

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
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67
all docs

67
docs citations

67
times ranked

2992
citing authors

#	ARTICLE	IF	CITATIONS
1	Status of GPCR Modeling and Docking as Reflected by Community-wide GPCR Dock 2010 Assessment. Structure, 2011, 19, 1108-1126.	3.3	269
2	The dipeptidyl peptidase IV family in cancer and cell biology. FEBS Journal, 2010, 277, 1126-1144.	4.7	149
3	Phage display as a technology delivering on the promise of peptide drug discovery. Drug Discovery Today, 2013, 18, 1144-1157.	6.4	135
4	GTP Binding and Signaling by Gh/Transglutaminase II Involves Distinct Residues in a Unique GTP-binding Pocket. Journal of Biological Chemistry, 2000, 275, 18259-18265.	3.4	91
5	Binding to human dipeptidyl peptidase IV by adenosine deaminase and antibodies that inhibit ligand binding involves overlapping, discontinuous sites on a predicted I ² propeller domain. FEBS Journal, 1999, 266, 798-810.	0.2	83
6	Allosteric Modulation of the Calcium-sensing Receptor by \hat{I}^3 -Glutamyl Peptides. Journal of Biological Chemistry, 2011, 286, 8786-8797.	3.4	82
7	Molecular pathogenesis of liver disease: an approach to hepatic inflammation, cirrhosis and liver transplant tolerance. Immunological Reviews, 2000, 174, 172-191.	6.0	77
8	Structural Determinants of the Interaction between the erbB2 Receptor and the Src Homology 2 Domain of Grb7. Journal of Biological Chemistry, 1997, 272, 8490-8497.	3.4	71
9	A Missense Mutation in Kynurenine Aminotransferase-1 in Spontaneously Hypertensive Rats. Journal of Biological Chemistry, 2002, 277, 35779-35782.	3.4	46
10	Homology model of Juvenile Hormone Esterase from the crop pest, <i>Heliothis virescens</i> . Proteins: Structure, Function and Bioinformatics, 1999, 34, 184-196.	2.6	42
11	Interactions of SKIP/NCoA-62, TFIIB, and Retinoid X Receptor with Vitamin D Receptor Helix H10 Residues. Journal of Biological Chemistry, 2003, 278, 8224-8228.	3.4	42
12	Inhibition of human kynurenine aminotransferase isozymes by estrogen and its derivatives. Scientific Reports, 2017, 7, 17559.	3.3	42
13	Functional Analysis of Novel Polymorphisms in the Human SLCO1A2 Gene that Encodes the Transporter OATP1A2. AAPS Journal, 2013, 15, 1099-1108.	4.4	41
14	Kynurenine Aminotransferase Isozyme Inhibitors: A Review. International Journal of Molecular Sciences, 2016, 17, 946.	4.1	41
15	Host-Guest Complexes of Carboxylated Pillar[n]arenes With Drugs. Journal of Pharmaceutical Sciences, 2016, 105, 3615-3625.	3.3	40
16	Reversible Inactivation of Human Dipeptidyl Peptidases 8 and 9 by Oxidation. The Open Enzyme Inhibition Journal, 2008, 1, 52-60.	2.0	39
17	A Novel Approach to the Design of Inhibitors of Human Secreted Phospholipase A2 Based on Native Peptide Inhibition. Journal of Biological Chemistry, 2001, 276, 33156-33164.	3.4	38
18	Functional characterization of nonsynonymous single nucleotide polymorphisms in the human organic anion transporter 4 (hOAT4). British Journal of Pharmacology, 2010, 159, 419-427.	5.4	34

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19	Kynurenine Aminotransferases and the Prospects of Inhibitors for the Treatment of Schizophrenia. <i>Current Medicinal Chemistry</i> , 2015, 22, 2902-2918.	2.4	34
20	Structural modelling and dynamics of proteins for insights into drug interactions. <i>Advanced Drug Delivery Reviews</i> , 2012, 64, 323-343.	13.7	32
21	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
22	Structural and Functional Aspects of Targeting the Secreted Human Group IIA Phospholipase A2. <i>Molecules</i> , 2020, 25, 4459.	3.8	26
23	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
24	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
25	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
26	Small-angle X-ray scattering of BAMLET at pH 12: A complex of β -lactalbumin and oleic acid. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1400-1408.	2.6	21
27	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
28	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
29	Comparative macrocycle binding of the anticancer drug phenanthriplatin by cucurbit[n]urils, β -cyclodextrin and para-sulfonatocalix[4]arene: a ¹ H NMR and molecular modelling study. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 2017, 87, 251-258.	1.6	18
30	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
31	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
32	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
33	Rhodopsin: Structure, signal transduction and oligomerisation. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 721-724.	2.8	13
34	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
35	Crystallization of human β -hexosaminidase B. <i>Journal of Molecular Biology</i> , 1992, 227, 577-580.	4.2	12
36	High resolution crystal structures of human kynurenine aminotransferase bound to PLP cofactor, and in complex with aminoxyacetate. <i>Protein Science</i> , 2017, 26, 727-736.	7.6	12

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37	Human Group IIA Phospholipase A2—Three Decades on from Its Discovery. <i>Molecules</i> , 2021, 26, 7267.	3.8	12
38	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
39	Modelling the structures of G protein-coupled receptors aided by three-dimensional validation. <i>BMC Bioinformatics</i> , 2008, 9, S14.	2.6	11
40	Relating Structure to Function in the Beta-Propeller Domain of Dipeptidyl Peptidase IV. , 2000, 477, 89-95.		10
41	Improvement of kynurenine aminotransferase-II inhibitors guided by mimicking sulfate esters. <i>PLoS ONE</i> , 2018, 13, e0196404.	2.5	10
42	BAMLET kills chemotherapy-resistant mesothelioma cells, holding oleic acid in an activated cytotoxic state. <i>PLoS ONE</i> , 2018, 13, e0203003.	2.5	10
43	Modeling of the structural features of integral-membrane proteins reverse-environment prediction of integral membrane protein structure (REPMPS). <i>Protein Science</i> , 2001, 10, 1529-1538.	7.6	9
44	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
45	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
46	Seasoned adaptive antibody immunity for highly pathogenic pandemic influenza in humans. <i>Immunology and Cell Biology</i> , 2012, 90, 149-158.	2.3	7
47	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
48	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
49	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
50	Essential Structural Features of Novel Antischizophrenic Drugs: A Review. <i>Medicinal Chemistry</i> , 2014, 10, 541-549.	1.5	7
51	The function of conserved amino acid residues adjacent to the effector domain in elongation factor G. , 1999, 37, 293-302.		6
52	Kink Characterization and Modeling in Transmembrane Protein Structures. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 2926-2936.	5.4	6
53	Comparison of the transmembrane helices of bovine rhodopsin in the crystal structure and the C β 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
54	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

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55	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
56	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
57	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
58	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
59	Djinn Lite: a tool for customised gene transcript modelling, annotation-data enrichment and exploration. <i>BMC Bioinformatics</i> , 2006, 7, 33.	2.6	2
60	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
61	Structural and Computational Approaches in Drug Design for G Protein-Coupled Receptors. , 2015, , 479-489.		2
62	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
63	In silico evaluation of the influence of the translocon on partitioning of membrane segments. <i>BMC Bioinformatics</i> , 2014, 15, 156.	2.6	1
64	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
65	A mechanistic perspective, clinical applications, and phage-display-assisted discovery of TNF $\hat{\pm}$ inhibitors. <i>Drug Discovery Today</i> , 2021, 27, 503-503.	6.4	1
66	Cover Image, Volume 85, Issue 7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C4.	2.6	0
67	Fragment Screening of Human Kynurenine Aminotransferase-II. <i>SLAS Discovery</i> , 2018, 23, 511-519.	2.7	0