

Ralf Schmid

List of Publications by Year in descending order

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54
papers

2,085
citations

236925

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56
docs citations

56
times ranked

3250
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Basis of the Negative Allosteric Modulation of 5-BDBD at Human P2X4 Receptors. <i>Molecular Pharmacology</i> , 2022, 101, 33-44.	2.3	12
2	Limitations of Monitoring Disease Progression Using Circulating Tumor DNA in Lymphoma: An Example From Primary Cutaneous DLBCL Leg-type. <i>HemaSphere</i> , 2022, 6, e690.	2.7	0
3	Identification of a distinct desensitisation gate in the ATP-gated P2X2 receptor. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 190-195.	2.1	2
4	Discovery of a heme-binding domain in a neuronal voltage-gated potassium channel. <i>Journal of Biological Chemistry</i> , 2020, 295, 13277-13286.	3.4	17
5	Discovery and Structure Relationships of Salicylanilide Derivatives as Potent, Non-acidic P2X1 Receptor Antagonists. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 6164-6178.	6.4	10
6	Homology Modeling of P2X Receptors. <i>Methods in Molecular Biology</i> , 2020, 2041, 65-75.	0.9	6
7	Mapping the Site of Action of Human P2X7 Receptor Antagonists AZ11645373, Brilliant Blue G, KN-62, Calmidazolium, and ZINC58368839 to the Intersubunit Allosteric Pocket. <i>Molecular Pharmacology</i> , 2019, 96, 355-363.	2.3	25
8	Cytosolic glucosylceramide regulates endolysosomal function in Niemann-Pick type C disease. <i>Neurobiology of Disease</i> , 2019, 127, 242-252.	4.4	23
9	Lipid-Protein Interactions in Niemann-Pick Type C Disease: Insights from Molecular Modeling. <i>International Journal of Molecular Sciences</i> , 2019, 20, 717.	4.1	19
10	Organization of ATP-gated P2X1 receptor intracellular termini in apo and desensitized states. <i>Journal of General Physiology</i> , 2019, 151, 146-155.	1.9	6
11	ATP-Gated P2X Receptor Channels: Molecular Insights into Functional Roles. <i>Annual Review of Physiology</i> , 2019, 81, 43-62.	13.1	44
12	A mechanism for CO regulation of ion channels. <i>Nature Communications</i> , 2018, 9, 907.	12.8	38
13	Mapping the Allosteric Action of Antagonists A740003 and A438079 Reveals a Role for the Left Flipper in Ligand Sensitivity at P2X7 Receptors. <i>Molecular Pharmacology</i> , 2018, 93, 553-562.	2.3	25
14	Mapping the binding site of the P2X receptor antagonist PPADS reveals the importance of orthosteric site charge and the cysteine-rich head region. <i>Journal of Biological Chemistry</i> , 2018, 293, 12820-12831.	3.4	19
15	Unique residues in the ATP gated human P2X7 receptor define a novel allosteric binding pocket for the selective antagonist AZ10606120. <i>Scientific Reports</i> , 2017, 7, 725.	3.3	58
16	Mechanistic insights from resolving ligand-dependent kinetics of conformational changes at ATP-gated P2X1R ion channels. <i>Scientific Reports</i> , 2016, 6, 32918.	3.3	14
17	A heme-binding domain controls regulation of ATP-dependent potassium channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3785-3790.	7.1	53
18	The Molecular Basis for Heme Modulation of KATP Channels. <i>Biophysical Journal</i> , 2015, 108, 437a.	0.5	0

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19	Structural Insights into Separase Architecture and Substrate Recognition through Computational Modelling of Caspase-Like and Death Domains. <i>PLoS Computational Biology</i> , 2015, 11, e1004548.	3.2	20
20	Use of Chimeras, Point Mutants, and Molecular Modeling to Map the Antagonist-binding Site of 4,4'-bis(4-(Carboxylbis-(imino-5,1,3-benzenetriylbis(carboxylimino)))tetrakisbenzene-1,3-disulfonic Acid (NF449) at P2X1 Receptors for ATP. <i>Journal of Biological Chemistry</i> , 2015, 290, 1559-1569.	3.4	7
21	Malaria Protein Kinase CK2 (PfCK2) Shows Novel Mechanisms of Regulation. <i>PLoS ONE</i> , 2014, 9, e85391.	2.5	14
22	Molecular Evolution of a Pervasive Natural Amino-Acid Substitution in <i>Drosophila</i> cryptochrome. <i>PLoS ONE</i> , 2014, 9, e86483.	2.5	10
23	A Canonical EF-loop Directs Ca ²⁺ -Sensitivity in Phospholipase C-2. <i>Journal of Cellular Biochemistry</i> , 2014, 115, 557-565.	2.6	12
24	The splicing landscape is globally reprogrammed during male meiosis. <i>Nucleic Acids Research</i> , 2013, 41, 10170-10184.	14.5	71
25	Agonist binding evokes extensive conformational changes in the extracellular domain of the ATP-gated human P2X1 receptor ion channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4663-4667.	7.1	51
26	Acinetobacter Insertion Sequence IS <i>Aba11</i> Belongs to a Novel Family That Encodes Transposases with a Signature HHEK Motif. <i>Applied and Environmental Microbiology</i> , 2012, 78, 471-480.	3.1	7
27	Mining Genomes of Marine Cyanobacteria for Elements of Zinc Homeostasis. <i>Frontiers in Microbiology</i> , 2012, 3, 142.	3.5	51
28	FASCAPLYSIN as a Specific Inhibitor for CDK4: Insights from Molecular Modelling. <i>PLoS ONE</i> , 2012, 7, e42612.	2.5	43
29	Cysteine Scanning Mutagenesis (Residues Glu52-Gly96) of the Human P2X1 Receptor for ATP. <i>Journal of Biological Chemistry</i> , 2011, 286, 29207-29217.	3.4	37
30	Cytosolic metal handling in plants: determinants for zinc specificity in metal transporters and metallothioneins. <i>Metallomics</i> , 2010, 2, 510.	2.4	71
31	Paths reunited: Initiation of the classical and lectin pathways of complement activation. <i>Immunobiology</i> , 2010, 215, 1-11.	1.9	135
32	Flavones as Colorectal Cancer Chemopreventive Agents: Phenol-Methylation Enhances Efficacy. <i>Cancer Prevention Research</i> , 2009, 2, 743-750.	1.5	52
33	Analogous Interactions in Initiating Complexes of the Classical and Lectin Pathways of Complement. <i>Journal of Immunology</i> , 2009, 182, 7708-7717.	0.8	59
34	MicroRNA and tasiRNA diversity in mature pollen of <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2009, 10, 643.	2.8	112
35	EST Processing: From Trace to Sequence. <i>Methods in Molecular Biology</i> , 2009, 533, 189-220.	0.9	3
36	Pitfalls of using out of date databases. Comment on Guo et al. and Guo et al.. <i>Journal of Theoretical Biology</i> , 2008, 255, 267.	1.7	0

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37	annot8: GO, EC and KEGG annotation of EST datasets. BMC Bioinformatics, 2008, 9, 180.	2.6	87
38	Developmentally regulated expression, alternative splicing and distinct sub-groupings in members of the Schistosoma mansoni venom allergen-like (SmVAL) gene family. BMC Genomics, 2008, 9, 89.	2.8	112
39	Structural analysis of the adenovirus type 2 E3/19K protein using mutagenesis and a panel of conformation-sensitive monoclonal antibodies. Molecular Immunology, 2008, 46, 16-26.	2.2	7
40	On the Extent and Origins of Genic Novelty in the Phylum Nematoda. PLoS Neglected Tropical Diseases, 2008, 2, e258.	3.0	68
41	Toward a property/function relationship for metallothioneins: Histidine coordination and unusual cluster composition in a zinc-metallothionein from plants. Proteins: Structure, Function and Bioinformatics, 2007, 68, 922-935.	2.6	52
42	Computational Genome Analysis: An Introduction. R. C. Deonier, S. TavarÃ© & M. S. Waterman. Springer. 2005. 515 pages. ISBN 0 387 98785 1. Price \$79.95. (hardback). Genetical Research, 2006, 87, 218-219.	0.9	1
43	Probing the substrate specificities of human PHOSPHO1 and PHOSPHO2. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1752, 73-82.	2.3	32
44	NEMBASE: a resource for parasitic nematode ESTs. Nucleic Acids Research, 2004, 32, 427D-430.	14.5	65
45	PartiGene--constructing partial genomes. Bioinformatics, 2004, 20, 1398-1404.	4.1	129
46	A transcriptomic analysis of the phylum Nematoda. Nature Genetics, 2004, 36, 1259-1267.	21.4	239
47	Functional properties of the alternative NADH:ubiquinone oxidoreductase from E. coli through comparative 3-D modelling. FEBS Letters, 2004, 578, 163-168.	2.8	22
48	A novel copper site in a cyanobacterial metallochaperone. Biochemical Journal, 2004, 378, 293-297.	3.7	29
49	Comparative modelling of human PHOSPHO1 reveals a new group of phosphatases within the haloacid dehalogenase superfamily. Protein Engineering, Design and Selection, 2003, 16, 889-895.	2.1	42
50	Exploring the primary electron acceptor (QA)-site of the bacterial reaction center from Rhodospirillum rubrum. FEBS Journal, 2002, 269, 1096-1108.	0.2	7
51	Temperature and Free Energy Dependence of the Direct Charge Recombination Rate from the Secondary Quinone in Bacterial Reaction Centers from Rhodospirillum rubrum. Journal of Physical Chemistry B, 2000, 104, 2928-2936.	2.6	40
52	Synthesis and redox potentials of methylated vitamin K derivatives. Journal of the Chemical Society Perkin Transactions II, 1999, , 1199-1202.	0.9	22
53	Temperature Dependence of the Direct Charge Recombination From QA- to QA+ in Bacterial Reaction Centers from Rhodospirillum rubrum. , 1998, , 829-832.		1
54	The Influence of Quinone Structure on Quinone Binding to the QA Site in Bacterial Reaction Centers from Rhodospirillum rubrum. , 1998, , 877-880.		2