Mutsuko Kukimoto-Niino

List of Publications by Year
in descending order

57 papers	2,526 citations	186265 28 h-index	197818 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. Blood, 2012, 119, 4451-4461.	1.4	200
2	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.	2.5	185
3	TNIK inhibition abrogates colorectal cancer stemness. Nature Communications, 2016, 7, 12586.	12.8	117
4	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.	3.4	115
5	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.	5.9	114
6	Structure of Alcaligenes faecalis Nitrite Reductase and a Copper Site Mutant, M150E, That Contains Zinc. Biochemistry, 1995, 34, 12107-12117.	2.5	102
7	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.	7.1	95
8	Crystal Structure of the Interleukin-15Â·Interleukin-15 Receptor Î± Complex. Journal of Biological Chemistry, 2007, 282, 37191-37204.	3.4	89
9	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.	2.5	80
10	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.	2.3	70
11	Immune regulatory functions of DOCK family proteins in health and disease. Experimental Cell Research, 2013, 319, 2343-2349.	2.6	70
12	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.	2.1	69
13	Blockade of Inflammatory Responses by a Small-Molecule Inhibitor of the Rac Activator DOCK2. Chemistry and Biology, 2012, 19, 488-497.	6.0	65
14	Structural Basis for the Exclusive Specificity of Slac2-a/Melanophilin for the Rab27 GTPases. Structure, 2008, 16, 1478-1490.	3.3	64
15	Crystal structure of the human receptor activityâ€modifying protein 1 extracellular domain. Protein Science, 2008, 17, 1907-1914.	7.6	57
16	Structural basis of interleukinâ€5 dimer recognition by its Î± receptor. Protein Science, 2012, 21, 850-864.	7.6	57
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.	2.1	55
18	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.	7.6	54

#	Article	IF	Citations
19	Gilteritinib overcomes lorlatinib resistance in ALK-rearranged cancer. Nature Communications, 2021, 12, 1261.	12.8	52
20	Crystal Structure of the GTP-binding Protein Obg from Thermus thermophilus HB8. Journal of Molecular Biology, 2004, 337, 761-770.	4.2	51
21	Targeting Ras-Driven Cancer Cell Survival and Invasion through Selective Inhibition of DOCK1. Cell Reports, 2017, 19, 969-980.	6.4	51
22	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.	4.2	45
23	Application of nitrite reductase from Alcaligenes faecalis S-6 for nitrite measurement. Biosensors and Bioelectronics, 1998, 13, 1-5.	10.1	40
24	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.	3.4	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. Journal of Molecular Biology, 2014, 426, 3016-3027.	4.2	37
26	Crystal Structure of the RUN Domain of the RAP2-interacting Protein x. Journal of Biological Chemistry, 2006, 281, 31843-31853.	3.4	36
27	Crystal structure of an enhancer of rudimentary homolog (ERH) at 2.1 Ã... resolution. Protein Science, 2005, 14, 1888-1893.	7.6	31
28	Tetrameric Interaction of the Ectoenzyme CD38 on the Cell Surface Enables Its Catalytic and Raft-Association Activities. Structure, 2012, 20, 1585-1595.	3.3	31
29	Cell-permeable Carboxyl-terminal p27Kip1 Peptide Exhibits Anti-tumor Activity by Inhibiting Pim-1 Kinase. Journal of Biological Chemistry, 2011, 286, 2681-2688.	3.4	29
30	Cholesterol sulfate is a DOCK2 inhibitor that mediates tissue-specific immune evasion in the eye. Science Signaling, 2018, 11, .	3.6	29
31	Inhibitor-bound structures of human pyruvate dehydrogenase kinase 4. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 763-773.	2.5	28
32	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.	2.8	27
33	Dimerization of DOCK2 Is Essential for DOCK2-Mediated Rac Activation and Lymphocyte Migration. PLoS ONE, 2012, 7, e46277.	2.5	27
34	A redox switch shapes the Lon protease exit pore to facultatively regulate proteolysis. Nature Chemical Biology, 2015, 11, 46-51.	8.0	25
35	Crystal structure of the probable haloacid dehalogenase PH0459 from Pyrococcus horikoshii OT3. Protein Science, 2006, 15, 373-377.	7.6	24
36	Crystal structure of human acetylcholinesterase in complex with tacrine: Implications for drug discovery. International Journal of Biological Macromolecules, 2022, 210, 172-181.	7.5	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. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 223-232.	2.5	22
38	Granzyme A Stimulates pDCs to Promote Adaptive Immunity via Induction of Type I IFN. Frontiers in Immunology, 2019, 10, 1450.	4.8	22
39	Reduced efficacy of a Src kinase inhibitor in crowded protein solution. Nature Communications, 2021, 12, 4099.	12.8	22
40	Cell-free synthesis of functional antibody fragments to provide a structural basis for antibodyâ€“antigen interaction. PLoS ONE, 2018, 13, e0193158.	2.5	20
41	Structural Basis for the Dual Substrate Specificity of DOCK7 Guanine Nucleotide Exchange Factor. Structure, 2019, 27, 741-748.e3.	3.3	19
42	Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex. Science Advances, 2021, 7, .	10.3	17
43	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.	3.4	15
44	Structural Basis for the Inhibition of Cyclin Gâ€Associated Kinase by Gefitinib. ChemistryOpen, 2018, 7, 713-719.	1.9	15
45	Structural insights into the small GTPase specificity of the DOCK guanine nucleotide exchange factors. Current Opinion in Structural Biology, 2021, 71, 249-258.	5.7	13
46	Crystal structures of possible lysine decarboxylases from Thermus thermophilus HB8. Protein Science, 2008, 13, 3038-3042.	7.6	11
47	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.	3.0	11
48	Gene Organization for Nitric Oxide Reduction inAlcaligenes faecalisS-6. Bioscience, Biotechnology and Biochemistry, 2000, 64, 852-857.	1.3	9
49	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.	3.0	9
50	A conserved PI(4,5)P2â€“binding domain is critical for immune regulatory function of DOCK8. Life Science Alliance, 2021, 4, e202000873.	2.8	9
51	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.	9.1	9
52	Crystal structure of a predicted phosphoribosyltransferase (TT1426) from Thermus thermophilus HB8 at 2.01 A resolution. Protein Science, 2005, 14, 823-827.	7.6	6
53	Identification of pyrrolo[2,3- d]pyrimidines as potent HCK and FLT3-ITD dual inhibitors. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 4994-4998.	2.2	6
54	Phosphorylated and non-phosphorylated HCK kinase domains produced by cell-free protein expression. Protein Expression and Purification, 2018, 150, 92-99.	1.3	6

#	Article	IF	Citations
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