Kenichiro Imai

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/317655/publications.pdf

Version: 2024-02-01

45
papers

2,029
citations

361413
20
h-index

265206
42
g-index

49
all docs

49
docs citations

49
times ranked

3463
citing authors

#	Article	IF	Citations
1	Role of the TOM Complex in Protein Import into Mitochondria: Structural Views. Annual Review of Biochemistry, 2022, 91, 679-703.	11.1	31
2	Entamoeba histolytica EHD1 Is Involved in Mitosome-Endosome Contact. MBio, 2022, 13, e0384921.	4.1	4
3	Lack of Hikeshi activates HSF1 activity under normal conditions and disturbs the heat-shock response. Life Science Alliance, 2022, 5, e202101241.	2.8	1
4	Structural snapshot of the mitochondrial protein import gate. FEBS Journal, 2021, 288, 5300-5310.	4.7	14
5	Distinct mutations in importin-Î² family nucleocytoplasmic transport receptors transportin-SR and importin-13 affect specific cargo binding. Scientific Reports, 2021, 11, 15649.	3.3	4
6	Mammalian BCAS3 and C16orf70 associate with the phagophore assembly site in response to selective and non-selective autophagy. Autophagy, 2021, 17, 2011-2036.	9.1	6
7	Unfolding is the driving force for mitochondrial import and degradation of the Parkinson's disease-related protein DJ-1. Journal of Cell Science, 2021, 134, .	2.0	3
8	<p>Current Challenges and Opportunities in Designing Proteinâ€“Protein Interaction Targeted Drugs</p>. Advances and Applications in Bioinformatics and Chemistry, 2020, Volume 13, 11-25.	2.6	34
9	Import of Entamoeba histolytica Mitosomal ATP Sulfurylase Relies on Internal Targeting Sequences. Microorganisms, 2020, 8, 1229.	3.6	2
10	Tools for the Recognition of Sorting Signals and the Prediction of Subcellular Localization of Proteins From Their Amino Acid Sequences. Frontiers in Genetics, 2020, 11, 607812.	2.3	17
11	Prediction of Protein Localization. , 2019, , 53-59.		1
12	An Entamoeba-Specific Mitosomal Membrane Protein with Potential Association to the Golgi Apparatus. Genes, 2019, 10, 367.	2.4	7
13	Novel lineageâ€specific transmembrane Î²â€barrel proteins in the endoplasmic reticulum of <i>EntamoebaÂhistolytica</i>. FEBS Journal, 2019, 286, 3416-3432.	4.7	4
14	Porin Associates with Tom22 to Regulate the Mitochondrial Protein Gate Assembly. Molecular Cell, 2019, 73, 1044-1055.e8.	9.7	47
15	Structure of the mitochondrial import gate reveals distinct preprotein paths. Nature, 2019, 575, 395-401.	27.8	146
16	Identification of new abscisic acid receptor agonists using a wheat cell-free based drug screening system. Scientific Reports, 2018, 8, 4268.	3.3	23
17	Origin and Evolutionary Alteration of the Mitochondrial Import System in Eukaryotic Lineages. Molecular Biology and Evolution, 2017, 34, 1574-1586.	8.9	52
18	Tyrosine phosphorylation of the GARU E3 ubiquitin ligase promotes gibberellin signalling by preventing GID1 degradation. Nature Communications, 2017, 8, 1004.	12.8	47

#	Article	IF	Citations
19	Hinge-Deficient IgG1 Fc Fusion: Application to Human Lactoferrin. Molecular Pharmaceutics, 2017, 14, 3025-3035.	4.6	7
20	Extensive cargo identification reveals distinct biological roles of the 12 importin pathways. ELife, 2017, 6, .	6.0	77
21	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
22	Functional conservation of the apoptotic machinery from coral to man: the diverse and complex Bcl-2 and caspase repertoires of Acropora millepora. BMC Genomics, 2016, 17, 62.	2.8	45
23	Screening and discovery of lineage-specific mitosomal membrane proteins in Entamoeba histolytica. Molecular and Biochemical Parasitology, 2016, 209, 10-17.	1.1	13
24	A Novel Mitosomal Î²-Barrel Outer Membrane Protein in Entamoeba. Scientific Reports, 2015, 5, 8545.	3.3	16
25	Conservation of structure and function in vertebrate c-FLIP proteins despite rapid evolutionary change. Biochemistry and Biophysics Reports, 2015, 3, 175-189.	1.3	5
26	Evolutionary analyses of caspaseâ€8 and its paralogs: Deep origins of the apoptotic signaling pathways. BioEssays, 2015, 37, 767-776.	2.5	48
27	MitoFates: Improved Prediction of Mitochondrial Targeting Sequences and Their Cleavage Sites*. Molecular and Cellular Proteomics, 2015, 14, 1113-1126.	3.8	470
28	Molecular architecture of the active mitochondrial protein gate. Science, 2015, 349, 1544-1548.	12.6	169
29	ScreenCap3: Improving prediction of caspaseâ€3 cleavage sites using experimentally verified noncleavage sites. Proteomics, 2014, 14, 2042-2046.	2.2	9
30	The Apoptotic Initiator Caspase-8: Its Functional Ubiquity and Genetic Diversity during Animal Evolution. Molecular Biology and Evolution, 2014, 31, 3282-3301.	8.9	25
31	Tam41 Is a CDP-Diacylglycerol Synthase Required for Cardiolipin Biosynthesis in Mitochondria. Cell Metabolism, 2013, 17, 709-718.	16.2	135
32	Localization Prediction and Structure-Based In Silico Analysis of Bacterial Proteins: With Emphasis on Outer Membrane Proteins. Methods in Molecular Biology, 2013, 939, 115-140.	0.9	3
33	Identification of Cargo Proteins Specific for the Nucleocytoplasmic Transport Carrier Transportin by Combination of an in Vitro Transport System and Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)-based Quantitative Proteomics. Molecular and Cellular Proteomics, 2013, 12, 145-157.	3.8	39
34	Prediction of leucine-rich nuclear export signal containing proteins with NESsential. Nucleic Acids Research, 2011, 39, e111-e111.	14.5	54
35	Eukaryote-wide sequence analysis of mitochondrial Î²-barrel outer membrane proteins. BMC Genomics, 2011, 12, 79.	2.8	36
36	Prediction of subcellular locations of proteins: Where to proceed?. Proteomics, 2010, 10, 3970-3983.	2.2	81

#	Article	IF	Citations
37	Mitochondrial Î²-Barrel Proteins, an Exclusive Club?. Cell, 2008, 135, 1158-1159.	28.9	11
38	SOSUI-GramN: high performance prediction for sub-cellular localization of proteins in Gram-negative bacteria. Bioinformation, 2008, 2, 417-421.	0.5	94
39	A Fourth Type of Secondary Structure Breaker. , 2007, , 165-170.		0
40	Physicochemical properties of amino acid sequences of G-proteins for understanding GPCR-G-protein coupling. Chem-Bio Informatics Journal, 2006, 6, 1-16.	0.3	2
41	Mechanisms of secondary structure breakers in soluble proteins. Biophysics (Nagoya-shi, Japan), 2005, 1, 55-65.	0.4	78
42	Secondary structure breakers and hairpin structures in myoglobin and hemoglobin. Chem-Bio Informatics Journal, 2005, 5, 65-77.	0.3	3
43	Common Pattern of Coarse-Grained Charge Distribution of Structurally Analogous Proteins. Chem-Bio Informatics Journal, 2003, 3, 194-200.	0.3	2
44	Effect of Carbonic Anhydrase II in Molten Globule State on Physical Properties of Dimyristoylphosphatidylcholine Liposome. Japanese Journal of Applied Physics, 2001, 40, 3521-3525.	1.5	1
45	Ultrasonic Properties of a Binary System of a Soluble Protein, Î±-Lactalbumin and Dimyristoyl Phosphatidylcholine Membrane. Japanese Journal of Applied Physics, 2000, 39, 2948-2949.	1.5	3