

Georg Kuenze

List of Publications by Year in descending order

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Version: 2024-02-01

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	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
2	The molecular basis of subtype selectivity of human kinin G-protein-coupled receptors. <i>Nature Chemical Biology</i> , 2018, 14, 284-290.	8.0	74
3	Binding of the three-repeat domain of tau to phospholipid membranes induces an aggregated-like state of the protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 2302-2313.	2.6	70
4	Mechanisms of KCNQ1 channel dysfunction in long QT syndrome involving voltage sensor domain mutations. <i>Science Advances</i> , 2018, 4, eaar2631.	10.3	64
5	Structure and physiological function of the human KCNQ1 channel voltage sensor intermediate state. <i>ELife</i> , 2020, 9, .	6.0	36
6	Chemoenzymatic Synthesis of Nonasulfated Tetrahyaluronan with a Paramagnetic Tag for Studying Its Complex with Interleukin-10. <i>Chemistry - A European Journal</i> , 2016, 22, 5563-5574.	3.3	35
7	Identification of the Glycosaminoglycan Binding Site of Interleukin-10 by NMR Spectroscopy. <i>Journal of Biological Chemistry</i> , 2016, 291, 3100-3113.	3.4	32
8	NMR characterization of the binding properties and conformation of glycosaminoglycans interacting with interleukin-10. <i>Glycobiology</i> , 2014, 24, 1036-1049.	2.5	28
9	Upgraded molecular models of the human KCNQ1 potassium channel. <i>PLoS ONE</i> , 2019, 14, e0220415.	2.5	26
10	Integrative Protein Modeling in RosettaNMR from Sparse Paramagnetic Restraints. <i>Structure</i> , 2019, 27, 1721-1734.e5.	3.3	25
11	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. <i>Biochemistry</i> , 2021, 60, 825-846.	2.5	24
12	Structures Illuminate Cardiac Ion Channel Functions in Health and in Long QT Syndrome. <i>Frontiers in Pharmacology</i> , 2020, 11, 550.	3.5	23
13	Integrated Structural Modeling of Full-Length LRH-1 Reveals Inter-domain Interactions Contribute to Receptor Structure and Function. <i>Structure</i> , 2020, 28, 830-846.e9.	3.3	22
14	Crystal Structure of an Intracellular Subtilisin Reveals Novel Structural Features Unique to this Subtilisin Family. <i>Structure</i> , 2010, 18, 744-755.	3.3	20
15	Allosteric mechanism for KCNE1 modulation of KCNQ1 potassium channel activation. <i>ELife</i> , 2020, 9, .	6.0	19
16	Regulation of an intracellular subtilisin protease activity by a short propeptide sequence through an original combined dual mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3536-3541.	7.1	18
17	Structure and Function of the Transmembrane Domain of NsaS, an Antibiotic Sensing Histidine Kinase in <i>Staphylococcus aureus</i> . <i>Journal of the American Chemical Society</i> , 2018, 140, 7471-7485.	13.7	17
18	Investigation of the structure of regulatory proteins interacting with glycosaminoglycans by combining NMR spectroscopy and molecular modeling – the beginning of a wonderful friendship. <i>Biological Chemistry</i> , 2021, 402, 1337-1355.	2.5	16

#	ARTICLE	IF	CITATIONS
19	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947.	12.8	16
20	Site-specific dynamic nuclear polarization in a Gd(III)-labeled protein. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 25455-25466.	2.8	15
21	The role of substrate specificity and metal binding in defining the activity and structure of an intracellular subtilisin. <i>FEBS Open Bio</i> , 2012, 2, 209-215.	2.3	12
22	A unified structural model of the mammalian translocator protein (TSPO). <i>Journal of Biomolecular NMR</i> , 2019, 73, 347-364.	2.8	12
23	Structural determinants of cholesterol recognition in helical integral membrane proteins. <i>Biophysical Journal</i> , 2021, 120, 1592-1604.	0.5	12
24	Protein structure prediction using sparse NOE and RDC restraints with Rosetta in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1341-1350.	2.6	11
25	Molecular Simulations Reveal Distinct Energetic and Kinetic Binding Properties of [¹⁸ F]PI-2620 on Tau Filaments from 3R/4R and 4R Tauopathies. <i>ACS Chemical Neuroscience</i> , 2022, 13, 2222-2234.	3.5	10
26	An arginine residue in the outer segment of hASIC1a TM1 affects both proton affinity and channel desensitization. <i>Journal of General Physiology</i> , 2021, 153, .	1.9	8
27	Backbone ¹ H, ¹⁵ N, ¹³ C and side chain ¹³ C ^β NMR chemical shift assignment of murine interleukin-10. <i>Biomolecular NMR Assignments</i> , 2014, 8, 375-378.	0.8	5
28	Predicting the functional impact of KCNQ1 variants with artificial neural networks. <i>PLoS Computational Biology</i> , 2022, 18, e1010038.	3.2	5
29	Disease-linked supertrafficking of a potassium channel. <i>Journal of Biological Chemistry</i> , 2021, 296, 100423.	3.4	3
30	Paramagnetic spin labeling of a bacterial DnaB helicase for solid-state NMR. <i>Journal of Magnetic Resonance</i> , 2021, 332, 107075.	2.1	2
31	Rational Structure-Based Rescaffolding Approach to De Novo Design of Interleukin 10 (IL-10) Receptor-1 Mimetics. <i>PLoS ONE</i> , 2016, 11, e0154046.	2.5	2
32	Structure and Physiological Function of the KCNQ1 Channel Voltage Sensor Intermediate State. <i>Biophysical Journal</i> , 2020, 118, 333a.	0.5	0