Benjamin D Bax

List of Publications by Year
in descending order

47	3,359	218381	223531
papers	citations	26 h-index	46 g-index

51	51	51	4291
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Type IIA topoisomerase inhibition by a new class of antibacterial agents. Nature, 2010, 466, 935-940.	13.7	672
2	Inhibition of PAD4 activity is sufficient to disrupt mouse and human NET formation. Nature Chemical Biology, 2015, 11, 189-191.	3.9	544
3	Structural basis of quinolone inhibition of type IIA topoisomerases and target-mediated resistance. Nature Structural and Molecular Biology, 2010, 17, 1152-1153.	3.6	255
4	The Structure of Phosphorylated GSK-3Î² Complexed with a Peptide, FRATtide, that Inhibits Î²-Catenin Phosphorylation. Structure, 2001, 9, 1143-1152.	1.6	186
5	The structure of rat ADP-ribosylation factor-1 (ARF-1) complexed to GDP determined from two different crystal forms. Nature Structural and Molecular Biology, 1995, 2, 797-806.	3.6	107
6	Structural basis of DNA gyrase inhibition by antibacterial QPT-1, anticancer drug etoposide and moxifloxacin. Nature Communications, 2015, 6, 10048.	5.8	100
7	Protein Arginine Deiminase 2 Binds Calcium in an Ordered Fashion: Implications for Inhibitor Design. ACS Chemical Biology, 2015, 10, 1043-1053.	1.6	99
8	Mechanistic and Structural Basis for the Actions of the Antibacterial Gepotidacin against Staphylococcus aureus Gyrase. ACS Infectious Diseases, 2019, 5, 570-581.	1.8	99
9	High resolution structure of an oligomeric eye lens Î²-crystallin. Journal of Molecular Biology, 1991, 222, 1067-1083.	2.0	89
10	GSK-3 inhibition by adenoviral FRAT1 overexpression is neuroprotective and induces Tau dephosphorylation and Î²-catenin stabilisation without elevation of glycogen synthase activity. FEBS Letters, 2001, 507, 288-294.	1.3	82
11	DNA Topoisomerase Inhibitors: Trapping a DNA-Cleaving Machine in Motion. Journal of Molecular Biology, 2019, 431, 3427-3449.	2.0	79
12	Structure of mouse 7S NGF: a complex of nerve growth factor with four binding proteins. Structure, 1997, 5, 1275-1285.	1.6	68
13	Challenges for and current status of research into positive modulators of AMPA receptors. British Journal of Pharmacology, 2010, 160, 181-190.	2.7	66
14	Integration of Lead Optimization with Crystallography for a Membrane-Bound Ion Channel Target: Discovery of a New Class of AMPA Receptor Positive Allosteric Modulators. Journal of Medicinal Chemistry, 2011, 54, 78-94.	2.9	61
15	Crystallizing Membrane Proteins in the Lipidic Mesophase. Experience with Human Prostaglandin E2 Synthase 1 and an Evolving Strategy. Crystal Growth and Design, 2014, 14, 2034-2047.	1.4	61
16	Novel hydroxyl tricyclics (e.g., GSK966587) as potent inhibitors of bacterial type IIA topoisomerases. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 5437-5441.	1.0	58
17	5-Aryl-4-carboxamide-1,3-oxazoles: Potent and selective GSK-3 inhibitors. Bioorganic and Medicinal Chemistry Letters, 2012, 22, 1989-1994.	1.0	53
18	Thiophene antibacterials that allosterically stabilize DNA-cleavage complexes with DNA gyrase. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4492-E4500.	3.3	51

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19	Evolutionary and functional relationships between the basic and acidic Î²-crystallins. Experimental Eye Research, 1988, 46, 375-403.	1.2	50
20	Close packing of an oligomeric eye lens Î²-crystallin induces loss of symmetry and ordering of sequence extensions. Journal of Molecular Biology, 1994, 236, 1250-1258.	2.0	46
21	Discovery of N-[(2S)-5-(6-Fluoro-3-pyridinyl)-2,3-dihydro-1H-inden-2-yl]-2-propanesulfonamide, a Novel Clinical AMPA Receptor Positive Modulator. Journal of Medicinal Chemistry, 2010, 53, 5801-5812.	2.9	44
22	Getting the chemistry right: protonation, tautomers and the importance of H atoms in biological chemistry. Acta Crystallographica Section D: Structural Biology, 2017, 73, 131-140.	1.1	44
23	The Structure of MSK1 Reveals a Novel Autoinhibitory Conformation for a Dual Kinase Protein. Structure, 2004, 12, 1067-1077.	1.6	42
24	Novel tricyclics (e.g., GSK945237) as potent inhibitors of bacterial type IIA topoisomerases. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 2464-2469.	1.0	39
25	Structural and functional analysis of the nucleotide and DNA binding activities of the human PIF1 helicase. Nucleic Acids Research, 2019, 47, 3208-3222.	6.5	36
26	1-Aryl-3,4-dihydroisoquinoline inhibitors of JNK3. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 2230-2234.	1.0	34
27	Structural aspects of the functional modules in human protein kinase-CÎ± deduced from comparative analyses. , 1996, 26, 217-235.		29
28	The three-dimensional structure of cytosolic bovine retinal creatine kinase. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 187-193.	2.5	24
29	Identification of 2-(4-pyridyl)thienopyridinones as GSK-3Î² inhibitors. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 4823-4827.	1.0	23
30	A new class of antibacterials, the imidazopyrazinones, reveal structural transitions involved in DNA gyrase poisoning and mechanisms of resistance. Nucleic Acids Research, 2018, 46, 4114-4128.	6.5	23
31	Mechanism of Action of Mycobacterium tuberculosis Gyrase Inhibitors: A Novel Class of Gyrase Poisons. ACS Infectious Diseases, 2018, 4, 1211-1222.	1.8	23
32	ADP ribosylation factor 1 mutants identify a phospholipase D effector region and reveal that phospholipase D participates in lysosomal secretion but is not sufficient for recruitment of coatomer I. Biochemical Journal, 1999, 341, 185.	1.7	21
33	Crystallization and initial crystallographic analysis of covalent DNA-cleavage complexes of Staphyloccocus aureus DNA gyrase with QPT-1, moxifloxacin and etoposide. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1242-1246.	0.4	19
34	Coupling the core of the anticancer drug etoposide to an oligonucleotide induces topoisomerase II-mediated cleavage at specific DNA sequences. Nucleic Acids Research, 2018, 46, 2218-2233.	6.5	19
35	Structure-guided design of antibacterials that allosterically inhibit DNA gyrase. Bioorganic and Medicinal Chemistry Letters, 2019, 29, 1407-1412.	1.0	19
36	Crystallization of a new form of the eye lens protein Î²B2-crystallin. Journal of Molecular Biology, 1989, 208, 715-717.	2.0	15

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37	From PIM1 to PI3KÎ´ via GSK3Î²: Target Hopping through the Kinome. ACS Medicinal Chemistry Letters, 2017, 8, 1093-1098.	1.3	15
38	Prediction of the threeâ€dimensional structures of the nerve growth factor and epidermal growth factor binding proteins (kallikreins) and an hypothetical structure of the high molecular weight complex of epidermal growth factor with its binding protein. Protein Science, 1993, 2, 1229-1241.	3.1	12
39	Crystallization and structure of ebselen bound to Cys141 of human inositol monophosphatase. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 469-476.	0.4	9
40	Proteinâ€“Protein Interactions: Putting the pieces together. Current Biology, 1995, 5, 1119-1121.	1.8	8
41	Purification, crystallization and preliminary X-ray crystallographic studies of theMycobacterium tuberculosisDNA gyrase ATPase domain. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 679-682.	0.7	7
42	Conformational flexibility within the small domain of human serine racemase. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 65-73.	0.4	4
43	Crystallization and Preliminary X-ray Diffraction Studies on ADP-ribosylation Factor 1. Journal of Molecular Biology, 1994, 244, 651-653.	2.0	2
44	Structures of the Human SPAK and OSR1 Conserved Câ€Terminal (CCT) Domains**. ChemBioChem, 2022, 23, .	1.3	2
45	Purification, crystallization and preliminary crystallographic analysis of bovine cytosolic brain-type creatine kinase. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 989-990.	2.5	1
46	Tyrosine 121 moves revealing a ligandable pocket that couples catalysis to ATP-binding in serine racemase. Communications Biology, 2022, 5, 346.	2.0	1
47	Common themes and surprising differences in small G-proteins. Biochemical Society Transactions, 1997, 25, 989-991.	1.6	0