John B Bruning

List of Publications by Year
in descending order

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90 papers	3,615 citations	218677 26 h-index	144013 57 g-index
95 all docs	95 docs citations	95 times ranked	5280 citing authors

#	Article	IF	Citations
1	Antidiabetic actions of a non-agonist PPARÎ³ ligand blocking Cdk5-mediated phosphorylation. Nature, 2011, 477, 477-481.	27.8	484
2	Partial Agonists Activate PPARÎ³ Using a Helix 12 Independent Mechanism. Structure, 2007, 15, 1258-1271.	3.3	321
3	Structural and Thermodynamic Analysis of Human PCNA with Peptides Derived from DNA Polymerase-Î´ p66 Subunit and Flap Endonuclease-1. Structure, 2004, 12, 2209-2219.	3.3	190
4	DNA binding alters coactivator interaction surfaces of the intact VDRâ€“RXR complex. Nature Structural and Molecular Biology, 2011, 18, 556-563.	8.2	185
5	Review of the Structural and Dynamic Mechanisms of PPARÎ³Partial Agonism. PPAR Research, 2015, 2015, 1-15.	2.4	151
6	NFÎºB selectivity of estrogen receptor ligands revealed by comparative crystallographic analyses. Nature Chemical Biology, 2008, 4, 241-247.	8.0	149
7	Rare variants in single-minded 1 (SIM1) are associated with severe obesity. Journal of Clinical Investigation, 2013, 123, 3042-3050.	8.2	135
8	Structural plasticity in the oestrogen receptor ligandâ€binding domain. EMBO Reports, 2007, 8, 563-568.	4.5	125
9	Coupling of receptor conformation and ligand orientation determine graded activity. Nature Chemical Biology, 2010, 6, 837-843.	8.0	121
10	Structure of the Mycobacterium tuberculosis <scp>d</scp> -Alanine: <scp>d</scp> -Alanine Ligase, a Target of the Antituberculosis Drug <scp>d</scp> -Cycloserine. Antimicrobial Agents and Chemotherapy, 2011, 55, 291-301.	3.2	121
11	Loss-of-function mutations in SIM1 contribute to obesity and Prader-Williâ€like features. Journal of Clinical Investigation, 2013, 123, 3037-3041.	8.2	105
12	Structural mechanism for signal transduction in RXR nuclear receptor heterodimers. Nature Communications, 2015, 6, 8013.	12.8	101
13	Pharmacological repression of PPARÎ³ promotes osteogenesis. Nature Communications, 2015, 6, 7443.	12.8	99
14	Prediction of the tissue-specificity of selective estrogen receptor modulators by using a single biochemical method. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7171-7176.	7.1	87
15	Elemental Isomerism: A Boron-Nitrogen Surrogate for a Carbon-Carbon Double Bond Increases the Chemical Diversity of Estrogen Receptor Ligands. Chemistry and Biology, 2007, 14, 659-669.	6.0	66
16	PPARG Post-translational Modifications Regulate Bone Formation and Bone Resorption. EBioMedicine, 2016, 10, 174-184.	6.1	64
17	Expressing a moth abcc2 gene in transgenic Drosophila causes susceptibility to Bt Cry1Ac without requiring a cadherin-like protein receptor. Insect Biochemistry and Molecular Biology, 2017, 80, 61-70.	2.7	44
18	PPARÎ³ in Complex with an Antagonist and Inverse Agonist: a Tumble and Trap Mechanism of the Activation Helix. IScience, 2018, 5, 69-79.	4.1	40

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19	Structural Insights into the Mechanism of the Allosteric Transitions of Mycobacterium tuberculosis cAMP Receptor Protein. Journal of Biological Chemistry, 2009, 284, 36581-36591.	3.4	39
20	The TB Structural Genomics Consortium: A decade of progress. Tuberculosis, 2011, 91, 155-172.	1.9	39
21	HDX reveals the conformational dynamics of DNA sequence specific VDR co-activator interactions. Nature Communications, 2017, 8, 923.	12.8	39
22	The therapeutic potential of inhibiting PPARÎ³ phosphorylation to treat type 2 diabetes. Journal of Biological Chemistry, 2021, 297, 101030.	3.4	35
23	SR2067 Reveals a Unique Kinetic and Structural Signature for PPARÎ³ Partial Agonism. ACS Chemical Biology, 2016, 11, 273-283.	3.4	34
24	Shooting three inflammatory targets with a single bullet: Novel multi-targeting anti-inflammatory glitazones. European Journal of Medicinal Chemistry, 2019, 167, 562-582.	5.5	33
25	Understanding the Mechanistic Requirements for Efficient and Stereoselective Alkene Epoxidation by a Cytochrome P450 Enzyme. ACS Catalysis, 2021, 11, 1995-2010.	11.2	30
26	An Altered Heme Environment in an Engineered Cytochrome P450 Enzyme Enables the Switch from Monooxygenase to Peroxygenase Activity. ACS Catalysis, 2022, 12, 1614-1625.	11.2	29
27	CYP199A4 catalyses the efficient demethylation and demethenylation of para-substituted benzoic acid derivatives. RSC Advances, 2015, 5, 52007-52018.	3.6	28
28	Structure, Mechanism, and Inhibition of Aspergillus fumigatus Thioredoxin Reductase. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	28
29	Cytochrome P450 CYP199A4 from Rhodopseudomonas palustris Catalyzes Heteroatom Dealkylations, Sulfoxidation, and Amide and Cyclic Hemiacetal Formation. ACS Catalysis, 2018, 8, 5915-5927.	11.2	27
30	Macrocyclic Protease Inhibitors with Reduced Peptide Character. Angewandte Chemie - International Edition, 2014, 53, 7828-7831.	13.8	26
31	p21 Exploits Residue Tyr151 as a Tether for High-Affinity PCNA Binding. Biochemistry, 2015, 54, 3483-3493.	2.5	26
32	New insights into the evolutionary history of plant sorbitol dehydrogenase. BMC Plant Biology, 2015, 15, 101.	3.6	26
33	Structural insights into the role of the acid-alcohol pair of residues required for dioxygen activation in cytochrome P450 enzymes. Journal of Biological Inorganic Chemistry, 2020, 25, 583-596.	2.6	26
34	Chemical Crosslinking Mass Spectrometry Reveals the Conformational Landscape of the Activation Helix of PPARÎ³; a Model for Ligand-Dependent Antagonism. Structure, 2018, 26, 1431-1439.e6.	3.3	24
35	Targeting PCNA with Peptide Mimetics for Therapeutic Purposes. ChemBioChem, 2020, 21, 442-450.	2.6	24
36	Human Variants in the Neuronal Basic Helix-Loop-Helix/Per-Arnt-Sim (bHLH/PAS) Transcription Factor Complex NPAS4/ARNT2 Disrupt Function. PLoS ONE, 2014, 9, e85768.	2.5	22

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37	Structureâ€“Activity Relationship of 2,4-Dichloro-N-(3,5-dichloro-4-(quinolin-3-yloxy)phenyl)benzenesulfonamide (INT131) Analogs for PPARÎ³-Targeted Antidiabetics. Journal of Medicinal Chemistry, 2017, 60, 4584-4593.	6.4	22
38	Investigation of the requirements for efficient and selective cytochrome P450 monooxygenase catalysis across different reactions. Journal of Inorganic Biochemistry, 2020, 203, 110913.	3.5	22
39	d-Alanineâ€“d-alanine ligase as a model for the activation of ATP-grasp enzymes by monovalent cations. Journal of Biological Chemistry, 2020, 295, 7894-7904.	3.4	21
40	Biophysical Techniques for Distinguishing Ligand Binding Modes in Cytochrome P450 Monooxygenases. Biochemistry, 2020, 59, 1038-1050.	2.5	20
41	Structure, Activity, and Inhibition of the Carboxyltransferase Î²-Subunit of Acetyl Coenzyme A Carboxylase (AccD6) from Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2014, 58, 6122-6132.	3.2	18
42	Mechanisms Governing Precise Protein Biotinylation. Trends in Biochemical Sciences, 2017, 42, 383-394.	7.5	18
43	Vanishing white matter: Eukaryotic initiation factor 2B model and the impact of missense mutations. Molecular Genetics & Genomic Medicine, 2021, 9, e1593.	1.2	17
44	Rational Design of a 3₁₀â€Helical PIPâ€Box Mimetic Targeting PCNA, the Human Sliding Clamp. Chemistry - A European Journal, 2018, 24, 11325-11331.	3.3	16
45	X-ray crystal structure of rivoglitazone bound to PPARÎ³ and PPAR subtype selectivity of TZDs. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 1981-1991.	2.4	15
46	An aldo-keto reductase with 2-keto-l-gulonate reductase activity functions in l-tartaric acid biosynthesis from vitamin C in Vitis vinifera. Journal of Biological Chemistry, 2019, 294, 15932-15946.	3.4	14
47	Different Geometric Requirements for Cytochrome P450-Catalyzed Aliphatic Versus Aromatic Hydroxylation Results in Chemoselective Oxidation. ACS Catalysis, 2022, 12, 1258-1267.	11.2	14
48	Structural and functional characterisation of the cytochrome P450 enzyme CYP268A2 fromMycobacterium marinum. Biochemical Journal, 2018, 475, 705-722.	3.7	13
49	Targeting Unconventional Pathways in Pursuit of Novel Antifungals. Frontiers in Molecular Biosciences, 2020, 7, 621366.	3.5	12
50	A comparison of steroid and lipid binding cytochrome P450s from Mycobacterium marinum and Mycobacterium tuberculosis. Journal of Inorganic Biochemistry, 2020, 209, 111116.	3.5	12
51	A mechanistic study on the inhibition of Î±-chymotrypsin by a macrocyclic peptidomimetic aldehyde. Organic and Biomolecular Chemistry, 2016, 14, 6970-6978.	2.8	11
52	Structure of the sliding clamp from the fungal pathogen Aspergillus fumigatus (Afum PCNA) and interactions with Human p21. FEBS Journal, 2017, 284, 985-1002.	4.7	11
53	JAK2 Alterations in Acute Lymphoblastic Leukemia: Molecular Insights for Superior Precision Medicine Strategies. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	11
54	Characterization of human variants in obesity-related SIM1 protein identifies a hot-spot for dimerization with the partner protein ARNT2. Biochemical Journal, 2014, 461, 403-412.	3.7	10

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55	Acquired JAK2 mutations confer resistance to JAK inhibitors in cell models of acute lymphoblastic leukemia. Npj Precision Oncology, 2021, 5, 75.	5.4	10
56	Unlocking the PIP-box: A peptide library reveals interactions that drive high-affinity binding to human PCNA. Journal of Biological Chemistry, 2021, 296, 100773.	3.4	9
57	Structure of the Apo Form of Bacillus stearothermophilus Phosphofructokinase. Biochemistry, 2012, 51, 769-775.	2.5	8
58	Unique Polypharmacology Nuclear Receptor Modulator Blocks Inflammatory Signaling Pathways. ACS Chemical Biology, 2019, 14, 1051-1062.	3.4	8
59	Constitutive JAK/STAT signaling is the primary mechanism of resistance to JAKi in TYK2-rearranged acute lymphoblastic leukemia. Cancer Letters, 2021, 512, 28-37.	7.2	8
60	Mycobacterium tuberculosis Dethiobiotin Synthetase Facilitates Nucleoside Triphosphate Promiscuity through Alternate Binding Modes. ACS Catalysis, 2018, 8, 10774-10783.	11.2	7
61	An antimony-phosphomolybdate microassay of ATPase activity through the detection of inorganic phosphate. Analytical Biochemistry, 2021, 623, 114170.	2.4	7
62	Nucleoside selectivity of Aspergillus fumigatus nucleosideâ€diphosphate kinase. FEBS Journal, 2021, 288, 2398-2417.	4.7	6
63	Immunogenicity study of engineered ferritins with C- and N-terminus insertion of Epstein-Barr nuclear antigen 1 epitope. Vaccine, 2021, 39, 4830-4841.	3.8	6
64	The Stereoselective Oxidation of para â€Substituted Benzenes by a Cytochrome P450 Biocatalyst. Chemistry - A European Journal, 2021, 27, 14765-14777.	3.3	6
65	Inhibition of Mycobacterium tuberculosis Dethiobiotin Synthase (MtDTBS): Toward Next-Generation Antituberculosis Agents. ACS Chemical Biology, 2021, 16, 2339-2347.	3.4	6
66	To Be, or Not to Be, an Inhibitor: A Comparison of Azole Interactions with and Oxidation by a Cytochrome P450 Enzyme. Inorganic Chemistry, 2022, 61, 236-245.	4.0	6
67	Redefining the Role of the Quaternary Shift in Bacillus stearothermophilus Phosphofructokinase. Biochemistry, 2013, 52, 5421-5429.	2.5	5
68	Precipitantâ€“ligand exchange technique reveals the ADP binding mode inMycobacterium tuberculosisdethiobiotin synthetase. Acta Crystallographica Section D: Structural Biology, 2018, 74, 965-972.	2.3	5
69	Sulfonamide-Based Inhibitors of Biotin Protein Ligase as New Antibiotic Leads. ACS Chemical Biology, 2019, 14, 1990-1997.	3.4	5
70	A cell permeable bimane-constrained PCNA-interacting peptide. RSC Chemical Biology, 2021, 2, 1499-1508.	4.1	5
71	TSC-insensitive Rheb mutations induce oncogenic transformation through a combination of constitutively active mTORC1 signalling and proteome remodelling. Cellular and Molecular Life Sciences, 2021, 78, 4035-4052.	5.4	5
72	Structural and Dynamic Elucidation of a Non-acid PPARÎ³ Partial Agonist: SR1988. Nuclear Receptor Research, 2018, 5, .	2.5	5

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73	A comparison of the bacterial CYP51 cytochrome P450 enzymes from Mycobacterium marinum and Mycobacterium tuberculosis. Journal of Steroid Biochemistry and Molecular Biology, 2022, 221, 106097.	2.5	5
74	Structure ofAspergillus fumigatusCytosolic Thiolase: Trapped Tetrahedral Reaction Intermediates and Activation by Monovalent Cations. ACS Catalysis, 2018, 8, 1973-1989.	11.2	4
75	Crystal Structure of Bovine Alpha-Chymotrypsin in Space Group P65. Crystals, 2018, 8, 460.	2.2	4
76	The characterisation of two members of the cytochrome P450 CYP150 family: CYP150A5 and CYP150A6 from Mycobacterium marinum. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 925-934.	2.4	4
77	Approaches to Introduce Helical Structure in Cysteineâ€Containing Peptides with a Bimane Group. ChemBioChem, 2021, 22, 2711-2720.	2.6	4
78	Obtaining Crystals of PPARÎ³ Ligand Binding Domain Bound to Small Molecules. Methods in Molecular Biology, 2019, 1966, 253-260.	0.9	3
79	Combining random microseed matrix screening and the magic triangle for the efficient structure solution of a potential lysin from bacteriophage P68. Acta Crystallographica Section D: Structural Biology, 2019, 75, 670-681.	2.3	3
80	The role of N-terminal heterocycles in hydrogen bonding to Î±-chymotrypsin. Bioorganic and Medicinal Chemistry Letters, 2019, 29, 396-399.	2.2	2
81	Simplified heavy-atom derivatization of protein structures via co-crystallization with the MAD tetragon tetrabromoterephthalic acid. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 156-162.	0.8	2
82	Structural insights into the antifungal drug target guanosine monophosphate synthase from Aspergillus fumigatus. Acta Crystallographica Section D: Structural Biology, 2022, 78, 248-259.	2.3	2
83	Structural plasticity in the oestrogen receptor ligandâ€binding domain. EMBO Reports, 2007, 8, 610-610.	4.5	1
84	Engineering potassium activation into biosynthetic thiolase. Biochemical Journal, 2021, 478, 3047-3062.	3.7	1
85	Redefining the Role of the Quaternary Shift in the Allosteric Inhibition ofÂBacillus Stearothermophilus Phosphofructokinase. Biophysical Journal, 2010, 98, 39a.	0.5	0
86	Rational Design of a 310 -Helical PIP-Box Mimetic Targeting PCNA, the Human Sliding Clamp. Chemistry - A European Journal, 2018, 24, 11238-11238.	3.3	0
87	A turn-on fluorescent PCNA sensor. Bioorganic and Medicinal Chemistry Letters, 2021, 41, 128031.	2.2	0
88	Derivatization of Protein Crystals with I3C using Random Microseed Matrix Screening. Journal of Visualized Experiments, 2021, , .	0.3	0
89	PPARÎ± and Î´ Ligand Design: Honing the Traditional Empirical Method with a More Holistic Overview. , 2021, , 111-178.		0
90	A structural model of the human plasminogen and Aspergillus fumigatus enolase complex. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1509-1520.	2.6	0