## **Richard Bayliss**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7470181/publications.pdf

Version: 2024-02-01

77 papers

4,856 citations

38 h-index 66 g-index

77 all docs

77 docs citations

77 times ranked

7625 citing authors

#	Article	IF	CITATIONS
1	Exploring the Conformational Landscape and Stability of Aurora A Using Ion-Mobility Mass Spectrometry and Molecular Modeling. Journal of the American Society for Mass Spectrometry, 2022, 33, 420-435.	1.2	3
2	Combined inhibition of Aurora-A and ATR kinases results in regression of MYCN-amplified neuroblastoma. Nature Cancer, 2021, 2, 312-326.	5.7	50
3	Drugging the "Undruggable―MYCN Oncogenic Transcription Factor: Overcoming Previous Obstacles to Impact Childhood Cancers. Cancer Research, 2021, 81, 1627-1632.	0.4	25
4	Phaseâ€separated foci of EML4â€ALK facilitate signalling and depend upon an active kinase conformation. EMBO Reports, 2021, 22, e53693.	2.0	31
5	Defining endogenous TACC3–chTOG–clathrin–GTSE1 interactions at the mitotic spindle using induced relocalization. Journal of Cell Science, 2021, 134, .	1.2	7
6	Covalent Aurora A regulation by the metabolic integrator coenzyme A. Redox Biology, 2020, 28, 101318.	3.9	45
7	Discovery and Optimization of wt-RET/KDR-Selective Inhibitors of RET <sup>V804M</sup> Kinase. ACS Medicinal Chemistry Letters, 2020, 11, 497-505.	1.3	8
8	EML4-ALK V3 oncogenic fusion proteins promote microtubule stabilization and accelerated migration through NEK9 and NEK7. Journal of Cell Science, 2020, 133, .	1.2	30
9	2-Arylamino-6-ethynylpurines are cysteine-targeting irreversible inhibitors of Nek2 kinase. RSC Medicinal Chemistry, 2020, 11, 707-731.	1.7	8
10	Orally bioavailable CDK9/2 inhibitor shows mechanism-based therapeutic potential in MYCN-driven neuroblastoma. Journal of Clinical Investigation, 2020, 130, 5875-5892.	3.9	40
11	Mitotic phosphorylation by NEK6 and NEK7 reduces the microtubule affinity of EML4 to promote chromosome congression. Science Signaling, 2019, 12, .	1.6	30
12	Construction of a Shapeâ€Diverse Fragment Set: Design, Synthesis and Screen against Auroraâ€A Kinase. Chemistry - A European Journal, 2019, 25, 6831-6839.	1.7	26
13	Binding to an Unusual Inactive Kinase Conformation by Highly Selective Inhibitors of Inositol-Requiring Enzyme $1\hat{l}_{\pm}$ Kinase-Endoribonuclease. Journal of Medicinal Chemistry, 2019, 62, 2447-2465.	2.9	23
14	Solution NMR assignment of the C-terminal domain of human chTOG. Biomolecular NMR Assignments, 2018, 12, 221-224.	0.4	5
15	Mitotic spindle association of TACC3 requires Auroraâ€Aâ€dependent stabilization of a cryptic αâ€helix. EMBO Journal, 2018, 37, .	<b>3.</b> 5	55
16	New tools for evaluating protein tyrosine sulfation and carbohydrate sulfation. Biochemical Journal, 2018, 475, 3035-3037.	1.7	6
17	Type II Kinase Inhibitors Targeting Cys-Gatekeeper Kinases Display Orthogonality with Wild Type and Ala/Gly-Gatekeeper Kinases. ACS Chemical Biology, 2018, 13, 2956-2965.	1.6	10
18	Synthesis and profiling of a 3-aminopyridin-2-one-based kinase targeted fragment library: Identification of 3-amino-5-(pyridin-4-yl)pyridin-2(1H)-one scaffold for monopolar spindle 1 (MPS1) and Aurora kinases inhibition. Bioorganic and Medicinal Chemistry, 2018, 26, 3021-3029.	1.4	7

#	Article	IF	CITATIONS
19	Mitotic phosphorylation regulates Hsp72 spindle localization by uncoupling ATP binding from substrate release. Science Signaling, $2018,11,.$	1.6	8
20	A moving target: structure and disorder in pursuit of Myc inhibitors. Biochemical Society Transactions, 2017, 45, 709-717.	1.6	26
21	Neurodevelopmental protein Musashi-1 interacts with the Zika genome and promotes viral replication. Science, 2017, 357, 83-88.	6.0	152
22	Switching Auroraâ€A kinase on and off at an allosteric site. FEBS Journal, 2017, 284, 2947-2954.	2.2	27
23	Differential protein stability and clinical responses of EML4-ALK fusion variants to various ALK inhibitors in advanced ALK-rearranged non-small cell lung cancer. Annals of Oncology, 2017, 28, 791-797.	0.6	178
24	Characterization of Three Druggable Hot-Spots in the Aurora-A/TPX2 Interaction Using Biochemical, Biophysical, and Fragment-Based Approaches. ACS Chemical Biology, 2017, 12, 2906-2914.	1.6	40
25	Hsp72 and Nek6 Cooperate to Cluster Amplified Centrosomes in Cancer Cells. Cancer Research, 2017, 77, 4785-4796.	0.4	24
26	EML4-ALK Variants: Biological and Molecular Properties, and the Implications for Patients. Cancers, 2017, 9, 118.	1.7	147
27	Mitotic Regulation by NEK Kinase Networks. Frontiers in Cell and Developmental Biology, 2017, 5, 102.	1.8	68
28	Structure-guided design of purine-based probes for selective Nek2 inhibition. Oncotarget, 2017, 8, 19089-19124.	0.8	13
29	A closed conformation of the Caenorhabditis elegans separase–securin complex. Open Biology, 2016, 6, 160032.	1.5	10
30	Detection of Ligandâ€induced Conformational Changes in the Activation Loop of Auroraâ€A Kinase by PELDOR Spectroscopy. ChemistryOpen, 2016, 5, 531-534.	0.9	5
31	Structure of a Potential Therapeutic Antibody Bound to Interleukin-16 (IL-16). Journal of Biological Chemistry, 2016, 291, 16840-16848.	1.6	11
32	Allosteric inhibition of Aurora-A kinase by a synthetic vNAR domain. Open Biology, 2016, 6, 160089.	1.5	39
33	Structural basis of N-Myc binding by Aurora-A and its destabilization by kinase inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13726-13731.	3.3	130
34	EML proteins in microtubule regulation and human disease. Biochemical Society Transactions, 2016, 44, 1281-1288.	1.6	24
35	A TPX2 Proteomimetic Has Enhanced Affinity for Aurora-A Due to Hydrocarbon Stapling of a Helix. ACS Chemical Biology, 2016, 11, 3383-3390.	1.6	20
36	Molecular mechanisms that underpin EML4-ALK driven cancers and their response to targeted drugs. Cellular and Molecular Life Sciences, 2016, 73, 1209-1224.	2.4	80

#	Article	IF	CITATIONS
37	Structural Insights into Separase Architecture and Substrate Recognition through Computational Modelling of Caspase-Like and Death Domains. PLoS Computational Biology, 2015, 11, e1004548.	1.5	20
38	Efficient genetic encoding of phosphoserine and its nonhydrolyzable analog. Nature Chemical Biology, 2015, 11, 496-503.	3.9	189
39	Solution NMR assignment of the cryptic sixth TOG domain of mini spindles. Biomolecular NMR Assignments, 2015, 9, 411-413.	0.4	5
40	TACC3–ch-TOG track the growing tips of microtubules independently of clathrin and Aurora-A phosphorylation. Biology Open, 2015, 4, 170-179.	0.6	43
41	Hsp72 is targeted to the mitotic spindle by Nek6 to promote K-fiber assembly and mitotic progression. Journal of Cell Biology, 2015, 209, 349-358.	2.3	44
42	7-(Pyrazol-4-yl)-3H-imidazo[4,5-b]pyridine-based derivatives for kinase inhibition: Co-crystallisation studies with Aurora-A reveal distinct differences in the orientation of the pyrazole N1-substituent. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 4203-4209.	1.0	13
43	Aurora-A-Dependent Control of TACC3 Influences the Rate of Mitotic Spindle Assembly. PLoS Genetics, 2015, 11, e1005345.	1.5	43
44	Diverse Functionalization of Aurora-A Kinase at Specified Surface and Buried Sites by Native Chemical Modification. PLoS ONE, 2014, 9, e103935.	1.1	10
45	Crystal structure of EML1 reveals the basis for Hsp90 dependence of oncogenic EML4-ALK by disruption of an atypical $\hat{l}^2$ -propeller domain. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5195-5200.	3.3	93
46	The primary cilium. Organogenesis, 2014, 10, 62-68.	0.4	70
47	Crystal structures of the phosphorylated <scp>BRI</scp> 1 kinase domain and implications for brassinosteroid signal initiation. Plant Journal, 2014, 78, 31-43.	2.8	142
48	A Kinetic Test Characterizes Kinase Intramolecular and Intermolecular Autophosphorylation Mechanisms. Science Signaling, 2013, 6, ra54.	1.6	51
49	Aurora Isoform Selectivity: Design and Synthesis of Imidazo[4,5- <i>b</i> ) pyridine Derivatives as Highly Selective Inhibitors of Aurora-A Kinase in Cells. Journal of Medicinal Chemistry, 2013, 56, 9122-9135.	2.9	70
50	Insights into Aurora-A Kinase Activation Using Unnatural Amino Acids Incorporated by Chemical Modification. ACS Chemical Biology, 2013, 8, 2184-2191.	1.6	39
51	Coordination of adjacent domains mediates TACC3–ch-TOG–clathrin assembly and mitotic spindle binding. Journal of Cell Biology, 2013, 202, 463-478.	2.3	76
52	The structural mechanisms that underpin mitotic kinase activation. Biochemical Society Transactions, 2013, 41, 1037-1041.	1.6	14
53	Activation of Aurora-A Kinase by Protein Partner Binding and Phosphorylation Are Independent and Synergistic. Journal of Biological Chemistry, 2012, 287, 1150-1157.	1.6	91
54	Cell cycle regulation by the NEK family of protein kinases. Journal of Cell Science, 2012, 125, 4423-33.	1.2	289

#	Article	lF	Citations
55	The Nek8 protein kinase, mutated in the human cystic kidney disease nephronophthisis, is both activated and degraded during ciliogenesis. Human Molecular Genetics, 2012, 21, 1155-1171.	1.4	55
56	On the molecular mechanisms of mitotic kinase activation. Open Biology, 2012, 2, 120136.	1.5	92
57	Optimization of Imidazo[4,5- <i>b</i> ]pyridine-Based Kinase Inhibitors: Identification of a Dual FLT3/Aurora Kinase Inhibitor as an Orally Bioavailable Preclinical Development Candidate for the Treatment of Acute Myeloid Leukemia. Journal of Medicinal Chemistry, 2012, 55, 8721-8734.	2.9	61
58	Design of Potent and Selective Hybrid Inhibitors of the Mitotic Kinase Nek2: Structure–Activity Relationship, Structural Biology, and Cellular Activity. Journal of Medicinal Chemistry, 2012, 55, 3228-3241.	2.9	59
59	Structure-based design of imidazo[1,2-a]pyrazine derivatives as selective inhibitors of Aurora-A kinase in cells. Bioorganic and Medicinal Chemistry Letters, 2010, 20, 5988-5993.	1.0	30
60	Structural Basis of Poly(ADP-ribose) Recognition by the Multizinc Binding Domain of Checkpoint with Forkhead-associated and RING Domains (CHFR). Journal of Biological Chemistry, 2010, 285, 39348-39358.	1.6	54
61	Crystal structure of an Aurora-A mutant that mimics Aurora-B bound to MLN8054: insights into selectivity and drug design. Biochemical Journal, 2010, 427, 19-28.	1.7	86
62	A Pocket on the Surface of the N-Terminal BRCT Domain of Mcph1 Is Required to Prevent Abnormal Chromosome Condensation. Journal of Molecular Biology, 2010, 395, 908-915.	2.0	12
63	A Cancer-associated Aurora A Mutant Is Mislocalized and Misregulated Due to Loss of Interaction with TPX2. Journal of Biological Chemistry, 2009, 284, 33177-33184.	1.6	40
64	<i>Agrobacterium</i> VirB10 domain requirements for type IV secretion and T pilus biogenesis. Molecular Microbiology, 2009, 71, 779-794.	1.2	79
65	Insights into the Conformational Variability and Regulation of Human Nek2 Kinase. Journal of Molecular Biology, 2009, 386, 476-485.	2.0	47
66	An Autoinhibitory Tyrosine Motif in the Cell-Cycle-Regulated Nek7 Kinase Is Released through Binding of Nek9. Molecular Cell, 2009, 36, 560-570.	4.5	83
67	NMR structure of a complex between the VirB9/VirB7 interaction domains of the pKM101 type IV secretion system. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1673-1678.	3.3	48
68	Functional Tat Transport of Unstructured, Small, Hydrophilic Proteins. Journal of Biological Chemistry, 2007, 282, 33257-33264.	1.6	60
69	Identification, structure and mode of action of a new regulator of the Helicobacter pylori HP0525 ATPase. EMBO Journal, 2007, 26, 4926-4934.	3.5	34
70	A Large Domain Swap in the VirB11 ATPase of Brucella suis Leaves the Hexameric Assembly Intact. Journal of Molecular Biology, 2006, 360, 56-66.	2.0	67
71	Dimerization and interactions of Brucella suis VirB8 with VirB4 and VirB10 are required for its biological activity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7252-7257.	3.3	48
72	Structural Basis of Aurora-A Activation by TPX2 at the Mitotic Spindle. Molecular Cell, 2003, 12, 851-862.	4.5	541

#	Article	IF	CITATIONS
73	GLFG and FxFG Nucleoporins Bind to Overlapping Sites on Importin- $\hat{l}^2$ . Journal of Biological Chemistry, 2002, 277, 50597-50606.	1.6	203
74	Structural basis for the interaction between NTF2 and nucleoporin FxFG repeats. EMBO Journal, 2002, 21, 2843-2853.	3.5	146
75	Molecular mechanism of translocation through nuclear pore complexes during nuclear protein import. FEBS Letters, 2001, 498, 145-149.	1.3	101
76	Functional Analysis of the Hydrophobic Patch on Nuclear Transport Factor 2 Involved in Interactions with the Nuclear Porein Vivo. Journal of Biological Chemistry, 2001, 276, 38820-38829.	1.6	26
77	Interaction between NTF2 and xFxFG-containing nucleoporins is required to mediate nuclear import of RanGDP 1 1Edited by I. B. Holland. Journal of Molecular Biology, 1999, 293, 579-593.	2.0	171