mode of Nek2A to the <scp>APC</scp> /C allows its ubiquitination during prometaphase. <i>EMBO Reports</i> , 2020, 21, e49831.	4.5	18
12	Cyclin A2 degradation during the spindle assembly checkpoint requires multiple binding modes to the APC/C. <i>Nature Communications</i> , 2019, 10, 3863.	12.8	36
13	Structure of the inner kinetochore CCAN complex assembled onto a centromeric nucleosome. <i>Nature</i> , 2019, 574, 278-282.	27.8	113
14	A MAD way to regulate mitosis. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 135-135.	37.0	0
15	Architecture of the CBF3¢romere complex of the budding yeast kinetochore. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 1103-1110.	8.2	23
16	Methods for Preparing Cryo-EM Grids of Large Macromolecular Complexes. <i>Methods in Molecular Biology</i> , 2018, 1844, 209-215.	0.9	1
17	Mechanism for remodelling of the cell cycle checkpoint protein MAD2 by the ATPase TRIP13. <i>Nature</i> , 2018, 559, 274-278.	27.8	109
18	Cryo-EM structure of a metazoan separase&securin complex at near-atomic resolution. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 414-418.	8.2	65

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19	Visualizing the complex functions and mechanisms of the anaphase promoting complex/cyclosome (APC/C). <i>Open Biology</i> , 2017, 7, 170204.	3.6	133
20	The potential of cryo-electron microscopy for structure-based drug design. <i>Essays in Biochemistry</i> , 2017, 61, 543-560.	4.7	34
21	Data collection with a tailored X-ray beam size at 2.69 Å wavelength (4.6 keV): sulfur SAD phasing of Cdc23Nterm. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 403-412.	2.3	10
22	Editorial overview: Macromolecular machines and assemblies. <i>Current Opinion in Structural Biology</i> , 2016, 37, vi-viii.	5.7	0
23	Molecular mechanism of APC/C activation by mitotic phosphorylation. <i>Nature</i> , 2016, 533, 260-264.	27.8	159
24	WD40 domain of Apc1 is critical for the coactivator-induced allosteric transition that stimulates APC/C catalytic activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10547-10552.	7.1	16
25	Molecular basis of APC/C regulation by the spindle assembly checkpoint. <i>Nature</i> , 2016, 536, 431-436.	27.8	178
26	Recombinant expression and reconstitution of multiprotein complexes by the USER cloning method in the insect cell-baculovirus expression system. <i>Methods</i> , 2016, 95, 13-25.	3.8	49
27	Understanding the structural basis for controlling chromosome division. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2015, 373, 20130392.	3.4	10
28	Atomic structure of the APC/C and its mechanism of protein ubiquitination. <i>Nature</i> , 2015, 522, 450-454.	27.8	208
29	Atomic-Resolution Structures of the APC/C Subunits Apc4 and the Apc5 N-Terminal Domain. <i>Journal of Molecular Biology</i> , 2015, 427, 3300-3315.	4.2	10
30	Molecular architecture and mechanism of the anaphase-promoting complex. <i>Nature</i> , 2014, 513, 388-393.	27.8	180
31	Insights into the anaphase-promoting complex: a molecular machine that regulates mitosis. <i>Current Opinion in Structural Biology</i> , 2014, 29, 1-9.	5.7	99
32	The Four Canonical TPR Subunits of Human APC/C Form Related Homo-Dimeric Structures and Stack in Parallel to Form a TPR Suprahelix. <i>Journal of Molecular Biology</i> , 2013, 425, 4236-4248.	4.2	20
33	Baculovirus expression: tackling the complexity challenge. <i>Current Opinion in Structural Biology</i> , 2013, 23, 357-364.	5.7	28
34	Insights into Degron Recognition by APC/C Coactivators from the Structure of an Acm1-Cdh1 Complex. <i>Molecular Cell</i> , 2013, 50, 649-660.	9.7	115
35	Recombinant expression, reconstitution and structure of human anaphase-promoting complex (APC/C). <i>Biochemical Journal</i> , 2013, 449, 365-371.	3.7	48
36	Structure of the mitotic checkpoint complex. <i>Nature</i> , 2012, 484, 208-213.	27.8	270

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37	The Structure of the 26S Proteasome Subunit Rpn2 Reveals Its PC Repeat Domain as a Closed Toroid of Two Concentric α -Helical Rings. <i>Structure</i> , 2012, 20, 513-521.	3.3	60
38	Structure, function and mechanism of the anaphase promoting complex (APC/C). <i>Quarterly Reviews of Biophysics</i> , 2011, 44, 153-190.	5.7	80
39	Structures of APC/CCdh1 with substrates identify Cdh1 and Apc10 as the D-box co-receptor. <i>Nature</i> , 2011, 470, 274-278.	27.8	176
40	Structural basis for the subunit assembly of the anaphase-promoting complex. <i>Nature</i> , 2011, 470, 227-232.	27.8	150
41	Structural insights into anaphase-promoting complex function and mechanism. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 3605-3624.	4.0	73
42	Multiple Factors Confer Specific Cdc42 and Rac Protein Activation by Dedicator of Cytokinesis (DOCK) Nucleotide Exchange Factors. <i>Journal of Biological Chemistry</i> , 2011, 286, 25341-25351.	3.4	81
43	The APC/C subunit Cdc16/Cut9 is a contiguous tetratricopeptide repeat superhelix with a homo-dimer interface similar to Cdc27. <i>EMBO Journal</i> , 2010, 29, 3733-3744.	7.8	68
44	Molecular Structure of the N-terminal Domain of the APC/C Subunit Cdc27 Reveals a Homo-dimeric Tetratricopeptide Repeat Architecture. <i>Journal of Molecular Biology</i> , 2010, 397, 1316-1328.	4.2	29
45	Activation of Rho GTPases by DOCK Exchange Factors Is Mediated by a Nucleotide Sensor. <i>Science</i> , 2009, 325, 1398-1402.	12.6	103
46	An α -Helical Extension of the ELMO1 Pleckstrin Homology Domain Mediates Direct Interaction to DOCK180 and Is Critical in Rac Signaling. <i>Molecular Biology of the Cell</i> , 2008, 19, 4837-4851.	2.1	85
47	Structural Analysis of the Anaphase-Promoting Complex Reveals Multiple Active Sites and Insights into Polyubiquitylation. <i>Molecular Cell</i> , 2005, 20, 855-866.	9.7	81
48	The role of cysteine residues as redox-sensitive regulatory switches. <i>Current Opinion in Structural Biology</i> , 2004, 14, 679-686.	5.7	293
49	Mechanism of Activation of the RAF-ERK Signaling Pathway by Oncogenic Mutations of B-RAF. <i>Cell</i> , 2004, 116, 855-867.	28.9	2,479
50	Doc1 mediates the activity of the anaphase-promoting complex by contributing to substrate recognition. <i>EMBO Journal</i> , 2003, 22, 786-796.	7.8	176
51	Implications for the Ubiquitination Reaction of the Anaphase-promoting Complex from the Crystal Structure of the Doc1/Apc10 Subunit. <i>Journal of Molecular Biology</i> , 2002, 316, 955-968.	4.2	48
52	Protein Tyrosine Phosphatases: X-Ray Crystallographic Observation of Cysteinyl-Phosphate Reaction Intermediate. <i>Methods in Enzymology</i> , 2002, 354, 237-251.	1.0	0