Georg Kuenze

List of Publications by Year
in descending order

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32 papers	1,179 citations	567281 15 h-index	454955 30 g-index
41 all docs	41 docs citations	41 times ranked	1752 citing authors

#	Article	IF	Citations
1	Predicting the functional impact of KCNQ1 variants with artificial neural networks. PLoS Computational Biology, 2022, 18, e1010038.	3.2	5
2	Molecular Simulations Reveal Distinct Energetic and Kinetic Binding Properties of [¹⁸F]PI-2620 on Tau Filaments from 3R/4R and 4R Tauopathies. ACS Chemical Neuroscience, 2022, 13, 2222-2234.	3.5	10
3	Disease-linked supertrafficking of a potassium channel. Journal of Biological Chemistry, 2021, 296, 100423.	3.4	3
4	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. Biochemistry, 2021, 60, 825-846.	2.5	24
5	Investigation of the structure of regulatory proteins interacting with glycosaminoglycans by combining NMR spectroscopy and molecular modelingÂâ€“ the beginning of a wonderful friendship. Biological Chemistry, 2021, 402, 1337-1355.	2.5	16
6	An arginine residue in the outer segment of hASIC1a TM1 affects both proton affinity and channel desensitization. Journal of General Physiology, 2021, 153, .	1.9	8
7	Structural determinants of cholesterol recognition in helical integral membrane proteins. Biophysical Journal, 2021, 120, 1592-1604.	0.5	12
8	Paramagnetic spin labeling of a bacterial DnaB helicase for solid-state NMR. Journal of Magnetic Resonance, 2021, 332, 107075.	2.1	2
9	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
10	Site-specific dynamic nuclear polarization in a Gd(iii)-labeled protein. Physical Chemistry Chemical Physics, 2020, 22, 25455-25466.	2.8	15
11	Integrated Structural Modeling of Full-Length LRH-1 Reveals Inter-domain Interactions Contribute to Receptor Structure and Function. Structure, 2020, 28, 830-846.e9.	3.3	22
12	Structures Illuminate Cardiac Ion Channel Functions in Health and in Long QT Syndrome. Frontiers in Pharmacology, 2020, 11, 550.	3.5	23
13	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
14	Structure and physiological function of the human KCNQ1 channel voltage sensor intermediate state. ELife, 2020, 9, .	6.0	36
15	Allosteric mechanism for KCNE1 modulation of KCNQ1 potassium channel activation. ELife, 2020, 9, .	6.0	19
16	Structure and Physiological Function of the KCNQ1 Channel Voltage Sensor Intermediate State. Biophysical Journal, 2020, 118, 333a.	0.5	0
17	Protein structure prediction using sparse NOE and RDC restraints with Rosetta in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1341-1350.	2.6	11
18	Integrative Protein Modeling in RosettaNMR from Sparse Paramagnetic Restraints. Structure, 2019, 27, 1721-1734.e5.	3.3	25

#	Article	IF	Citations
19	A unified structural model of the mammalian translocator protein (TSPO). Journal of Biomolecular NMR, 2019, 73, 347-364.	2.8	12
20	Upgraded molecular models of the human KCNQ1 potassium channel. PLoS ONE, 2019, 14, e0220415.	2.5	26
21	The molecular basis of subtype selectivity of human kinin G-protein-coupled receptors. Nature Chemical Biology, 2018, 14, 284-290.	8.0	74
22	Mechanisms of KCNQ1 channel dysfunction in long QT syndrome involving voltage sensor domain mutations. Science Advances, 2018, 4, eaar2631.	10.3	64
23	Structure and Function of the Transmembrane Domain of NsaS, an Antibiotic Sensing Histidine Kinase in Staphylococcus aureus. Journal of the American Chemical Society, 2018, 140, 7471-7485.	13.7	17
24	Chemoenzymatic Synthesis of Nonasulfated Tetrahyaluronan with a Paramagnetic Tag for Studying Its Complex with Interleukinâ€10. Chemistry - A European Journal, 2016, 22, 5563-5574.	3.3	35
25	Identification of the Glycosaminoglycan Binding Site of Interleukin-10 by NMR Spectroscopy. Journal of Biological Chemistry, 2016, 291, 3100-3113.	3.4	32
26	Rational Structure-Based Rescaffolding Approach to De Novo Design of Interleukin 10 (IL-10) Receptor-1 Mimetics. PLoS ONE, 2016, 11, e0154046.	2.5	2
27	NMR characterization of the binding properties and conformation of glycosaminoglycans interacting with interleukin-10. Glycobiology, 2014, 24, 1036-1049.	2.5	28
28	Backbone 1H, 15N, 13C and side chain 13CÎ² NMR chemical shift assignment of murine interleukin-10. Biomolecular NMR Assignments, 2014, 8, 375-378.	0.8	5
29	The role of substrate specificity and metal binding in defining the activity and structure of an intracellular subtilisin. FEBS Open Bio, 2012, 2, 209-215.	2.3	12
30	Binding of the three-repeat domain of tau to phospholipid membranes induces an aggregated-like state of the protein. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 2302-2313.	2.6	70
31	Regulation of an intracellular subtilisin protease activity by a short propeptide sequence through an original combined dual mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3536-3541.	7.1	18
32	Crystal Structure of an Intracellular Subtilisin Reveals Novel Structural Features Unique to this Subtilisin Family. Structure, 2010, 18, 744-755.	3.3	20