Markus G Rudolph

List of Publications by Year
in descending order

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55 papers	2,627 citations	201575 27 h-index	189801 50 g-index
56 all docs	56 docs citations	56 times ranked	3700 citing authors

#	Article	IF	Citations
1	The specificity of TCR/pMHC interaction. Current Opinion in Immunology, 2002, 14, 52-65.	2.4	273
2	TIP47 functions in the biogenesis of lipid droplets. Journal of Cell Biology, 2009, 185, 641-655.	2.3	226
3	A Functional Hot Spot for Antigen Recognition in a Superagonist TCR/MHC Complex. Immunity, 2000, 12, 251-261.	6.6	202
4	The Cdc42/Rac Interactive Binding Region Motif of the Wiskott Aldrich Syndrome Protein (WASP) Is Necessary but Not Sufficient for Tight Binding to Cdc42 and Structure Formation. Journal of Biological Chemistry, 1998, 273, 18067-18076.	1.6	128
5	A Real-World Perspective on Molecular Design. Journal of Medicinal Chemistry, 2016, 59, 4087-4102.	2.9	102
6	Structural and Thermodynamic Correlates of T Cell Signaling. Annual Review of Biophysics and Biomolecular Structure, 2002, 31, 121-149.	18.3	101
7	Structural Comparison of Allogeneic and Syngeneic T Cell Receptorâ€“Peptide-Major Histocompatibility Complex Complexes. Journal of Experimental Medicine, 2002, 195, 1175-1186.	4.2	96
8	Crystal Structure of the Borna Disease Virus Nucleoprotein. Structure, 2003, 11, 1219-1226.	1.6	95
9	Conformational Switch and Role of Phosphorylation in PAK Activation. Molecular and Cellular Biology, 2001, 21, 5179-5189.	1.1	94
10	Crystal structure of the murine NK cellâ€“activating receptor NKG2D at 1.95 Ã.... Nature Immunology, 2001, 2, 248-254.	7.0	85
11	Biochemical Analysis of SopE from Salmonella typhimurium, a Highly Efficient Guanosine Nucleotide Exchange Factor for RhoGTPases. Journal of Biological Chemistry, 1999, 274, 30501-30509.	1.6	83
12	The structure of human Î±-2,6-sialyltransferase reveals the binding mode of complex glycans. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1826-1838.	2.5	71
13	Thermodynamics of Ras/Effector and Cdc42/Effector Interactions Probed by Isothermal Titration Calorimetry. Journal of Biological Chemistry, 2001, 276, 23914-23921.	1.6	67
14	Structure of the Human Fatty Acid Synthase KSâ€“MAT Didomain as a Framework for Inhibitor Design. Journal of Molecular Biology, 2010, 397, 508-519.	2.0	57
15	Discovery of novel and orally active FXR agonists for the potential treatment of dyslipidemia & diabetes. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 191-194.	1.0	55
16	The Crystal Structures of Kbm1 and Kbm8 Reveal that Subtle Changes in the Peptide Environment Impact Thermostability and Alloreactivity. Immunity, 2001, 14, 231-242.	6.6	54
17	A novel dimerization motif in the C-terminal domain of the Thermus thermophilus DEAD box helicase Hera confers substantial flexibility â€. Nucleic Acids Research, 2009, 37, 421-430.	6.5	53
18	Structures of the Human Orotidine-5â€²-Monophosphate Decarboxylase Support a Covalent Mechanism and Provide a Framework for Drug Design. Structure, 2008, 16, 82-92.	1.6	51

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19	Discovery of a microbial transglutaminase enabling highly site-specific labeling of proteins. Journal of Biological Chemistry, 2017, 292, 15622-15635.	1.6	46
20	Molecular Recognition at the Active Site of Catecholâ€Oâ€Methyltransferase: Energetically Favorable Replacement of a Water Molecule Imported by a Bisubstrate Inhibitor. Angewandte Chemie - International Edition, 2009, 48, 9092-9096.	7.2	39
21	When core competence is not enough: functional interplay of the DEAD-box helicase core with ancillary domains and auxiliary factors in RNA binding and unwinding. Biological Chemistry, 2015, 396, 849-865.	1.2	39
22	Crystal Structure and Nucleotide Binding of the Thermus thermophilus RNA Helicase Hera N-terminal Domain. Journal of Molecular Biology, 2006, 361, 731-743.	2.0	36
23	Molecular Recognition at the Active Site of Catecholâ€Oâ€methyltransferase (COMT): Adenine Replacements in Bisubstrate Inhibitors. Chemistry - A European Journal, 2011, 17, 6369-6381.	1.7	35
24	Ligand channel in pharmacologically stabilized rhodopsin. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3640-3645.	3.3	34
25	Probing the oxygen-binding site of the human formylglycine-generating enzyme using halide ions. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 621-627.	2.5	32
26	A Hinge in the Distal End of the PACSIN 2 F-BAR Domain May Contribute to Membrane-Curvature Sensing. Journal of Molecular Biology, 2010, 400, 129-136.	2.0	31
27	Mapping the conformational space accessible to catechol-O-methyltransferase. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2163-2174.	2.5	30
28	Catechol-O-methyltransferase in complex with substituted 3â€²-deoxyribose bisubstrate inhibitors. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 253-260.	2.5	28
29	Crystal structures of Thermotoga maritima reverse gyrase: inferences for the mechanism of positive DNA supercoiling. Nucleic Acids Research, 2013, 41, 1058-1070.	6.5	27
30	Crystal Structure of Human pFGE, the Paralog of the Cα-formylglycine-generating Enzyme. Journal of Biological Chemistry, 2005, 280, 15180-15187.	1.6	26
31	Mapping the Spectrum of Conformational States of the DNA- and C-Gates in Bacillus subtilis Gyrase. Journal of Molecular Biology, 2013, 425, 2632-2640.	2.0	26
32	Combined pseudo-merohedral twinning, non-crystallographic symmetry and pseudo-translation in a monoclinic crystal form of the γδ T-cell ligand T10. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 656-664.	2.5	24
33	On the Mechanism of a Polyunsaturated Fatty Acid Double Bond Isomerase from Propionibacterium acnes. Journal of Biological Chemistry, 2009, 284, 8005-8012.	1.6	24
34	Crystal structure of Rab9 complexed to GDP reveals a dimer with an active conformation of switch II. FEBS Letters, 2004, 568, 23-29.	1.3	22
35	Recognition of two distinct elements in the RNA substrate by the RNA-binding domain of the T. thermophilus DEAD box helicase Hera. Nucleic Acids Research, 2013, 41, 6259-6272.	6.5	22
36	The Thermus thermophilus DEAD box helicase Hera contains a modified RNA recognition motif domain loosely connected to the helicase core. Rna, 2009, 15, 1993-2001.	1.6	21

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37	Design of Potent and Druglike Nonphenolic Inhibitors for Catechol O-Methyltransferase Derived from a Fragment Screening Approach Targeting the S-Adenosyl-<scp>l</scp>-methionine Pocket. Journal of Medicinal Chemistry, 2016, 59, 10163-10175.	2.9	20
38	The latch modulates nucleotide and DNA binding to the helicase-like domain of Thermotoga maritima reverse gyrase and is required for positive DNA supercoiling. Nucleic Acids Research, 2011, 39, 1789-1800.	6.5	18
39	A Peptide That Antagonizes TCR-Mediated Reactions with Both Syngeneic and Allogeneic Agonists: Functional and Structural Aspects. Journal of Immunology, 2004, 172, 2994-3002.	0.4	16
40	Design and synthesis of selective, dual fatty acid binding protein 4 and 5 inhibitors. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 5092-5097.	1.0	16
41	Crystal Structures of the Human Doublecortin C- and N-terminal Domains in Complex with Specific Antibodies. Journal of Biological Chemistry, 2016, 291, 16292-16306.	1.6	16
42	Use of multiple anomalous dispersion to phase highly merohedrally twinned crystals of interleukin-1Î². Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 290-298.	2.5	14
43	Crystal Structures of Two Rat MHC Class Ia (RT1-A) Molecules that are Associated Differentially with Peptide Transporter Alleles TAP-A and TAP-B. Journal of Molecular Biology, 2002, 324, 975-990.	2.0	12
44	De novocalcium/sulfur SAD phasing of the human formylglycine-generating enzyme using in-house data. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1057-1066.	2.5	12
45	Pseudo-merohedral twinning in monoclinic crystals of human orotidine-5â€²-monophosphate decarboxylase. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 744-749.	2.5	11
46	Atomic resolution structure of a lysine-specific endoproteinase fromLysobacter enzymogenessuggests a hydroxyl group bound to the oxyanion hole. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1832-1843.	2.5	10
47	Small molecule AX-024 reduces T cell proliferation independently of CD3Ïµ/Nck1 interaction, which is governed by a domain swap in the Nck1-SH3.1 domain. Journal of Biological Chemistry, 2020, 295, 7849-7864.	1.6	10
48	Domain swap in the C-terminal ubiquitin-like domain of human doublecortin. Acta Crystallographica Section D: Structural Biology, 2018, 74, 450-462.	1.1	10
49	Crystal structure of an isolated VÎ± domain of the 2C T-cell receptor. Journal of Molecular Biology, 2001, 314, 1-8.	2.0	8
50	The novel fluorescent CDPâ€analogue (PÎ²)MABAâ€CDP is a specific probe for the NMP binding site of UMP/CMP kinase. Protein Science, 1999, 8, 2697-2704.	3.1	8
51	Biophysical Chemistry. , 0, , .		4
52	Purification, crystallization and preliminary X-ray analysis of the GTP-binding protein Rab9 implicated in endosome-to-TGN vesicle trafficking. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 580-582.	2.5	3
53	Structure of a 13-fold superhelix (almost) determined from first principles. IUCrJ, 2015, 2, 177-187.	1.0	3
54	Synthesis, Characterization, and in vivo Evaluation of a Novel Potent Autotaxin-Inhibitor. Frontiers in Pharmacology, 2021, 12, 699535.	1.6	1

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55	Reply to Alarcon and Borroto: Small molecule AX-024 reduces T cell proliferation independently of CD3ĵµ-Nck1 interaction at SH3.1. Journal of Biological Chemistry, 2020, 295, 10077.	1.6	0