Dmitri B Kireev

List of Publications by Year
in descending order

64	3,035	186209 28	161767 54
papers	citations	h-index	g-index

72	72	72	4119
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Reprogramming CBX8-PRC1 function with a positive allosteric modulator. Cell Chemical Biology, 2022, 29, 555-571.e11.	2.5	12
2	A chemical probe targeting the PWWP domain alters NSD2 nucleolar localization. Nature Chemical Biology, 2022, 18, 56-63.	3.9	41
3	Multivalent DNA and nucleosome acidic patch interactions specify VRK1 mitotic localization and activity. Nucleic Acids Research, 2022, 50, 4355-4371.	6.5	9
4	Use of AD Informer Set compounds to explore validity of novel targets in Alzheimer's disease pathology. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2022, 8, e12253.	1.8	3
5	AD Informer Set: Chemical tools to facilitate Alzheimer's disease drug discovery. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2022, 8, e12246.	1.8	4
6	MERTK activation drives osimertinib resistance in EGFR-mutant nonâ€“small cell lung cancer. Journal of Clinical Investigation, 2022, 132, .	3.9	12
7	UNC5293, a potent, orally available and highly MERTK-selective inhibitor. European Journal of Medicinal Chemistry, 2021, 220, 113534.	2.6	4
8	Discovery and Development of Cyclic Peptide Inhibitors of CIB1. ACS Medicinal Chemistry Letters, 2021, 12, 1832-1839.	1.3	14
9	Off-Pocket Activity Cliffs: A Puzzling Facet of Molecular Recognition. Journal of Chemical Information and Modeling, 2020, 60, 152-161.	2.5	9
10	Integrating DNA-encoded chemical libraries with virtual combinatorial library screening: Optimizing a PARP10 inhibitor. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 127464.	1.0	13
11	Design and Construction of a Focused DNA-Encoded Library for Multivalent Chromatin Reader Proteins. Molecules, 2020, 25, 979.	1.7	12
12	Data-Driven Construction of Antitumor Agents with Controlled Polypharmacology. Journal of the American Chemical Society, 2019, 141, 15700-15709.	6.6	12
13	Discovery and Characterization of a Cellular Potent Positive Allosteric Modulator of the Polycomb Repressive Complex 1 Chromodomain, CBX7. Cell Chemical Biology, 2019, 26, 1365-1379.e22.	2.5	38
14	Discovery of selective activators of PRC2 mutant EED-I363M. Scientific Reports, 2019, 9, 6524.	1.6	12
15	Synthesis and Antibacterial Evaluation of Cephalosporin Isosteres. Asian Journal of Organic Chemistry, 2019, 8, 1053-1057.	1.3	4
16	A Focused DNA-Encoded Chemical Library for the Discovery of Inhibitors of NAD⁺-Dependent Enzymes. Journal of the American Chemical Society, 2019, 141, 5169-5181.	6.6	84
17	Dynamics of Substrate Processing by PPIP5K2, a Versatile Catalytic Machine. Structure, 2019, 27, 1022-1028.e2.	1.6	9
18	Quantitative Characterization of Bivalent Probes for a Dual Bromodomain Protein, Transcription Initiation Factor TFIID Subunit 1. Biochemistry, 2018, 57, 2140-2149.	1.2	16

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19	Highly Selective MERTK Inhibitors Achieved by a Single Methyl Group. Journal of Medicinal Chemistry, 2018, 61, 10242-10254.	2.9	20
20	Use of Protein Kinaseâ€“Focused Compound Libraries for the Discovery of New Inositol Phosphate Kinase Inhibitors. SLAS Discovery, 2018, 23, 982-988.	1.4	15
21	Application of Integrated Drug Screening/Kinome Analysis to Identify Inhibitors of Gemcitabine-Resistant Pancreatic Cancer Cell Growth. SLAS Discovery, 2018, 23, 850-861.	1.4	11
22	Identification of Cosalane as an Inhibitor of Human and Murine CCâ€“Chemokine Receptor 7 Signaling via a High-Throughput Screen. SLAS Discovery, 2018, 23, 1083-1091.	1.4	10
23	Discovery of Macrocyclic Pyrimidines as MerTKâ€Specific Inhibitors. ChemMedChem, 2017, 12, 207-213.	1.6	25
24	A High-Throughput Screening-Compatible Strategy for the Identification of Inositol Pyrophosphate Kinase Inhibitors. PLoS ONE, 2016, 11, e0164378.	1.1	2
25	Computational Chemical Biology of Methyllysine Histone Effectors. , 2016, , 273-296.		0
26	Design and Synthesis of Novel Macrocyclic Mer Tyrosine Kinase Inhibitors. ACS Medicinal Chemistry Letters, 2016, 7, 1044-1049.	1.3	19
27	Structure-Based Virtual Screening of Commercially Available Compound Libraries. Methods in Molecular Biology, 2016, 1439, 65-76.	0.4	4
28	Chromodomain Ligand Optimization via Target-Class Directed Combinatorial Repurposing. ACS Chemical Biology, 2016, 11, 2475-2483.	1.6	46
29	Identification of Small Molecule Inhibitors That Block the Toxoplasma gondii Rhoptry Kinase ROP18. ACS Infectious Diseases, 2016, 2, 194-206.	1.8	20
30	The MERTK/FLT3 inhibitor MRX-2843 overcomes resistance-conferring FLT3 mutations in acute myeloid leukemia. JCI Insight, 2016, 1, e85630.	2.3	55
31	Development of a High-Throughput Screening Assay to Identify Inhibitors of the Lipid Kinase PIP5K1C. Journal of Biomolecular Screening, 2015, 20, 655-662.	2.6	16
32	UNC2025, a Potent and Orally Bioavailable MER/FLT3 Dual Inhibitor. Journal of Medicinal Chemistry, 2014, 57, 7031-7041.	2.9	125
33	Structural Proteinâ€“Ligand Interaction Fingerprints (SPLIF) for Structure-Based Virtual Screening: Method and Benchmark Study. Journal of Chemical Information and Modeling, 2014, 54, 2555-2561.	2.5	128
34	The structureâ€“activity relationships of L3MBTL3 inhibitors: flexibility of the dimer interface. MedChemComm, 2013, 4, 1501.	3.5	24
35	Discovery of Mer Specific Tyrosine Kinase Inhibitors for the Treatment and Prevention of Thrombosis. Journal of Medicinal Chemistry, 2013, 56, 9693-9700.	2.9	43
36	Pseudo-Cyclization through Intramolecular Hydrogen Bond Enables Discovery of Pyridine Substituted Pyrimidines as New Mer Kinase Inhibitors. Journal of Medicinal Chemistry, 2013, 56, 9683-9692.	2.9	54

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37	Small-Molecule Ligands of Methyl-Lysine Binding Proteins: Optimization of Selectivity for L3MBTL3. Journal of Medicinal Chemistry, 2013, 56, 7358-7371.	2.9	66
38	Discovery of a chemical probe for the L3MBTL3 methyllysine reader domain. Nature Chemical Biology, 2013, 9, 184-191.	3.9	160
39	UNC1062, a new and potent Mer inhibitor. European Journal of Medicinal Chemistry, 2013, 65, 83-93.	2.6	58
40	Multivalent histone engagement by the linked tandem Tudor and PHD domains of UHRF1 is required for the epigenetic inheritance of DNA methylation. Genes and Development, 2013, 27, 1288-1298.	2.7	155
41	Inhibitors of Streptococcus pneumoniae Surface Endonuclease EndA Discovered by High-Throughput Screening Using a PicoGreen Fluorescence Assay. Journal of Biomolecular Screening, 2013, 18, 247-257.	2.6	12
42	UNC569, a Novel Small-Molecule Mer Inhibitor with Efficacy against Acute Lymphoblastic Leukemia In Vitro and In Vivo. Molecular Cancer Therapeutics, 2013, 12, 2367-2377.	1.9	53
43	Structureâ€“activity relationships of methyl-lysine reader antagonists. MedChemComm, 2012, 3, 45-51.	3.5	33
44	Development of a High-Throughput Assay for Identifying Inhibitors of TBK1 and IKKÎµ. PLoS ONE, 2012, 7, e41494.	1.1	34
45	Discovery of Small Molecule Mer Kinase Inhibitors for the Treatment of Pediatric Acute Lymphoblastic Leukemia. ACS Medicinal Chemistry Letters, 2012, 3, 129-134.	1.3	67
46	High-Throughput Screening for RecA Inhibitors Using a Transcreener Adenosine 5â€²-O-Diphosphate Assay. Assay and Drug Development Technologies, 2012, 10, 260-268.	0.6	31
47	Assessment of free energy predictors for ligand binding to a methyllysine histone code reader. Journal of Computational Chemistry, 2012, 33, 659-665.	1.5	8
48	Mer Receptor Tyrosine Kinase Is A Potential Therapeutic Target in Acute Myeloid Leukemia. Blood, 2012, 120, 1317-1317.	0.6	2
49	Evaluation of UNC569, a Novel Small Molecule Mer Inhibitor for the Treatment of ALL in Vitro and in Vivo.. Blood, 2012, 120, 2607-2607.	0.6	0
50	A chemical probe selectively inhibits G9a and GLP methyltransferase activity in cells. Nature Chemical Biology, 2011, 7, 566-574.	3.9	465
51	Biophysical Probes Reveal a â€œCompromiseâ€•Nature of the Methyl-lysine Binding Pocket in L3MBTL1. Journal of the American Chemical Society, 2011, 133, 5357-5362.	6.6	35
52	Small-Molecule Ligands of Methyl-Lysine Binding Proteins. Journal of Medicinal Chemistry, 2011, 54, 2504-2511.	2.9	115
53	UNC569 As Novel Small Molecule Mer Receptor Tyrosine Kinase Inhibitor for Treatment of ALL. Blood, 2011, 118, 2589-2589.	0.6	17
54	Identification of Non-Peptide Malignant Brain Tumor (MBT) Repeat Antagonists by Virtual Screening of Commercially Available Compounds. Journal of Medicinal Chemistry, 2010, 53, 7625-7631.	2.9	52

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55	Screening for Inhibitors of Low-Affinity Epigenetic Peptide-Protein Interactions: An AlphaScreenâ„¢-Based Assay for Antagonists of Methyl-Lysine Binding Proteins. Journal of Biomolecular Screening, 2010, 15, 62-71.	2.6	88
56	Protein Lysine Methyltransferase G9a Inhibitors: Design, Synthesis, and Structure Activity Relationships of 2,4-Diamino-7-aminoalkoxy-quinazolines.. Journal of Medicinal Chemistry, 2010, 53, 5844-5857.	2.9	177
57	Discovery of a 2,4-Diamino-7-aminoalkoxyquinazoline as a Potent and Selective Inhibitor of Histone Lysine Methyltransferase G9a. Journal of Medicinal Chemistry, 2009, 52, 7950-7953.	2.9	206
58	A CoMFA Study of Enantiomeric Organophoshorus Inhibitors of Acetylcholinesterase. Journal of Molecular Modeling, 2000, 6, 618-629.	0.8	10
59	Automated docking of 82 N-benzylpiperidine derivatives to mouse acetylcholinesterase and comparative molecular field analysis with 'natural' alignment. Journal of Computer-Aided Molecular Design, 1999, 13, 355-371.	1.3	27
60	3D Model of the Acetylcholinesterase Catalytic Cavity Probed by Stereospecific Organophosphorous Inhibitors. Journal of Molecular Modeling, 1998, 4, 323-334.	0.8	5
61	A 3D QSAR Study of a Series of HEPT Analogues:Â The Influence of Conformational Mobility on HIV-1 Reverse Transcriptase Inhibition. Journal of Medicinal Chemistry, 1997, 40, 4257-4264.	2.9	59
62	Molecular modeling and quantitative structure-activity studies of anti-HIV-1 2-heteroarylquinoline-4-amines. European Journal of Medicinal Chemistry, 1995, 30, 395-402.	2.6	22
63	ChemNet: A Novel Neural Network Based Method for Graph/Property Mapping. Journal of Chemical Information and Computer Sciences, 1995, 35, 175-180.	2.8	36
64	Complete Thermodynamic Description of H-Bonding in the Framework of Multiplicative Approach. QSAR and Combinatorial Science, 1992, 11, 49-63.	1.4	103