

# Mutsuko Kukimoto-Niino

## List of Publications by Year in descending order

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57  
papers

2,526  
citations

186209

28  
h-index

197736

49  
g-index

57  
all docs

57  
docs citations

57  
times ranked

4076  
citing authors

#	ARTICLE	IF	CITATIONS
1	DOCK8 is a Cdc42 activator critical for interstitial dendritic cell migration during immune responses. <i>Blood</i> , 2012, 119, 4451-4461.	0.6	200
2	X-ray Structure and Site-Directed Mutagenesis of a Nitrite Reductase from <i>Alcaligenes Faecalis</i> S-6: Roles of Two Copper Atoms in Nitrite Reduction. <i>Biochemistry</i> , 1994, 33, 5246-5252.	1.2	185
3	TNIK inhibition abrogates colorectal cancer stemness. <i>Nature Communications</i> , 2016, 7, 12586.	5.8	117
4	Catalytic Roles for Two Water Bridged Residues (Asp-98 and His-255) in the Active Site of Copper-containing Nitrite Reductase. <i>Journal of Biological Chemistry</i> , 2000, 275, 23957-23964.	1.6	115
5	Structural basis for the altered drug sensitivities of non-small cell lung cancer-associated mutants of human epidermal growth factor receptor. <i>Oncogene</i> , 2013, 32, 27-38.	2.6	114
6	Structure of <i>Alcaligenes faecalis</i> Nitrite Reductase and a Copper Site Mutant, M150E, That Contains Zinc. <i>Biochemistry</i> , 1995, 34, 12107-12117.	1.2	102
7	Structural basis for mutual relief of the Rac guanine nucleotide exchange factor DOCK2 and its partner ELMO1 from their autoinhibited forms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3305-3310.	3.3	95
8	Crystal Structure of the Interleukin-15-Interleukin-15 Receptor $\beta$ Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 37191-37204.	1.6	89
9	Site-Directed Mutants of Pseudoazurin: Explanation of Increased Redox Potentials from X-ray Structures and from Calculation of Redox Potential Differences. <i>Biochemistry</i> , 1997, 36, 13160-13179.	1.2	80
10	A Rac GTPase-Activating Protein, MgcRacGAP, Is a Nuclear Localizing Signal-Containing Nuclear Chaperone in the Activation of STAT Transcription Factors. <i>Molecular and Cellular Biology</i> , 2009, 29, 1796-1813.	1.1	70
11	Immune regulatory functions of DOCK family proteins in health and disease. <i>Experimental Cell Research</i> , 2013, 319, 2343-2349.	1.2	70
12	Identification of interaction site of pseudoazurin with its redox partner, copper-containing nitrite reductase from <i>Alcaligenes faecalis</i> S-6. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 153-158.	1.0	69
13	Blockade of Inflammatory Responses by a Small-Molecule Inhibitor of the Rac Activator DOCK2. <i>Chemistry and Biology</i> , 2012, 19, 488-497.	6.2	65
14	Structural Basis for the Exclusive Specificity of Slac2-a/Melanophilin for the Rab27 GTPases. <i>Structure</i> , 2008, 16, 1478-1490.	1.6	64
15	Crystal structure of the human receptor activity-modifying protein 1 extracellular domain. <i>Protein Science</i> , 2008, 17, 1907-1914.	3.1	57
16	Structural basis of interleukin-5 dimer recognition by its $\beta$ receptor. <i>Protein Science</i> , 2012, 21, 850-864.	3.1	57
17	Lysosome-associated membrane proteins-1 and -2 (LAMP-1 and LAMP-2) assemble via distinct modes. <i>Biochemical and Biophysical Research Communications</i> , 2016, 479, 489-495.	1.0	55
18	Structural basis for extracellular interactions between calcitonin receptor-like receptor and receptor activity-modifying protein 2 for adrenomedullin-specific binding. <i>Protein Science</i> , 2012, 21, 199-210.	3.1	54

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19	Gilteritinib overcomes lorlatinib resistance in ALK-rearranged cancer. <i>Nature Communications</i> , 2021, 12, 1261.	5.8	52
20	Crystal Structure of the GTP-binding Protein Obg from <i>Thermus thermophilus</i> HB8. <i>Journal of Molecular Biology</i> , 2004, 337, 761-770.	2.0	51
21	Targeting Ras-Driven Cancer Cell Survival and Invasion through Selective Inhibition of DOCK1. <i>Cell Reports</i> , 2017, 19, 969-980.	2.9	51
22	The Crystal Structure of Mouse Nup35 Reveals Atypical RNP Motifs and Novel Homodimerization of the RRM Domain. <i>Journal of Molecular Biology</i> , 2006, 363, 114-124.	2.0	45
23	Application of nitrite reductase from <i>Alcaligenes faecalis</i> S-6 for nitrite measurement. <i>Biosensors and Bioelectronics</i> , 1998, 13, 1-5.	5.3	40
24	Crystal Structure of the Ca <sup>2+</sup> /Calmodulin-dependent Protein Kinase Kinase in Complex with the Inhibitor STO-609. <i>Journal of Biological Chemistry</i> , 2011, 286, 22570-22579.	1.6	37
25	Structural Basis for the Specific Recognition of the Major Antigenic Peptide from the Japanese Cedar Pollen Allergen Cry j 1 by HLA-DP5. <i>Journal of Molecular Biology</i> , 2014, 426, 3016-3027.	2.0	37
26	Crystal Structure of the RUN Domain of the RAP2-interacting Protein x. <i>Journal of Biological Chemistry</i> , 2006, 281, 31843-31853.	1.6	36
27	Crystal structure of an enhancer of rudimentary homolog (ERH) at 2.1 Å... resolution. <i>Protein Science</i> , 2005, 14, 1888-1893.	3.1	31
28	Tetrameric Interaction of the Ectoenzyme CD38 on the Cell Surface Enables Its Catalytic and Raft-Association Activities. <i>Structure</i> , 2012, 20, 1585-1595.	1.6	31
29	Cell-permeable Carboxyl-terminal p27Kip1 Peptide Exhibits Anti-tumor Activity by Inhibiting Pim-1 Kinase. <i>Journal of Biological Chemistry</i> , 2011, 286, 2681-2688.	1.6	29
30	Cholesterol sulfate is a DOCK2 inhibitor that mediates tissue-specific immune evasion in the eye. <i>Science Signaling</i> , 2018, 11, .	1.6	29
31	Inhibitor-bound structures of human pyruvate dehydrogenase kinase 4. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 763-773.	2.5	28
32	Site-directed mutagenesis of azurin from <i>Pseudomonas aeruginosa</i> enhances the formation of an electron-transfer complex with a copper-containing nitrite reductase from <i>Alcaligenes faecalis</i> S-6. <i>FEBS Letters</i> , 1996, 394, 87-90.	1.3	27
33	Dimerization of DOCK2 Is Essential for DOCK2-Mediated Rac Activation and Lymphocyte Migration. <i>PLoS ONE</i> , 2012, 7, e46277.	1.1	27
34	A redox switch shapes the Lon protease exit pore to facultatively regulate proteolysis. <i>Nature Chemical Biology</i> , 2015, 11, 46-51.	3.9	25
35	Crystal structure of the probable haloacid dehalogenase PH0459 from <i>Pyrococcus horikoshii</i> OT3. <i>Protein Science</i> , 2006, 15, 373-377.	3.1	24
36	Crystal structure of human acetylcholinesterase in complex with tacrine: Implications for drug discovery. <i>International Journal of Biological Macromolecules</i> , 2022, 210, 172-181.	3.6	23

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37	Direct inter-subdomain interactions switch between the closed and open forms of the Hsp70 nucleotide-binding domain in the nucleotide-free state. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 223-232.	2.5	22
38	Granzyme A Stimulates pDCs to Promote Adaptive Immunity via Induction of Type I IFN. <i>Frontiers in Immunology</i> , 2019, 10, 1450.	2.2	22
39	Reduced efficacy of a Src kinase inhibitor in crowded protein solution. <i>Nature Communications</i> , 2021, 12, 4099.	5.8	22
40	Cell-free synthesis of functional antibody fragments to provide a structural basis for antibody-antigen interaction. <i>PLoS ONE</i> , 2018, 13, e0193158.	1.1	20
41	Structural Basis for the Dual Substrate Specificity of DOCK7 Guanine Nucleotide Exchange Factor. <i>Structure</i> , 2019, 27, 741-748.e3.	1.6	19
42	Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex. <i>Science Advances</i> , 2021, 7, .	4.7	17
43	Identification of Critical Residues in G13 for Stimulation of p115RhoGEF Activity and the Structure of the G13-p115RhoGEF Regulator of G Protein Signaling Homology (RH) Domain Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 20625-20636.	1.6	15
44	Structural Basis for the Inhibition of Cyclin G-associated Kinase by Gefitinib. <i>ChemistryOpen</i> , 2018, 7, 713-719.	0.9	15
45	Structural insights into the small GTPase specificity of the DOCK guanine nucleotide exchange factors. <i>Current Opinion in Structural Biology</i> , 2021, 71, 249-258.	2.6	13
46	Crystal structures of possible lysine decarboxylases from <i>Thermus thermophilus</i> HB8. <i>Protein Science</i> , 2008, 13, 3038-3042.	3.1	11
47	Identification of novel drug-resistant EGFR mutant inhibitors by in silico screening using comprehensive assessments of protein structures. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 3756-3767.	1.4	11
48	Gene Organization for Nitric Oxide Reduction in <i>Alcaligenes faecalis</i> S-6. <i>Bioscience, Biotechnology and Biochemistry</i> , 2000, 64, 852-857.	0.6	9
49	Activity cliff for 7-substituted pyrrolo-pyrimidine inhibitors of HCK explained in terms of predicted basicity of the amine nitrogen. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 4259-4264.	1.4	9
50	A conserved PI(4,5)P2-binding domain is critical for immune regulatory function of DOCK8. <i>Life Science Alliance</i> , 2021, 4, e202000873.	1.3	9
51	Direct homophilic interaction of LAMP2A with the two-domain architecture revealed by site-directed photo-crosslinks and steric hindrances in mammalian cells. <i>Autophagy</i> , 2021, 17, 4286-4304.	4.3	9
52	Crystal structure of a predicted phosphoribosyltransferase (TT1426) from <i>Thermus thermophilus</i> HB8 at 2.01 Å resolution. <i>Protein Science</i> , 2005, 14, 823-827.	3.1	6
53	Identification of pyrrolo[2,3-d]pyrimidines as potent HCK and FLT3-ITD dual inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 4994-4998.	1.0	6
54	Phosphorylated and non-phosphorylated HCK kinase domains produced by cell-free protein expression. <i>Protein Expression and Purification</i> , 2018, 150, 92-99.	0.6	6

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55	Structure of the UNC5H2 death domain. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1502-1509.	2.5	4
56	Title is missing!. Kagaku To Seibutsu, 2008, 46, 153-155.	0.0	0
57	Structural Basis for the Dual Substrate Specificity of DOCK7 Guanine Nucleotide Exchange Factor. SSRN Electronic Journal, 0, , .	0.4	0