Mutsuko Kukimoto-Niino

List of Publications by Year
in descending order

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	Crystal structure of human acetylcholinesterase in complex with tacrine: Implications for drug discovery. International Journal of Biological Macromolecules, 2022, 210, 172-181.	3.6	23
2	A conserved PI(4,5)P2â€“binding domain is critical for immune regulatory function of DOCK8. Life Science Alliance, 2021, 4, e202000873.	1.3	9
3	Gilteritinib overcomes lorlatinib resistance in ALK-rearranged cancer. Nature Communications, 2021, 12, 1261.	5.8	52
4	Direct homophilic interaction of LAMP2A with the two-domain architecture revealed by site-directed photo-crosslinks and steric hindrances in mammalian cells. Autophagy, 2021, 17, 4286-4304.	4.3	9
5	Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex. Science Advances, 2021, 7, .	4.7	17
6	Reduced efficacy of a Src kinase inhibitor in crowded protein solution. Nature Communications, 2021, 12, 4099.	5.8	22
7	Structural insights into the small GTPase specificity of the DOCK guanine nucleotide exchange factors. Current Opinion in Structural Biology, 2021, 71, 249-258.	2.6	13
8	Granzyme A Stimulates pDCs to Promote Adaptive Immunity via Induction of Type I IFN. Frontiers in Immunology, 2019, 10, 1450.	2.2	22
9	Structural Basis for the Dual Substrate Specificity of DOCK7 Guanine Nucleotide Exchange Factor. Structure, 2019, 27, 741-748.e3.	1.6	19
10	Structural Basis for the Inhibition of Cyclin Gâ€Associated Kinase by Gefitinib. ChemistryOpen, 2018, 7, 713-719.	0.9	15
11	Phosphorylated and non-phosphorylated HCK kinase domains produced by cell-free protein expression. Protein Expression and Purification, 2018, 150, 92-99.	0.6	6
12	Cholesterol sulfate is a DOCK2 inhibitor that mediates tissue-specific immune evasion in the eye. Science Signaling, 2018, 11, .	1.6	29
13	Cell-free synthesis of functional antibody fragments to provide a structural basis for antibodyâ€“antigen interaction. PLoS ONE, 2018, 13, e0193158.	1.1	20
14	Targeting Ras-Driven Cancer Cell Survival and Invasion through Selective Inhibition of DOCK1. Cell Reports, 2017, 19, 969-980.	2.9	51
15	Activity cliff for 7-substituted pyrrolo-pyrimidine inhibitors of HCK explained in terms of predicted basicity of the amine nitrogen. Bioorganic and Medicinal Chemistry, 2017, 25, 4259-4264.	1.4	9
16	Identification of pyrrolo[2,3- d]pyrimidines as potent HCK and FLT3-ITD dual inhibitors. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 4994-4998.	1.0	6
17	Lysosome-associated membrane proteins-1 and -2 (LAMP-1 and LAMP-2) assemble via distinct modes. Biochemical and Biophysical Research Communications, 2016, 479, 489-495.	1.0	55
18	TNIK inhibition abrogates colorectal cancer stemness. Nature Communications, 2016, 7, 12586.	5.8	117

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19	A redox switch shapes the Lon protease exit pore to facultatively regulate proteolysis. Nature Chemical Biology, 2015, 11, 46-51.	3.9	25
20	Structural Basis for the Specific Recognition of the Major Antigenic Peptide from the Japanese Cedar Pollen Allergen Cry j 1 by HLA-DP5. Journal of Molecular Biology, 2014, 426, 3016-3027.	2.0	37
21	Structural basis for the altered drug sensitivities of non-small cell lung cancer-associated mutants of human epidermal growth factor receptor. Oncogene, 2013, 32, 27-38.	2.6	114
22	Immune regulatory functions of DOCK family proteins in health and disease. Experimental Cell Research, 2013, 319, 2343-2349.	1.2	70
23	Tetrameric Interaction of the Ectoenzyme CD38 on the Cell Surface Enables Its Catalytic and Raft-Association Activities. Structure, 2012, 20, 1585-1595.	1.6	31
24	Structural basis for mutual relief of the Rac guanine nucleotide exchange factor DOCK2 and its partner ELMO1 from their autoinhibited forms. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3305-3310.	3.3	95
25	Identification of novel drug-resistant EGFR mutant inhibitors by in silico screening using comprehensive assessments of protein structures. Bioorganic and Medicinal Chemistry, 2012, 20, 3756-3767.	1.4	11
26	DOCK8 is a Cdc42 activator critical for interstitial dendritic cell migration during immune responses. Blood, 2012, 119, 4451-4461.	0.6	200
27	Dimerization of DOCK2 Is Essential for DOCK2-Mediated Rac Activation and Lymphocyte Migration. PLoS ONE, 2012, 7, e46277.	1.1	27
28	Structural basis for extracellular interactions between calcitonin receptorâ€like receptor and receptor activityâ€modifying protein 2 for adrenomedullinâ€specific binding. Protein Science, 2012, 21, 199-210.	3.1	54
29	Structural basis of interleukinâ€5 dimer recognition by its Î± receptor. Protein Science, 2012, 21, 850-864.	3.1	57
30	Blockade of Inflammatory Responses by a Small-Molecule Inhibitor of the Rac Activator DOCK2. Chemistry and Biology, 2012, 19, 488-497.	6.2	65
31	Inhibitor-bound structures of human pyruvate dehydrogenase kinase 4. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 763-773.	2.5	28
32	Crystal Structure of the Ca2+/Calmodulin-dependent Protein Kinase Kinase in Complex with the Inhibitor STO-609. Journal of Biological Chemistry, 2011, 286, 22570-22579.	1.6	37
33	Identification of Critical Residues in GÎ±13 for Stimulation of p115RhoGEF Activity and the Structure of the GÎ±13-p115RhoGEF Regulator of G Protein Signaling Homology (RH) Domain Complex. Journal of Biological Chemistry, 2011, 286, 20625-20636.	1.6	15
34	Cell-permeable Carboxyl-terminal p27Kip1 Peptide Exhibits Anti-tumor Activity by Inhibiting Pim-1 Kinase. Journal of Biological Chemistry, 2011, 286, 2681-2688.	1.6	29
35	Direct inter-subdomain interactions switch between the closed and open forms of the Hsp70 nucleotide-binding domain in the nucleotide-free state. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 223-232.	2.5	22
36	A Rac GTPase-Activating Protein, MgcRacGAP, Is a Nuclear Localizing Signal-Containing Nuclear Chaperone in the Activation of STAT Transcription Factors. Molecular and Cellular Biology, 2009, 29, 1796-1813.	1.1	70

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37	Structural Basis for the Exclusive Specificity of Slac2-a/Melanophilin for the Rab27 GTPases. Structure, 2008, 16, 1478-1490.	1.6	64
38	Crystal structure of the human receptor activityâ€modifying protein 1 extracellular domain. Protein Science, 2008, 17, 1907-1914.	3.1	57
39	Crystal structures of possible lysine decarboxylases from Thermus thermophilus HB8. Protein Science, 2008, 13, 3038-3042.	3.1	11
40	Title is missing!. Kagaku To Seibutsu, 2008, 46, 153-155.	0.0	0
41	Crystal Structure of the Interleukin-15Â·Interleukin-15 Receptor Î± Complex. Journal of Biological Chemistry, 2007, 282, 37191-37204.	1.6	89
42	Crystal structure of the probable haloacid dehalogenase PH0459 from Pyrococcus horikoshii OT3. Protein Science, 2006, 15, 373-377.	3.1	24
43	The Crystal Structure of Mouse Nup35 Reveals Atypical RNP Motifs and Novel Homodimerization of the RRM Domain. Journal of Molecular Biology, 2006, 363, 114-124.	2.0	45
44	Structure of the UNC5H2 death domain. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1502-1509.	2.5	4
45	Crystal Structure of the RUN Domain of the RAP2-interacting Protein x. Journal of Biological Chemistry, 2006, 281, 31843-31853.	1.6	36
46	Crystal structure of an enhancer of rudimentary homolog (ERH) at 2.1 Ã... resolution. Protein Science, 2005, 14, 1888-1893.	3.1	31
47	Crystal structure of a predicted phosphoribosyltransferase (TT1426) from Thermus thermophilus HB8 at 2.01 A resolution. Protein Science, 2005, 14, 823-827.	3.1	6
48	Crystal Structure of the GTP-binding Protein Obg from Thermus thermophilus HB8. Journal of Molecular Biology, 2004, 337, 761-770.	2.0	51
49	Catalytic Roles for Two Water Bridged Residues (Asp-98 and His-255) in the Active Site of Copper-containing Nitrite Reductase. Journal of Biological Chemistry, 2000, 275, 23957-23964.	1.6	115
50	Gene Organization for Nitric Oxide Reduction inAlcaligenes faecalisS-6. Bioscience, Biotechnology and Biochemistry, 2000, 64, 852-857.	0.6	9
51	Application of nitrite reductase from Alcaligenes faecalis S-6 for nitrite measurement. Biosensors and Bioelectronics, 1998, 13, 1-5.	5.3	40
52	Site-Directed Mutants of Pseudoazurin:â€‰ Explanation of Increased Redox Potentials from X-ray Structures and from Calculation of Redox Potential Differences,. Biochemistry, 1997, 36, 13160-13179.	1.2	80
53	Site-directed mutagenesis of azurin fromPseudomonas aeruginosaenhances the formation of an electron-transfer complex with a copper-containing nitrite reductase fromAlcaligenes faecalisS-6. FEBS Letters, 1996, 394, 87-90.	1.3	27
54	Identification of interaction site of pseudoazurin with its redox partner, copper-containing nitrite reductase from Alcaligenes faecalis S-6. Protein Engineering, Design and Selection, 1995, 8, 153-158.	1.0	69

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55	Structure of Alcaligenes faecalis Nitrite Reductase and a Copper Site Mutant, M150E, That Contains Zinc. Biochemistry, 1995, 34, 12107-12117.	1.2	102
56	X-ray Structure and Site-Directed Mutagenesis of a Nitrite Reductase from Alcaligenes Faecalis S-6: Roles of Two Copper Atoms in Nitrite Reduction. Biochemistry, 1994, 33, 5246-5252.	1.2	185
57	Structural Basis for the Dual Substrate Specificity of DOCK7 Guanine Nucleotide Exchange Factor. SSRN Electronic Journal, 0, , .	0.4	0