Do-Hyung Kim

List of Publications by Year
in descending order

58 papers	21,269 citations	136740 32 h-index	149479 56 g-index
59 all docs	59 docs citations	59 times ranked	32304 citing authors

#	Article	IF	Citations
1	Defective autophagy and increased apoptosis contribute toward the pathogenesis of FKRP-associated muscular dystrophies. Stem Cell Reports, 2021, 16, 2752-2767.	2.3	5
2	Efficient Cross-Correlation Filtering of One- and Two-Color Single Molecule Localization Microscopy Data. Frontiers in Bioinformatics, 2021, 1, .	1.0	4
3	GABARAPs and LC3s have opposite roles in regulating ULK1 for autophagy induction. Autophagy, 2020, 16, 600-614.	4.3	75
4	A Novel Mechanism for NF-ÎºB-activation via IÎºB-aggregation: Implications for Hepatic Mallory-Denk-Body Induced Inflammation. Molecular and Cellular Proteomics, 2020, 19, 1968-1986.	2.5	17
5	Unconventional Secretion of Adipocyte Fatty Acid Binding Protein 4 Is Mediated By Autophagic Proteins in a Sirtuin-1â€“Dependent Manner. Diabetes, 2019, 68, 1767-1777.	0.3	32
6	ULK1 phosphorylates Ser30 of BECN1 in association with ATG14 to stimulate autophagy induction. Autophagy, 2018, 14, 584-597.	4.3	121
7	<i>N</i>-(1-Benzyl-3,5-dimethyl-1<i>H</i>-pyrazol-4-yl)benzamides: Antiproliferative Activity and Effects on mTORC1 and Autophagy. ACS Medicinal Chemistry Letters, 2017, 8, 90-95.	1.3	12
8	Down regulation of Peroxiredoxin-3 in 3T3-L1 adipocytes leads to oxidation of Rictor in the mammalian-target of rapamycin complex 2 (mTORC2). Biochemical and Biophysical Research Communications, 2017, 493, 1311-1317.	1.0	6
9	Uncoordinated 51â€like kinase 2 signaling pathway regulates epithelialâ€mesenchymal transition in A549 lung cancer cells. FEBS Letters, 2016, 590, 1365-1374.	1.3	32
10	The ULK1 complex mediates MTORC1 signaling to the autophagy initiation machinery via binding and phosphorylating ATG14. Autophagy, 2016, 12, 547-564.	4.3	243
11	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	4.3	4,701
12	mTORC1 Coordinates Protein Synthesis and Immunoproteasome Formation via PRAS40 to Prevent Accumulation of Protein Stress. Molecular Cell, 2016, 61, 625-639.	4.5	59
13	An expanded role for mTORC1 in autophagy. Molecular and Cellular Oncology, 2016, 3, e1010958.	0.3	9
14	Immunoproteasome Inhibition to Target AML with Activated RAS Pathways. Blood, 2016, 128, 577-577.	0.6	0
15	mRNA 3â€²-UTR shortening is a molecular signature of mTORC1 activation. Nature Communications, 2015, 6, 7218.	5.8	55
16	mTORC1 Phosphorylates UVRAG to Negatively Regulate Autophagosome and Endosome Maturation. Molecular Cell, 2015, 57, 207-218.	4.5	218
17	Epigenetic Regulation of Autophagy by the Methyltransferase G9a. Molecular and Cellular Biology, 2013, 33, 3983-3993.	1.1	177
18	dRAGging Amino Acid-mTORC1 Signaling by SH3BP4. Molecules and Cells, 2013, 35, 1-6.	1.0	16

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19	Distinct functions of<i><i>Ulk1</i></i>and<i><i>Ulk2</i></i>in the regulation of lipid metabolism in adipocytes. Autophagy, 2013, 9, 2103-2114.	4.3	76
20	Potyvirus NIa Protease. , 2013, , 2427-2432.		0
21	Crystal Structure of the Gtr1pGTP-Gtr2pGDP Protein Complex Reveals Large Structural Rearrangements Triggered by GTP-to-GDP Conversion. Journal of Biological Chemistry, 2012, 287, 29648-29653.	1.6	60
22	SH3BP4 Is a Negative Regulator of Amino Acid-Rag GTPase-mTORC1 Signaling. Molecular Cell, 2012, 46, 833-846.	4.5	76
23	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	4.3	3,122
24	Hsp90-Cdc37 Chaperone Complex Regulates Ulk1- and Atg13-Mediated Mitophagy. Molecular Cell, 2011, 43, 572-585.	4.5	211
25	ULK1 inhibits the kinase activity of mTORC1 and cell proliferation. Autophagy, 2011, 7, 1212-1221.	4.3	143
26	mTOR regulation of autophagy. FEBS Letters, 2010, 584, 1287-1295.	1.3	1,790
27	Cyclic AMP Controls mTOR through Regulation of the Dynamic Interaction between Rheb and Phosphodiesterase 4D. Molecular and Cellular Biology, 2010, 30, 5406-5420.	1.1	65
28	Quantitative Nuclear Proteomics Identifies mTOR Regulation of DNA Damage Response. Molecular and Cellular Proteomics, 2010, 9, 403-414.	2.5	37
29	Glycolytic Flux Signals to mTOR through Glyceraldehyde-3-Phosphate Dehydrogenase-Mediated Regulation of Rheb. Molecular and Cellular Biology, 2009, 29, 3991-4001.	1.1	156
30	ULK-Atg13-FIP200 Complexes Mediate mTOR Signaling to the Autophagy Machinery. Molecular Biology of the Cell, 2009, 20, 1992-2003.	0.9	1,725
31	GÎ²L regulates TNFÎ±-induced NF-ÐºB signaling by directly inhibiting the activation of IÐºB kinase. Cellular Signalling, 2008, 20, 2127-2133.	1.7	8
32	Hsf1 Activation Inhibits Rapamycin Resistance and TOR Signaling in Yeast Revealed by Combined Proteomic and Genetic Analysis. PLoS ONE, 2008, 3, e1598.	1.1	41
33	PRR5, a Novel Component of mTOR Complex 2, Regulates Platelet-derived Growth Factor Receptor Î² Expression and Signaling. Journal of Biological Chemistry, 2007, 282, 25604-25612.	1.6	174
34	Insulin signalling to mTOR mediated by the Akt/PKB substrate PRAS40. Nature Cell Biology, 2007, 9, 316-323.	4.6	1,023
35	PLD2 forms a functional complex with mTOR/raptor to transduce mitogenic signals. Cellular Signalling, 2006, 18, 2283-2291.	1.7	52
36	Rictor, a Novel Binding Partner of mTOR, Defines a Rapamycin-Insensitive and Raptor-Independent Pathway that Regulates the Cytoskeleton. Current Biology, 2004, 14, 1296-1302.	1.8	2,370

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37	GÎ²L, a Positive Regulator of the Rapamycin-Sensitive Pathway Required for the Nutrient-Sensitive Interaction between Raptor and mTOR. Molecular Cell, 2003, 11, 895-904.	4.5	883
38	Contribution of Conserved Amino Acids at the Dimeric Interface to the Conformational Stability and the Structural Integrity of the Active Site in Ketosteroid Isomerase from Pseudomonas putida Biotype B. Journal of Biochemistry, 2003, 134, 101-110.	0.9	5
39	mTOR Interacts with Raptor to Form a Nutrient-Sensitive Complex that Signals to the Cell Growth Machinery. Cell, 2002, 110, 163-175.	13.5	2,673
40	15N NMR Relaxation Studies of Backbone Dynamics in Free and Steroid-Bound Î”5-3-Ketosteroid Isomerase from Pseudomonas testosteroni. Biochemistry, 2001, 40, 3967-3973.	1.2	31
41	Folding Mechanism of Ketosteroid Isomerase from Comamonas testosteroni. Biochemistry, 2001, 40, 5011-5017.	1.2	17
42	Maintenance of Î±-Helical Structures by Phenyl Rings in the Active-Site Tyrosine Triad Contributes to Catalysis and Stability of Ketosteroid Isomerase fromPseudomonas putidaBiotype Bâ€. Biochemistry, 2001, 40, 13529-13537.	1.2	10
43	The Role of Tyr248 Probed by Mutant Bovine Carboxypeptidase A:Â Insight into the Catalytic Mechanism of Carboxypeptidase Aâ€. Biochemistry, 2001, 40, 10197-10203.	1.2	39
44	Roles of dimerization in folding and stability of ketosteroid isomerase from Pseudomonas putida biotype B. Protein Science, 2001, 10, 741-752.	3.1	17
45	Temperature and salt effects on proteolytic function of turnip mosaic potyvirus nuclear inclusion protein a exhibiting a low-temperature optimum activity. BBA - Proteins and Proteomics, 2000, 1480, 29-40.	2.1	6
46	Molecular Cloning, Expression, and Purification of Nuclear Inclusion A Protease from Tobacco Vein Mottling Virus. Molecules and Cells, 2000, 10, 148-155.	1.0	8
47	Characterization of Active-Site Residues of the NIa Protease from Tobacco Vein Mottling Virus. Molecules and Cells, 2000, 10, 505-511.	1.0	10
48	Local Structural Elements in the Mostly Unstructured Transcriptional Activation Domain of Human p53. Journal of Biological Chemistry, 2000, 275, 29426-29432.	1.6	307
49	Role of Catalytic Residues in Enzymatic Mechanisms of Homologous Ketosteroid Isomerasesâ€,â€¡. Biochemistry, 2000, 39, 13891-13896.	1.2	37
50	Equilibrium and Kinetic Analysis of Folding of Ketosteroid Isomerase from Comamonas testosteroni. Biochemistry, 2000, 39, 13084-13092.	1.2	15
51	Contribution of the Hydrogen-Bond Network Involving a Tyrosine Triad in the Active Site to the Structure and Function of a Highly Proficient Ketosteroid Isomerase fromPseudomonas putidaBiotype Bâ€,â€¡. Biochemistry, 2000, 39, 4581-4589.	1.2	42
52	Asp-99 Donates a Hydrogen Bond Not to Tyr-14 but to the Steroid Directly in the Catalytic Mechanism of Î”5-3-Ketosteroid Isomerase fromPseudomonas putidaBiotype Bâ€. Biochemistry, 2000, 39, 903-909.	1.2	49
53	Roles of Active Site Aromatic Residues in Catalysis by Ketosteroid Isomerase from Pseudomonas putida Biotype B. Biochemistry, 1999, 38, 13810-13819.	1.2	19
54	Effects of Mutations in the C-terminal Region of NIa Protease oncis-Cleavage between NIa and NIb. Virology, 1998, 241, 94-100.	1.1	9

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55	Characterization of NIa Protease from Turnip Mosaic Potyvirus Exhibiting a Low-Temperature Optimum Catalytic Activity. Virology, 1996, 221, 245-249.	1.1	16
56	Effects of Internal Cleavages and Mutations in the C-Terminal Region of NIa Protease of Turnip Mosaic Potyvirus on the Catalytic Activity. Virology, 1996, 226, 183-190.	1.1	24
57	Expression, Purification, and Identification of a Novel Self-Cleavage Site of the NIa C-Terminal 27-kDa Protease of Turnip Mosaic Potyvirus C5. Virology, 1995, 213, 517-525.	1.1	30
58	Transactivation Ability of p53 Transcriptional Activation Domain Is Directly Related to the Binding Affinity to TATA-binding Protein. Journal of Biological Chemistry, 1995, 270, 25014-25019.	1.6	106