

Kenji Inaba

List of Publications by Year in descending order

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76
papers

3,371
citations

147801

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149698

56
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83
all docs

83
docs citations

83
times ranked

3422
citing authors

#	ARTICLE	IF	CITATIONS
1	CysteinyI-tRNA synthetase governs cysteine polysulfidation and mitochondrial bioenergetics. <i>Nature Communications</i> , 2017, 8, 1177.	12.8	373
2	Crystal Structure of the DsbB-DsbA Complex Reveals a Mechanism of Disulfide Bond Generation. <i>Cell</i> , 2006, 127, 789-801.	28.9	233
3	The disulfide bond formation (Dsb) system. <i>Current Opinion in Structural Biology</i> , 2008, 18, 450-458.	5.7	143
4	Structural Basis of an ERAD Pathway Mediated by the ER-Resident Protein Disulfide Reductase ERdj5. <i>Molecular Cell</i> , 2011, 41, 432-444.	9.7	130
5	Synergistic cooperation of PDI family members in peroxiredoxin 4-driven oxidative protein folding. <i>Scientific Reports</i> , 2013, 3, 2456.	3.3	118
6	Crystal structures of human Ero1 α reveal the mechanisms of regulated and targeted oxidation of PDI. <i>EMBO Journal</i> , 2010, 29, 3330-3343.	7.8	113
7	Structures and functions of protein disulfide isomerase family members involved in proteostasis in the endoplasmic reticulum. <i>Free Radical Biology and Medicine</i> , 2015, 83, 314-322.	2.9	94
8	Structure and mechanisms of the DsbB-DsbA disulfide bond generation machine. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2008, 1783, 520-529.	4.1	88
9	Paradoxical redox properties of DsbB and DsbA in the protein disulfide-introducing reaction cascade. <i>EMBO Journal</i> , 2002, 21, 2646-2654.	7.8	85
10	Preparation of Selenoinsulin as a Long-Lasting Insulin Analogue. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 5522-5526.	13.8	80
11	Structure, Mechanism, and Evolution of Ero1 Family Enzymes. <i>Antioxidants and Redox Signaling</i> , 2012, 16, 790-799.	5.4	79
12	Disulfide Bond Formation System in <i>Escherichia coli</i> . <i>Journal of Biochemistry</i> , 2009, 146, 591-597.	1.7	75
13	Dynamic nature of disulphide bond formation catalysts revealed by crystal structures of DsbB. <i>EMBO Journal</i> , 2009, 28, 779-791.	7.8	74
14	Redox-assisted regulation of Ca ²⁺ homeostasis in the endoplasmic reticulum by disulfide reductase ERdj5. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6055-E6063.	7.1	74
15	Disulfide bond formation network in the three biological kingdoms, bacteria, fungi and mammals. <i>FEBS Journal</i> , 2012, 279, 2262-2271.	4.7	71
16	A pH-Regulated Quality Control Cycle for Surveillance of Secretory Protein Assembly. <i>Molecular Cell</i> , 2013, 50, 783-792.	9.7	70
17	The Protein Disulfide Isomerase Family: from proteostasis to pathogenesis. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129338.	2.4	66
18	Molecular Bases of Cyclic and Specific Disulfide Interchange between Human ERO1 α Protein and Protein-disulfide Isomerase (PDI). <i>Journal of Biological Chemistry</i> , 2011, 286, 16261-16271.	3.4	63

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19	Critical role of a thiolate-quinone charge transfer complex and its adduct form in de novo disulfide bond generation by DsbB. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 287-292.	7.1	60
20	A PDI-catalyzed thiolate-disulfide switch regulates the production of hydrogen peroxide by human Ero1. Free Radical Biology and Medicine, 2015, 83, 361-372.	2.9	59
21	Redox-Dependent Domain Rearrangement of Protein Disulfide Isomerase Coupled with Exposure of Its Substrate-Binding Hydrophobic Surface. Journal of Molecular Biology, 2010, 396, 361-374.	4.2	58
22	Dynamic assembly of protein disulfide isomerase in catalysis of oxidative folding. Nature Chemical Biology, 2019, 15, 499-509.	8.0	58
23	DsbB Elicits a Red-shift of Bound Ubiquinone during the Catalysis of DsbA Oxidation. Journal of Biological Chemistry, 2004, 279, 6761-6768.	3.4	57
24	Structural basis of a Ni acquisition cycle for [NiFe] hydrogenase by Ni-metallochaperone HypA and its enhancer. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7701-7706.	7.1	54
25	Zinc regulates ERp44-dependent protein quality control in the early secretory pathway. Nature Communications, 2019, 10, 603.	12.8	52
26	A Pair of Circularly Permutated PDZ Domains Control RseP, the S2P Family Intramembrane Protease of Escherichia coli. Journal of Biological Chemistry, 2008, 283, 35042-35052.	3.4	50
27	Radically Different Thioredoxin Domain Arrangement of ERp46, an Efficient Disulfide Bond Introducer of the Mammalian PDI Family. Structure, 2014, 22, 431-443.	3.3	49
28	Reactivities of Quinone-free DsbB from Escherichia coli. Journal of Biological Chemistry, 2005, 280, 33035-33044.	3.4	43
29	Characterization of the Menaquinone-dependent Disulfide Bond Formation Pathway of Escherichia coli. Journal of Biological Chemistry, 2004, 279, 47057-47065.	3.4	38
30	Inhibition of the Functional Interplay between Endoplasmic Reticulum (ER) Oxidoreductin-1 \pm (Ero1 \pm) and Protein-disulfide Isomerase (PDI) by the Endocrine Disruptor Bisphenol A. Journal of Biological Chemistry, 2014, 289, 27004-27018.	3.4	38
31	One-Dimensional Sliding of p53 Along DNA Is Accelerated in the Presence of Ca ²⁺ or Mg ²⁺ at Millimolar Concentrations. Journal of Molecular Biology, 2015, 427, 2663-2678.	4.2	37
32	Progressive quality control of secretory proteins in the early secretory compartment by ERp44. Journal of Cell Science, 2014, 127, 4260-9.	2.0	36
33	Structural Basis of Sarco/Endoplasmic Reticulum Ca ²⁺ -ATPase 2b Regulation via Transmembrane Helix Interplay. Cell Reports, 2019, 27, 1221-1230.e3.	6.4	34
34	MBSJ MCC Young Scientist Award 2009â€“REVIEW: Structural basis of protein disulfide bond generation in the cell. Genes To Cells, 2010, 15, 935-943.	1.2	32
35	Structural basis of pH-dependent client binding by ERp44, a key regulator of protein secretion at the ERâ€“Golgi interface. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3224-E3232.	7.1	32
36	High-Resolution Crystal Structure of Arabidopsis FLOWERING LOCUS T Illuminates Its Phospholipid-Binding Site in Flowering. IScience, 2019, 21, 577-586.	4.1	30

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37	Quantitative Imaging of Labile Zn ²⁺ in the Golgi Apparatus Using a Localizable Small-Molecule Fluorescent Probe. <i>Cell Chemical Biology</i> , 2020, 27, 1521-1531.e8.	5.2	29
38	Homodimerization of Nemo-like kinase is essential for activation and nuclear localization. <i>Molecular Biology of the Cell</i> , 2011, 22, 266-277.	2.1	28
39	Organelle-Level Labile Zn ²⁺ Mapping Based on Targetable Fluorescent Sensors. <i>ACS Sensors</i> , 2022, 7, 748-757.	7.8	26
40	The Highly Dynamic Nature of ERdj5 Is Key to Efficient Elimination of Aberrant Protein Oligomers through ER-Associated Degradation. <i>Structure</i> , 2017, 25, 846-857.e4.	3.3	25
41	Characterization and optimization of two-chain folding pathways of insulin via native chain assembly. <i>Communications Chemistry</i> , 2018, 1, .	4.5	24
42	Conversion of two-state to multi-state folding kinetics on fusion of two protein foldons 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 2000, 302, 219-233.	4.2	23
43	Characterization of the endoplasmic reticulum-resident peroxidases GPx7 and GPx8 shows the higher oxidative activity of GPx7 and its linkage to oxidative protein folding. <i>Journal of Biological Chemistry</i> , 2020, 295, 12772-12785.	3.4	23
44	Cryo-EM structures of SERCA2b reveal the mechanism of regulation by the luminal extension tail. <i>Science Advances</i> , 2020, 6, eabb0147.	10.3	22
45	Structural and functional roles of heme binding module in globin proteins: identification of the segment regulating the heme binding structure. <i>Journal of Molecular Biology</i> , 1998, 283, 311-327.	4.2	21
46	Coupling effects of thiol and urea-type groups for promotion of oxidative protein folding. <i>Chemical Communications</i> , 2019, 55, 759-762.	4.1	21
47	Structural and Functional Roles of Modules in Hemoglobin. <i>Journal of Biological Chemistry</i> , 1997, 272, 30054-30060.	3.4	20
48	PDI Family Members as Guides for Client Folding and Assembly. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9351.	4.1	20
49	Preparation of Selenoinsulin as a Long-Lasting Insulin Analogue. <i>Angewandte Chemie</i> , 2017, 129, 5614-5618.	2.0	18
50	Visualization of structural dynamics of protein disulfide isomerase enzymes in catalysis of oxidative folding and reductive unfolding. <i>Current Opinion in Structural Biology</i> , 2021, 66, 49-57.	5.7	16
51	The membrane topology of vitamin K epoxide reductase is conserved between human isoforms and the bacterial enzyme. <i>Biochemical Journal</i> , 2016, 473, 851-858.	3.7	15
52	Human ER Oxidoreductin-1 \pm (Ero1 \pm) Undergoes Dual Regulation through Complementary Redox Interactions with Protein-Disulfide Isomerase. <i>Journal of Biological Chemistry</i> , 2016, 291, 23952-23964.	3.4	15
53	Identification of the physiological substrates of PDIp, a pancreas-specific protein-disulfide isomerase family member. <i>Journal of Biological Chemistry</i> , 2018, 293, 18421-18433.	3.4	15
54	Identification of the redox partners of ERdj5/JPDI, a PDI family member, from an animal tissue. <i>Biochemical and Biophysical Research Communications</i> , 2013, 440, 245-250.	2.1	14

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55	Antipsychotic olanzapine-induced misfolding of proinsulin in the endoplasmic reticulum accounts for atypical development of diabetes. <i>ELife</i> , 2020, 9, .	6.0	14
56	Structural and Functional Effects of Pseudo-module Substitution in Hemoglobin Subunits. <i>Journal of Biological Chemistry</i> , 1998, 273, 8080-8087.	3.4	13
57	Cysteines 208 and 241 in Ero1 α are required for maximal catalytic turnover. <i>Redox Biology</i> , 2016, 7, 14-20.	9.0	13
58	Observing the nonvectorial yet cotranslational folding of a multidomain protein, LDL receptor, in the ER of mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16401-16408.	7.1	12
59	The α -Proteobacteria <i>Wolbachia pipientis</i> Protein Disulfide Machinery Has a Regulatory Mechanism Absent in β -Proteobacteria. <i>PLoS ONE</i> , 2013, 8, e81440.	2.5	12
60	Methods to identify the substrates of thiolâ€disulfide oxidoreductases. <i>Protein Science</i> , 2018, 28, 30-40.	7.6	11
61	Structural basis of the conformational and functional regulation of human SERCA2b, the ubiquitous endoplasmic reticulum calcium pump. <i>BioEssays</i> , 2022, 44, e2200052.	2.5	10
62	Substitution of the Heme Binding Module in Hemoglobin α - and β -Subunits. <i>Journal of Biological Chemistry</i> , 2000, 275, 12438-12445.	3.4	8
63	A unique leucine-valine adhesive motif supports structure and function of protein disulfide isomerase P5 via dimerization. <i>Structure</i> , 2021, 29, 1357-1370.e6.	3.3	8
64	Cryoâ€EM analysis provides new mechanistic insight into ATP binding to Ca ²⁺ â€ATPase SERCA2b. <i>EMBO Journal</i> , 2021, 40, e108482.	7.8	8
65	Crystal structure of a protein with an artificial exon-shuffling, module M4-substituted chimera hemoglobin β ¹ , at 2.5 Å... resolution 1 1Edited by K. Nagei. <i>Journal of Molecular Biology</i> , 1999, 287, 369-382.	4.2	6
66	Protein disulfide bond generation in <i>Escherichia coli</i> DsbBâ€DsbA. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 199-201.	2.4	6
67	Ero1-Mediated Reoxidation of Protein Disulfide Isomerase Accelerates the Folding of Cone Snail Toxins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3418.	4.1	6
68	Ca ²⁺ Regulates ERp57-Calnexin Complex Formation. <i>Molecules</i> , 2021, 26, 2853.	3.8	6
69	Role of the Cytosolic Loop of DsbB in Catalytic Turnover of the Ubiquinoneâ€DsbB Complex. <i>Antioxidants and Redox Signaling</i> , 2006, 8, 743-752.	5.4	5
70	Distinct roles and actions of protein disulfide isomerase family enzymes in catalysis of nascent-chain disulfide bond formation. <i>IScience</i> , 2021, 24, 102296.	4.1	5
71	Design, construction, crystallization, and preliminary X-ray studies of a fine-tuning mutant (F133V) of module-substituted chimera hemoglobin. , 1998, 32, 263-267.		2
72	Functional Interplay between P5 and PDI/ERp72 to Drive Protein Folding. <i>Biology</i> , 2021, 10, 1112.	2.8	2

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73	Active Expression of Genes for Protein Modification Enzymes in Habu Venom Glands. <i>Toxins</i> , 2022, 14, 300.	3.4	1
74	2P-033 Structural and functional analyses of an ER-resident protein disulfide reductase, ERdj5(The Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	0.1	0
75	Cell Biology of Cysteine-Based Molecular Switches. <i>International Journal of Cell Biology</i> , 2014, 2014, 1-2.	2.5	0
76	A Chemical Ground of de novo Protein Disulfide Bond Generation in the Cell. <i>Seibutsu Butsuri</i> , 2006, 46, 257-262.	0.1	0