John B Bruning

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

86 2,663 22 51 h-index g-index citations papers 6.8 3,169 4.86 95 L-index avg, IF ext. papers ext. citations

#	Paper	IF	Citations
86	An Altered Heme Environment in an Engineered Cytochrome P450 Enzyme Enables the Switch from Monooxygenase to Peroxygenase Activity. <i>ACS Catalysis</i> , 2022 , 12, 1614-1625	13.1	2
85	Structural insights into the antifungal drug target guanosine monophosphate synthase from Aspergillus fumigatus <i>Acta Crystallographica Section D: Structural Biology</i> , 2022 , 78, 248-259	5.5	0
84	A comparison of the bacterial CYP51 cytochrome P450 enzymes from Mycobacterium marinum and Mycobacterium tuberculosis <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2022 , 106097	5.1	O
83	TSC-insensitive Rheb mutations induce oncogenic transformation through a combination of constitutively active mTORC1 signalling and proteome remodelling. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 4035-4052	10.3	O
82	Simplified heavy-atom derivatization of protein structures via co-crystallization with the MAD tetragon tetrabromoterephthalic acid. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021 , 77, 156-162	1.1	O
81	A turn-on fluorescent PCNA sensor. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021 , 41, 128031	2.9	
80	Approaches to Introduce Helical Structure in Cysteine-Containing Peptides with a Bimane Group. <i>ChemBioChem</i> , 2021 , 22, 2711-2720	3.8	1
79	An antimony-phosphomolybdate microassay of ATPase activity through the detection of inorganic phosphate. <i>Analytical Biochemistry</i> , 2021 , 623, 114170	3.1	2
78	Nucleoside selectivity of Aspergillus fumigatus nucleoside-diphosphate kinase. <i>FEBS Journal</i> , 2021 , 288, 2398-2417	5.7	2
77	Vanishing white matter: Eukaryotic initiation factor 2B model and the impact of missense mutations. <i>Molecular Genetics & amp; Genomic Medicine</i> , 2021 , 9, e1593	2.3	7
76	A cell permeable bimane-constrained PCNA-interacting peptide. RSC Chemical Biology, 2021, 2, 1499-15	i0 ₉ 8	O
75	Understanding the Mechanistic Requirements for Efficient and Stereoselective Alkene Epoxidation by a Cytochrome P450 Enzyme. <i>ACS Catalysis</i> , 2021 , 11, 1995-2010	13.1	7
74	Immunogenicity study of engineered ferritins with C- and N-terminus insertion of Epstein-Barr nuclear antigen 1 epitope. <i>Vaccine</i> , 2021 , 39, 4830-4841	4.1	3
73	Engineering potassium activation into biosynthetic thiolase. <i>Biochemical Journal</i> , 2021 , 478, 3047-3062	3.8	
72	Acquired JAK2 mutations confer resistance to JAK inhibitors in cell models of acute lymphoblastic leukemia. <i>Npj Precision Oncology</i> , 2021 , 5, 75	9.8	1
71	Constitutive JAK/STAT signaling is the primary mechanism of resistance to JAKi in TYK2-rearranged acute lymphoblastic leukemia. <i>Cancer Letters</i> , 2021 , 512, 28-37	9.9	2
70	The Stereoselective Oxidation of para-Substituted Benzenes by a Cytochrome P450 Biocatalyst. <i>Chemistry - A European Journal</i> , 2021 , 27, 14765-14777	4.8	1

(2019-2021)

69	The therapeutic potential of inhibiting PPARIphosphorylation to treat type 2 diabetes. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101030	5.4	5	
68	Inhibition of Dethiobiotin Synthase (DTBS): Toward Next-Generation Antituberculosis Agents. <i>ACS Chemical Biology</i> , 2021 , 16, 2339-2347	4.9	О	
67	Unlocking the PIP-box: A peptide library reveals interactions that drive high-affinity binding to human PCNA. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100773	5.4	1	
66	PPAR and Ligand Design: Honing the Traditional Empirical Method with a More Holistic Overview 2021 , 111-178			
65	Biophysical Techniques for Distinguishing Ligand Binding Modes in Cytochrome P450 Monooxygenases. <i>Biochemistry</i> , 2020 , 59, 1038-1050	3.2	6	
64	Structural insights into the role of the acid-alcohol pair of residues required for dioxygen activation in cytochrome P450 enzymes. <i>Journal of Biological Inorganic Chemistry</i> , 2020 , 25, 583-596	3.7	10	
63	d-Alanine-d-alanine ligase as a model for the activation of ATP-grasp enzymes by monovalent cations. <i>Journal of Biological Chemistry</i> , 2020 , 295, 7894-7904	5.4	6	
62	A comparison of steroid and lipid binding cytochrome P450s from Mycobacterium marinum and Mycobacterium tuberculosis. <i>Journal of Inorganic Biochemistry</i> , 2020 , 209, 111116	4.2	4	
61	Investigation of the requirements for efficient and selective cytochrome P450 monooxygenase catalysis across different reactions. <i>Journal of Inorganic Biochemistry</i> , 2020 , 203, 110913	4.2	9	
60	Targeting PCNA with Peptide Mimetics for Therapeutic Purposes. <i>ChemBioChem</i> , 2020 , 21, 442-450	3.8	12	
59	Targeting Unconventional Pathways in Pursuit of Novel Antifungals. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 621366	5.6	6	
58	Obtaining Crystals of PPARLigand Binding Domain Bound to Small Molecules. <i>Methods in Molecular Biology</i> , 2019 , 1966, 253-260	1.4	2	
57	The characterisation of two members of the cytochrome P450 CYP150 family: CYP150A5 and CYP150A6 from Mycobacterium marinum. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019 , 1863, 925-934	4	3	
56	Unique Polypharmacology Nuclear Receptor Modulator Blocks Inflammatory Signaling Pathways. <i>ACS Chemical Biology</i> , 2019 , 14, 1051-1062	4.9	7	
55	Sulfonamide-Based Inhibitors of Biotin Protein Ligase as New Antibiotic Leads. <i>ACS Chemical Biology</i> , 2019 , 14, 1990-1997	4.9	3	
54	An aldo-keto reductase with 2-keto-l-gulonate reductase activity functions in l-tartaric acid biosynthesis from vitamin C in. <i>Journal of Biological Chemistry</i> , 2019 , 294, 15932-15946	5.4	9	
53	Combining random microseed matrix screening and the magic triangle for the efficient structure solution of a potential lysin from bacteriophage P68. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019 , 75, 670-681	5.5	2	
52	Shooting three inflammatory targets with a single bullet: Novel multi-targeting anti-inflammatory glitazones. <i>European Journal of Medicinal Chemistry</i> , 2019 , 167, 562-582	6.8	20	

51	The role of N-terminal heterocycles in hydrogen bonding to Ethymotrypsin. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2019 , 29, 396-399	2.9	0
50	Structure, Mechanism, and Inhibition of Thioredoxin Reductase. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	13
49	Structural and functional characterisation of the cytochrome P450 enzyme CYP268A2 from. <i>Biochemical Journal</i> , 2018 , 475, 705-722	3.8	7
48	Structure of Aspergillus fumigatus Cytosolic Thiolase: Trapped Tetrahedral Reaction Intermediates and Activation by Monovalent Cations. <i>ACS Catalysis</i> , 2018 , 8, 1973-1989	13.1	3
47	Rational Design of a 310-Helical PIP-Box Mimetic Targeting PCNA, the Human Sliding Clamp. <i>Chemistry - A European Journal</i> , 2018 , 24, 11238-11238	4.8	
46	PPARIIn Complex with an Antagonist and Inverse Agonist: a Tumble and Trap Mechanism of the Activation Helix. <i>IScience</i> , 2018 , 5, 69-79	6.1	29
45	Rational Design of a 3 -Helical PIP-Box Mimetic Targeting PCNA, the Human Sliding Clamp. <i>Chemistry - A European Journal</i> , 2018 , 24, 11325-11331	4.8	9
44	Structural and Dynamic Elucidation of a Non-acid PPAR Partial Agonist: SR1988. <i>Nuclear Receptor Research</i> , 2018 , 5,	1.4	3
43	Crystal Structure of Bovine Alpha-Chymotrypsin in Space Group P65. Crystals, 2018, 8, 460	2.3	2
42	Precipitant-ligand exchange technique reveals the ADP binding mode in Mycobacterium tuberculosis dethiobiotin synthetase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 965-	-972	3
41	Mycobacterium tuberculosis Dethiobiotin Synthetase Facilitates Nucleoside Triphosphate Promiscuity through Alternate Binding Modes. <i>ACS Catalysis</i> , 2018 , 8, 10774-10783	13.1	6
40	Chemical Crosslinking Mass Spectrometry Reveals the Conformational Landscape of the Activation Helix of PPAR[]a Model for Ligand-Dependent Antagonism. <i>Structure</i> , 2018 , 26, 1431-1439.e6	5.2	14
39	Cytochrome P450 CYP199A4 from Rhodopseudomonas palustris Catalyzes Heteroatom Dealkylations, Sulfoxidation, and Amide and Cyclic Hemiacetal Formation. <i>ACS Catalysis</i> , 2018 , 8, 5915-5	5 927	14
38	Structure of the sliding clamp from the fungal pathogen Aspergillus fumigatus (AfumPCNA) and interactions with Human p21. <i>FEBS Journal</i> , 2017 , 284, 985-1002	5.7	6
37	Mechanisms Governing Precise Protein Biotinylation. <i>Trends in Biochemical Sciences</i> , 2017 , 42, 383-394	10.3	15
36	X-ray crystal structure of rivoglitazone bound to PPARIand PPAR subtype selectivity of TZDs. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 1981-1991	4	11
35	Structure-Activity Relationship of 2,4-Dichloro-N-(3,5-dichloro-4-(quinolin-3-yloxy)phenyl)benzenesulfonamide (INT131) Analogs for PPARETargeted Antidiabetics. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 4584-4593	8.3	14
34	Expressing a moth abcc2 gene in transgenic Drosophila causes susceptibility to Bt Cry1Ac without requiring a cadherin-like protein receptor. <i>Insect Biochemistry and Molecular Biology</i> , 2017 , 80, 61-70	4.5	35

(2012-2017)

33	HDX reveals the conformational dynamics of DNA sequence specific VDR co-activator interactions. <i>Nature Communications</i> , 2017 , 8, 923	17.4	22
32	A mechanistic study on the inhibition of Ethymotrypsin by a macrocyclic peptidomimetic aldehyde. Organic and Biomolecular Chemistry, 2016, 14, 6970-8	3.9	9
31	PPARG Post-translational Modifications Regulate Bone Formation and Bone Resorption. <i>EBioMedicine</i> , 2016 , 10, 174-84	8.8	45
30	SR2067 Reveals a Unique Kinetic and Structural Signature for PPARIPartial Agonism. <i>ACS Chemical Biology</i> , 2016 , 11, 273-83	4.9	30
29	New insights into the evolutionary history of plant sorbitol dehydrogenase. <i>BMC Plant Biology</i> , 2015 , 15, 101	5.3	12
28	Structural mechanism for signal transduction in RXR nuclear receptor heterodimers. <i>Nature Communications</i> , 2015 , 6, 8013	17.4	84
27	Review of the Structural and Dynamic Mechanisms of PPARIPartial Agonism. <i>PPAR Research</i> , 2015 , 2015, 816856	4.3	112
26	p21 Exploits Residue Tyr151 as a Tether for High-Affinity PCNA Binding. <i>Biochemistry</i> , 2015 , 54, 3483-9	33.2	21
25	Pharmacological repression of PPAR[promotes osteogenesis. <i>Nature Communications</i> , 2015 , 6, 7443	17.4	79
24	CYP199A4 catalyses the efficient demethylation and demethenylation of para-substituted benzoic acid derivatives. <i>RSC Advances</i> , 2015 , 5, 52007-52018	3.7	18
23	Structure, activity, and inhibition of the Carboxyltransferase Bubunit of acetyl coenzyme A carboxylase (AccD6) from Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 6122-32	5.9	16
22	Macrocyclic protease inhibitors with reduced peptide character. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 7828-31	16.4	21
21	Human variants in the neuronal basic helix-loop-helix/Per-Arnt-Sim (bHLH/PAS) transcription factor complex NPAS4/ARNT2 disrupt function. <i>PLoS ONE</i> , 2014 , 9, e85768	3.7	18
20	Characterization of human variants in obesity-related SIM1 protein identifies a hot-spot for dimerization with the partner protein ARNT2. <i>Biochemical Journal</i> , 2014 , 461, 403-12	3.8	7
19	Redefining the role of the quaternary shift in Bacillus stearothermophilus phosphofructokinase. <i>Biochemistry</i> , 2013 , 52, 5421-9	3.2	4
18	Rare variants in single-minded 1 (SIM1) are associated with severe obesity. <i>Journal of Clinical Investigation</i> , 2013 , 123, 3042-50	15.9	107
17	Loss-of-function mutations in SIM1 contribute to obesity and Prader-Willi-like features. <i>Journal of Clinical Investigation</i> , 2013 , 123, 3037-41	15.9	75
16	Structure of the apo form of Bacillus stearothermophilus phosphofructokinase. <i>Biochemistry</i> , 2012 , 51, 769-75	3.2	8

15	Antidiabetic actions of a non-agonist PPARIligand blocking Cdk5-mediated phosphorylation. <i>Nature</i> , 2011 , 477, 477-81	50.4	404
14	DNA binding alters coactivator interaction surfaces of the intact VDR-RXR complex. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 556-63	17.6	154
13	The TB Structural Genomics Consortium: a decade of progress. <i>Tuberculosis</i> , 2011 , 91, 155-72	2.6	33
12	Structure of the Mycobacterium tuberculosis D-alanine:D-alanine ligase, a target of the antituberculosis drug D-cycloserine. <i>Antimicrobial Agents and Chemotherapy</i> , 2011 , 55, 291-301	5.9	89
11	Coupling of receptor conformation and ligand orientation determine graded activity. <i>Nature Chemical Biology</i> , 2010 , 6, 837-43	11.7	102
10	Structural insights into the mechanism of the allosteric transitions of Mycobacterium tuberculosis cAMP receptor protein. <i>Journal of Biological Chemistry</i> , 2009 , 284, 36581-36591	5.4	30
9	NFkappaB selectivity of estrogen receptor ligands revealed by comparative crystallographic analyses. <i>Nature Chemical Biology</i> , 2008 , 4, 241-7	11.7	123
8	Prediction of the tissue-specificity of selective estrogen receptor modulators by using a single biochemical method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 7171-6	11.5	76
7	Elemental isomerism: a boron-nitrogen surrogate for a carbon-carbon double bond increases the chemical diversity of estrogen receptor ligands. <i>Chemistry and Biology</i> , 2007 , 14, 659-69		57
6	Structural plasticity in the oestrogen receptor ligand-binding domain. <i>EMBO Reports</i> , 2007 , 8, 563-8	6.5	109
5	Structural plasticity in the oestrogen receptor ligand-binding domain. <i>EMBO Reports</i> , 2007 , 8, 610-610	6.5	1
4	Partial agonists activate PPARgamma using a helix 12 independent mechanism. <i>Structure</i> , 2007 , 15, 125	58 5 . <u>7</u> 21	271
3	Structural and thermodynamic analysis of human PCNA with peptides derived from DNA polymerase-delta p66 subunit and flap endonuclease-1. <i>Structure</i> , 2004 , 12, 2209-19	5.2	163
2	Different Geometric Requirements for Cytochrome P450-Catalyzed Aliphatic Versus Aromatic Hydroxylation Results in Chemoselective Oxidation. <i>ACS Catalysis</i> ,1258-1267	13.1	O
1	Analysis of the mutation dynamics of SARS-CoV-2 reveals the spread history and emergence of RBD mutant with lower ACE2 binding affinity		46