

Ralf Schmid

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

2,085
citations

236925

25
h-index

233421

45
g-index

56
all docs

56
docs citations

56
times ranked

3250
citing authors

#	ARTICLE	IF	CITATIONS
1	A transcriptomic analysis of the phylum Nematoda. <i>Nature Genetics</i> , 2004, 36, 1259-1267.	21.4	239
2	Paths reunited: Initiation of the classical and lectin pathways of complement activation. <i>Immunobiology</i> , 2010, 215, 1-11.	1.9	135
3	PartiGene--constructing partial genomes. <i>Bioinformatics</i> , 2004, 20, 1398-1404.	4.1	129
4	Developmentally regulated expression, alternative splicing and distinct sub-groupings in members of the <i>Schistosoma mansoni</i> venom allergen-like (SmVAL) gene family. <i>BMC Genomics</i> , 2008, 9, 89.	2.8	112
5	MicroRNA and tasiRNA diversity in mature pollen of <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2009, 10, 643.	2.8	112
6	annot8: GO, EC and KEGG annotation of EST datasets. <i>BMC Bioinformatics</i> , 2008, 9, 180.	2.6	87
7	Cytosolic metal handling in plants: determinants for zinc specificity in metal transporters and metallothioneins. <i>Metallomics</i> , 2010, 2, 510.	2.4	71
8	The splicing landscape is globally reprogrammed during male meiosis. <i>Nucleic Acids Research</i> , 2013, 41, 10170-10184.	14.5	71
9	On the Extent and Origins of Genic Novelty in the Phylum Nematoda. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e258.	3.0	68
10	NEMBASE: a resource for parasitic nematode ESTs. <i>Nucleic Acids Research</i> , 2004, 32, 427D-430.	14.5	65
11	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
12	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
13	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
14	Toward a property/function relationship for metallothioneins: Histidine coordination and unusual cluster composition in a zinc-metallothionein from plants. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 922-935.	2.6	52
15	Flavones as Colorectal Cancer Chemopreventive Agents--Phenol-O-Methylation Enhances Efficacy. <i>Cancer Prevention Research</i> , 2009, 2, 743-750.	1.5	52
16	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
17	Mining Genomes of Marine Cyanobacteria for Elements of Zinc Homeostasis. <i>Frontiers in Microbiology</i> , 2012, 3, 142.	3.5	51
18	ATP-Gated P2X Receptor Channels: Molecular Insights into Functional Roles. <i>Annual Review of Physiology</i> , 2019, 81, 43-62.	13.1	44

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19	FASCAPLYSIN as a Specific Inhibitor for CDK4: Insights from Molecular Modelling. PLoS ONE, 2012, 7, e42612.	2.5	43
20	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
21	Temperature and Free Energy Dependence of the Direct Charge Recombination Rate from the Secondary Quinone in Bacterial Reaction Centers from Rhodobacter sphaeroides. Journal of Physical Chemistry B, 2000, 104, 2928-2936.	2.6	40
22	A mechanism for CO regulation of ion channels. Nature Communications, 2018, 9, 907.	12.8	38
23	Cysteine Scanning Mutagenesis (Residues Glu52â€“Gly96) of the Human P2X1 Receptor for ATP. Journal of Biological Chemistry, 2011, 286, 29207-29217.	3.4	37
24	Probing the substrate specificities of human PHOSPHO1 and PHOSPHO2. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1752, 73-82.	2.3	32
25	A novel copper site in a cyanobacterial metallochaperone. Biochemical Journal, 2004, 378, 293-297.	3.7	29
26	Mapping the Allosteric Action of Antagonists A740003 and A438079 Reveals a Role for the Left Flipper in Ligand Sensitivity at P2X7 Receptors. Molecular Pharmacology, 2018, 93, 553-562.	2.3	25
27	Mapping the Site of Action of Human P2X7 Receptor Antagonists AZ11645373, Brilliant Blue G, KN-62, Calmidazolium, and ZINC58368839 to the Intersubunit Allosteric Pocket. Molecular Pharmacology, 2019, 96, 355-363.	2.3	25
28	Cytosolic glucosylceramide regulates endolysosomal function in Niemann-Pick type C disease. Neurobiology of Disease, 2019, 127, 242-252.	4.4	23
29	Synthesis and redox potentials of methylated vitamin K derivatives. Journal of the Chemical Society Perkin Transactions II, 1999, , 1199-1202.	0.9	22
30	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
31	Structural Insights into Separase Architecture and Substrate Recognition through Computational Modelling of Caspase-Like and Death Domains. PLoS Computational Biology, 2015, 11, e1004548.	3.2	20
32	Mapping the binding site of the P2X receptor antagonist PPADS reveals the importance of orthosteric site charge and the cysteine-rich head region. Journal of Biological Chemistry, 2018, 293, 12820-12831.	3.4	19
33	Lipidâ€“Protein Interactions in Niemannâ€“Pick Type C Disease: Insights from Molecular Modeling. International Journal of Molecular Sciences, 2019, 20, 717.	4.1	19
34	Discovery of a heme-binding domain in a neuronal voltage-gated potassium channel. Journal of Biological Chemistry, 2020, 295, 13277-13286.	3.4	17
35	Malaria Protein Kinase CK2 (PfCK2) Shows Novel Mechanisms of Regulation. PLoS ONE, 2014, 9, e85391.	2.5	14
36	Mechanistic insights from resolving ligand-dependent kinetics of conformational changes at ATP-gated P2X1R ion channels. Scientific Reports, 2016, 6, 32918.	3.3	14

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37	A Canonical EF Δ Loop Directs Ca ²⁺ Sensitivity in Phospholipase C β 2. <i>Journal of Cellular Biochemistry</i> , 2014, 115, 557-565.	2.6	12
38	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
39	Molecular Evolution of a Pervasive Natural Amino-Acid Substitution in <i>Drosophila</i> cryptochrome. <i>PLoS ONE</i> , 2014, 9, e86483.	2.5	10
40	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
41	Exploring the primary electron acceptor (QA ⁻)-site of the bacterial reaction center from <i>Rhodobacter sphaeroides</i> . <i>FEBS Journal</i> , 2002, 269, 1096-1108.	0.2	7
42	Structural analysis of the adenovirus type 2 E3/19K protein using mutagenesis and a panel of conformation-sensitive monoclonal antibodies. <i>Molecular Immunology</i> , 2008, 46, 16-26.	2.2	7
43	<i>Acinetobacter</i> 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
44	Use of Chimeras, Point Mutants, and Molecular Modeling to Map the Antagonist-binding Site of 4,4'-((Carbonylbis(imino-5,1,3-benzenetriylbis(carbonylimino)))tetrakisbenzene-1,3-disulfonic Acid (NF449) at P2X1 Receptors for ATP. <i>Journal of Biological Chemistry</i> , 2015, 290, 1559-1569.	3.4	7
45	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
46	Homology Modeling of P2X Receptors. <i>Methods in Molecular Biology</i> , 2020, 2041, 65-75.	0.9	6
47	EST Processing: From Trace to Sequence. <i>Methods in Molecular Biology</i> , 2009, 533, 189-220.	0.9	3
48	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
49	The Influence of Quinone Structure on Quinone Binding to the QA Site in Bacterial Reaction Centers from <i>Rhodobacter Sphaeroides</i> . , 1998, , 877-880.		2
50	Computational Genome Analysis: An Introduction. R. C. Deonier, S. Tavar� & M. S. Waterman. Springer. 2005. 515 pages. ISBN 0 387 98785 1. Price \$79.95. (hardback). <i>Genetical Research</i> , 2006, 87, 218-219.	0.9	1
51	Temperature Dependence of the Direct Charge Recombination From Q _B - to D ⁺ in Bacterial Reaction Centers from <i>Rhodobacter Sphaeroides</i> . , 1998, , 829-832.		1
52	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
53	The Molecular Basis for Heme Modulation of KATP Channels. <i>Biophysical Journal</i> , 2015, 108, 437a.	0.5	0
54	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