

# William B Church

## List of Publications by Year in descending order

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67  
papers

1,898  
citations

304743

22  
h-index

265206

42  
g-index

67  
all docs

67  
docs citations

67  
times ranked

2992  
citing authors

#	ARTICLE	IF	CITATIONS
1	An improved production and purification protocol for recombinant soluble human fibroblast activation protein alpha. <i>Protein Expression and Purification</i> , 2021, 181, 105833.	1.3	2
2	A mechanistic perspective, clinical applications, and phage-display-assisted discovery of TNF $\pm$ inhibitors. <i>Drug Discovery Today</i> , 2021, 27, 503-503.	6.4	1
3	Human Group IIA Phospholipase A2 $\alpha$ —Three Decades on from Its Discovery. <i>Molecules</i> , 2021, 26, 7267.	3.8	12
4	Structural and Functional Aspects of Targeting the Secreted Human Group IIA Phospholipase A2. <i>Molecules</i> , 2020, 25, 4459.	3.8	26
5	A Novel Purification Procedure for Active Recombinant Human DPP4 and the Inability of DPP4 to Bind SARS-CoV-2. <i>Molecules</i> , 2020, 25, 5392.	3.8	26
6	Fragment Screening of Human Kynurenine Aminotransferase-II. <i>SLAS Discovery</i> , 2018, 23, 511-519.	2.7	0
7	Improvement of kynurenine aminotransferase-II inhibitors guided by mimicking sulfate esters. <i>PLoS ONE</i> , 2018, 13, e0196404.	2.5	10
8	BAMLET kills chemotherapy-resistant mesothelioma cells, holding oleic acid in an activated cytotoxic state. <i>PLoS ONE</i> , 2018, 13, e0203003.	2.5	10
9	Molecular dynamics simulations reveal structural insights into inhibitor binding modes and functionality in human Group IIA phospholipase A2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 827-842.	2.6	3
10	Comparative macrocycle binding of the anticancer drug phenanthriplatin by cucurbit[n]urils, $\beta$ -cyclodextrin and para-sulfonatocalix[4]arene: a 1H NMR and molecular modelling study. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 2017, 87, 251-258.	1.6	18
11	High resolution crystal structures of human kynurenine aminotransferase $\alpha$ bound to PLP cofactor, and in complex with aminooxyacetate. <i>Protein Science</i> , 2017, 26, 727-736.	7.6	12
12	Neutron scattering shows a droplet of oleic acid at the center of the BAMLET complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1371-1378.	2.6	7
13	Cover Image, Volume 85, Issue 7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C4.	2.6	0
14	Crystal structure and mechanistic analysis of a novel human kynurenine aminotransferase-2 reversible inhibitor. <i>Medicinal Chemistry Research</i> , 2017, 26, 2514-2519.	2.4	3
15	Inhibition of human kynurenine aminotransferase isozymes by estrogen and its derivatives. <i>Scientific Reports</i> , 2017, 7, 17559.	3.3	42
16	Structure of the PLP-Form of the Human Kynurenine Aminotransferase II in a Novel Spacegroup at 1.83 Å... Resolution. <i>International Journal of Molecular Sciences</i> , 2016, 17, 446.	4.1	13
17	Kynurenine Aminotransferase Isozyme Inhibitors: A Review. <i>International Journal of Molecular Sciences</i> , 2016, 17, 946.	4.1	41
18	Study of the Activity and Possible Mechanism of Action of a Reversible Inhibitor of Recombinant Human KAT-2: A Promising Lead in Neurodegenerative and Cognitive Disorders. <i>Molecules</i> , 2016, 21, 856.	3.8	17

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19	Host-Guest Complexes of Carboxylated Pillar[ n ]arenes With Drugs. <i>Journal of Pharmaceutical Sciences</i> , 2016, 105, 3615-3625.	3.3	40
20	Expression, purification and crystallization of human kynurenine aminotransferase 2 exploiting a highly optimized codon set. <i>Protein Expression and Purification</i> , 2016, 121, 41-45.	1.3	7
21	Structure and Potential Cellular Targets of HAMLET-like Anti-Cancer Compounds made from Milk Components. <i>Journal of Pharmacy and Pharmaceutical Sciences</i> , 2015, 18, 773.	2.1	21
22	Kynurenine Aminotransferases and the Prospects of Inhibitors for the Treatment of Schizophrenia. <i>Current Medicinal Chemistry</i> , 2015, 22, 2902-2918.	2.4	34
23	Structural and Computational Approaches in Drug Design for G Protein-Coupled Receptors. , 2015, , 479-489.		2
24	Homology Modeling of Human Kynurenine Aminotransferase III and Observations on Inhibitor Binding Using Molecular Docking. <i>Central Nervous System Agents in Medicinal Chemistry</i> , 2014, 14, 2-9.	1.1	7
25	Smallâ€angle Xâ€ray scattering of BAMLET at pH 12: A complex of Î±â€lactalbumin and oleic acid. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1400-1408.	2.6	21
26	In silico evaluation of the influence of the translocon on partitioning of membrane segments. <i>BMC Bioinformatics</i> , 2014, 15, 156.	2.6	1
27	The use of soluble protein structures in modeling helical proteins in a layered membrane. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 308-318.	3.5	1
28	Essential Structural Features of Novel Antischizophrenic Drugs: A Review. <i>Medicinal Chemistry</i> , 2014, 10, 541-549.	1.5	7
29	A benchmark server using high resolution protein structure data, and benchmark results for membrane helix predictions. <i>BMC Bioinformatics</i> , 2013, 14, 111.	2.6	9
30	Functional Analysis of Novel Polymorphisms in the Human SLCO1A2 Gene that Encodes the Transporter OATP1A2. <i>AAPS Journal</i> , 2013, 15, 1099-1108.	4.4	41
31	Kink Characterization and Modeling in Transmembrane Protein Structures. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 2926-2936.	5.4	6
32	Phage display as a technology delivering on the promise of peptide drug discovery. <i>Drug Discovery Today</i> , 2013, 18, 1144-1157.	6.4	135
33	Selective Inhibition of Human Group IIA-secreted Phospholipase A2 (hGIIA) Signaling Reveals Arachidonic Acid Metabolism Is Associated with Colocalization of hGIIA to Vimentin in Rheumatoid Synoviocytes. <i>Journal of Biological Chemistry</i> , 2013, 288, 15269-15279.	3.4	23
34	Seasoned adaptive antibody immunity for highly pathogenic pandemic influenza in humans. <i>Immunology and Cell Biology</i> , 2012, 90, 149-158.	2.3	7
35	Structural modelling and dynamics of proteins for insights into drug interactions. <i>Advanced Drug Delivery Reviews</i> , 2012, 64, 323-343.	13.7	32
36	Design and synthesis of novel inhibitors of human kynurenine aminotransferase-I. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2012, 22, 1579-1581.	2.2	15

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37	The modular structure of haemagglutinin/adhesin regions in gingipains of <i>Porphyromonas gingivalis</i> . <i>Molecular Microbiology</i> , 2011, 81, 1358-1373.	2.5	20
38	Status of GPCR Modeling and Docking as Reflected by Community-wide GPCR Dock 2010 Assessment. <i>Structure</i> , 2011, 19, 1108-1126.	3.3	269
39	Allosteric Modulation of the Calcium-sensing Receptor by $\hat{I}^3$ -Glutamyl Peptides. <i>Journal of Biological Chemistry</i> , 2011, 286, 8786-8797.	3.4	82
40	A Bifunctional Role for Group IIA Secreted Phospholipase A2 in Human Rheumatoid Fibroblast-like Synoviocyte Arachidonic Acid Metabolism. <i>Journal of Biological Chemistry</i> , 2011, 286, 2492-2503.	3.4	29
41	The molecular structure of the IsiA Photosystem I supercomplex, modelled from high-resolution, crystal structures of Photosystem I and the CP43 protein. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 457-465.	1.0	14
42	Functional characterization of nonsynonymous single nucleotide polymorphisms in the human organic anion transporter 4 (hOAT4). <i>British Journal of Pharmacology</i> , 2010, 159, 419-427.	5.4	34
43	The dipeptidyl peptidase IV family in cancer and cell biology. <i>FEBS Journal</i> , 2010, 277, 1126-1144.	4.7	149
44	Rhodopsin: Structure, signal transduction and oligomerisation. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 721-724.	2.8	13
45	Modelling the structures of G protein-coupled receptors aided by three-dimensional validation. <i>BMC Bioinformatics</i> , 2008, 9, S14.	2.6	11
46	Reversible Inactivation of Human Dipeptidyl Peptidases 8 and 9 by Oxidation. <i>The Open Enzyme Inhibition Journal</i> , 2008, 1, 52-60.	2.0	39
47	Comparative modeling of marsupial MHC class I molecules identifies structural polymorphisms affecting functional motifs. <i>Journal of Experimental Zoology</i> , 2007, 307A, 611-624.	1.2	3
48	Prediction of rotational orientation of transmembrane helical segments of integral membrane proteins using new environment-based propensities for amino acids derived from structural analyses. <i>FEBS Journal</i> , 2007, 274, 2653-2660.	4.7	11
49	Marked differences in the structures and protein associations of lymphocyte and monocyte CD4: Resolution of a novel CD4 isoform. <i>Immunology and Cell Biology</i> , 2006, 84, 154-165.	2.3	24
50	Djinn Lite: a tool for customised gene transcript modelling, annotation-data enrichment and exploration. <i>BMC Bioinformatics</i> , 2006, 7, 33.	2.6	2
51	Presence of transient helical segments in the galanin-like peptide evident from 1H NMR, circular dichroism, and prediction studies. <i>Journal of Structural Biology</i> , 2004, 146, 261-271.	2.8	7
52	Interactions of SKIP/NCoA-62, TFIIB, and Retinoid X Receptor with Vitamin D Receptor Helix H10 Residues. <i>Journal of Biological Chemistry</i> , 2003, 278, 8224-8228.	3.4	42
53	A Missense Mutation in Kynurenine Aminotransferase-1 in Spontaneously Hypertensive Rats. <i>Journal of Biological Chemistry</i> , 2002, 277, 35779-35782.	3.4	46
54	Comparison of the transmembrane helices of bovine rhodopsin in the crystal structure and the C $\hat{I}$ template based on cryo-electron microscopy maps and sequence analysis of the G protein-coupled receptors. <i>Molecular Simulation</i> , 2002, 28, 845-851.	2.0	5

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55	Modeling of the structural features of integral-membrane proteins reverse-environment prediction of integral membrane protein structure (REPIMPS). <i>Protein Science</i> , 2001, 10, 1529-1538.	7.6	9
56	A Novel Approach to the Design of Inhibitors of Human Secreted Phospholipase A2 Based on Native Peptide Inhibition. <i>Journal of Biological Chemistry</i> , 2001, 276, 33156-33164.	3.4	38
57	Crystallization and preliminary X-ray diffraction studies of a new crystal form of human secretory type IIA phospholipase A2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1482-1484.	2.5	1
58	Molecular pathogenesis of liver disease: an approach to hepatic inflammation, cirrhosis and liver transplant tolerance. <i>Immunological Reviews</i> , 2000, 174, 172-191.	6.0	77
59	GTP Binding and Signaling by Gh/Transglutaminase II Involves Distinct Residues in a Unique GTP-binding Pocket. <i>Journal of Biological Chemistry</i> , 2000, 275, 18259-18265.	3.4	91
60	Relating Structure to Function in the Beta-Propeller Domain of Dipeptidyl Peptidase IV. , 2000, 477, 89-95.		10
61	Binding to human dipeptidyl peptidase IV by adenosine deaminase and antibodies that inhibit ligand binding involves overlapping, discontinuous sites on a predicted $\hat{1}^2$ propeller domain. <i>FEBS Journal</i> , 1999, 266, 798-810.	0.2	83
62	Homology model of Juvenile Hormone Esterase from the crop pest, <i>Heliothis virescens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 34, 184-196.	2.6	42
63	The function of conserved amino acid residues adjacent to the effector domain in elongation factor G. , 1999, 37, 293-302.		6
64	Structural Determinants of the Interaction between the erbB2 Receptor and the Src Homology 2 Domain of Grb7. <i>Journal of Biological Chemistry</i> , 1997, 272, 8490-8497.	3.4	71
65	A homology-based model of Juvenile Hormone Esterase from the crop pest, <i>Heliothis virescens</i> . <i>Techniques in Protein Chemistry</i> , 1997, , 655-665.	0.3	4
66	Homology modeling of histidine-containing phosphocarrier protein and eosinophil-derived neurotoxin: Construction of models and comparison with experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 422-430.	2.6	2
67	Crystallization of human $\hat{1}^2$ -hexosaminidase B. <i>Journal of Molecular Biology</i> , 1992, 227, 577-580.	4.2	12