

Kenji Inaba

List of Publications by Year in descending order

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76
papers

3,371
citations

147566

31
h-index

155451

55
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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.	5.8	373
2	Crystal Structure of the DsbB-DsbA Complex Reveals a Mechanism of Disulfide Bond Generation. <i>Cell</i> , 2006, 127, 789-801.	13.5	233
3	The disulfide bond formation (Dsb) system. <i>Current Opinion in Structural Biology</i> , 2008, 18, 450-458.	2.6	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.	4.5	130
5	Synergistic cooperation of PDI family members in peroxiredoxin 4-driven oxidative protein folding. <i>Scientific Reports</i> , 2013, 3, 2456.	1.6	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.	3.5	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.	1.3	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.	1.9	88
9	Paradoxical redox properties of DsbB and DsbA in the protein disulfide-introducing reaction cascade. <i>EMBO Journal</i> , 2002, 21, 2646-2654.	3.5	85
10	Preparation of Selenoinsulin as a Long-Lasting Insulin Analogue. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 5522-5526.	7.2	80
11	Structure, Mechanism, and Evolution of Ero1 Family Enzymes. <i>Antioxidants and Redox Signaling</i> , 2012, 16, 790-799.	2.5	79
12	Disulfide Bond Formation System in <i>Escherichia coli</i> . <i>Journal of Biochemistry</i> , 2009, 146, 591-597.	0.9	75
13	Dynamic nature of disulphide bond formation catalysts revealed by crystal structures of DsbB. <i>EMBO Journal</i> , 2009, 28, 779-791.	3.5	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.	3.3	74
15	Disulfide bond formation network in the three biological kingdoms, bacteria, fungi and mammals. <i>FEBS Journal</i> , 2012, 279, 2262-2271.	2.2	71
16	A pH-Regulated Quality Control Cycle for Surveillance of Secretory Protein Assembly. <i>Molecular Cell</i> , 2013, 50, 783-792.	4.5	70
17	The Protein Disulfide Isomerase Family: from proteostasis to pathogenesis. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129338.	1.1	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.	1.6	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 287-292.	3.3	60
20	A PDI-catalyzed thiolate-disulfide switch regulates the production of hydrogen peroxide by human Ero1. <i>Free Radical Biology and Medicine</i> , 2015, 83, 361-372.	1.3	59
21	Redox-Dependent Domain Rearrangement of Protein Disulfide Isomerase Coupled with Exposure of Its Substrate-Binding Hydrophobic Surface. <i>Journal of Molecular Biology</i> , 2010, 396, 361-374.	2.0	58
22	Dynamic assembly of protein disulfide isomerase in catalysis of oxidative folding. <i>Nature Chemical Biology</i> , 2019, 15, 499-509.	3.9	58
23	DsbB Elicits a Red-shift of Bound Ubiquinone during the Catalysis of DsbA Oxidation. <i>Journal of Biological Chemistry</i> , 2004, 279, 6761-6768.	1.6	57
24	Structural basis of a Ni acquisition cycle for [NiFe] hydrogenase by Ni-metallochaperone HypA and its enhancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7701-7706.	3.3	54
25	Zinc regulates ERp44-dependent protein quality control in the early secretory pathway. <i>Nature Communications</i> , 2019, 10, 603.	5.8	52
26	A Pair of Circularly Permutated PDZ Domains Control RseP, the S2P Family Intramembrane Protease of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 35042-35052.	1.6	50
27	Radically Different Thioredoxin Domain Arrangement of ERp46, an Efficient Disulfide Bond Introducer of the Mammalian PDI Family. <i>Structure</i> , 2014, 22, 431-443.	1.6	49
28	Reactivities of Quinone-free DsbB from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 33035-33044.	1.6	43
29	Characterization of the Menaquinone-dependent Disulfide Bond Formation Pathway of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 47057-47065.	1.6	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. <i>Journal of Biological Chemistry</i> , 2014, 289, 27004-27018.	1.6	38
31	One-Dimensional Sliding of p53 Along DNA Is Accelerated in the Presence of Ca ²⁺ or Mg ²⁺ at Millimolar Concentrations. <i>Journal of Molecular Biology</i> , 2015, 427, 2663-2678.	2.0	37
32	Progressive quality control of secretory proteins in the early secretory compartment by ERp44. <i>Journal of Cell Science</i> , 2014, 127, 4260-9.	1.2	36
33	Structural Basis of Sarco/Endoplasmic Reticulum Ca ²⁺ -ATPase 2b Regulation via Transmembrane Helix Interplay. <i>Cell Reports</i> , 2019, 27, 1221-1230.e3.	2.9	34
34	MBSJ MCC Young Scientist Award 2009â€“REVIEW: Structural basis of protein disulfide bond generation in the cell. <i>Genes To Cells</i> , 2010, 15, 935-943.	0.5	32
35	Structural basis of pH-dependent client binding by ERp44, a key regulator of protein secretion at the ERâ€“Golgi interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3224-E3232.	3.3	32
36	High-Resolution Crystal Structure of Arabidopsis FLOWERING LOCUS T Illuminates Its Phospholipid-Binding Site in Flowering. <i>IScience</i> , 2019, 21, 577-586.	1.9	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.	2.5	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.	0.9	28
39	Organelle-Level Labile Zn ²⁺ Mapping Based on Targetable Fluorescent Sensors. <i>ACS Sensors</i> , 2022, 7, 748-757.	4.0	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.	1.6	25
41	Characterization and optimization of two-chain folding pathways of insulin via native chain assembly. <i>Communications Chemistry</i> , 2018, 1, .	2.0	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.	2.0	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.	1.6	23
44	Cryo-EM structures of SERCA2b reveal the mechanism of regulation by the luminal extension tail. <i>Science Advances</i> , 2020, 6, eabb0147.	4.7	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.	2.0	21
46	Coupling effects of thiol and urea-type groups for promotion of oxidative protein folding. <i>Chemical Communications</i> , 2019, 55, 759-762.	2.2	21
47	Structural and Functional Roles of Modules in Hemoglobin. <i>Journal of Biological Chemistry</i> , 1997, 272, 30054-30060.	1.6	20
48	PDI Family Members as Guides for Client Folding and Assembly. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9351.	1.8	20
49	Preparation of Selenoinsulin as a Long-Lasting Insulin Analogue. <i>Angewandte Chemie</i> , 2017, 129, 5614-5618.	1.6	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.	2.6	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.	1.7	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.	1.6	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.	1.6	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.	1.0	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, .	2.8	14
56	Structural and Functional Effects of Pseudo-module Substitution in Hemoglobin Subunits. <i>Journal of Biological Chemistry</i> , 1998, 273, 8080-8087.	1.6	13
57	Cysteines 208 and 241 in Ero1 \pm are required for maximal catalytic turnover. <i>Redox Biology</i> , 2016, 7, 14-20.	3.9	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.	3.3	12
59	The \pm -Proteobacteria <i>Wolbachia pipientis</i> Protein Disulfide Machinery Has a Regulatory Mechanism Absent in β -Proteobacteria. <i>PLoS ONE</i> , 2013, 8, e81440.	1.1	12
60	Methods to identify the substrates of thiolâ€disulfide oxidoreductases. <i>Protein Science</i> , 2018, 28, 30-40.	3.1	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.	1.2	10
62	Substitution of the Heme Binding Module in Hemoglobin $\hat{\pm}$ - and $\hat{2}$ -Subunits. <i>Journal of Biological Chemistry</i> , 2000, 275, 12438-12445.	1.6	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.	1.6	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.	3.5	8
65	Crystal structure of a protein with an artificial exon-shuffling, module M4-substituted chimera hemoglobin $\hat{2}\hat{1}\pm$, at 2.5 Å... resolution 1 1Edited by K. Nagei. <i>Journal of Molecular Biology</i> , 1999, 287, 369-382.	2.0	6
66	Protein disulfide bond generation in <i>Escherichia coli</i> DsbBâ€DsbA. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 199-201.	1.0	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.	1.8	6
68	Ca ²⁺ Regulates ERp57-Calnexin Complex Formation. <i>Molecules</i> , 2021, 26, 2853.	1.7	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.	2.5	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.	1.9	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.	1.3	2

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73	Active Expression of Genes for Protein Modification Enzymes in Habu Venom Glands. <i>Toxins</i> , 2022, 14, 300.	1.5	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	0.0	0
75	Cell Biology of Cysteine-Based Molecular Switches. <i>International Journal of Cell Biology</i> , 2014, 2014, 1-2.	1.0	0
76	A Chemical Ground of de novo Protein Disulfide Bond Generation in the Cell. <i>Seibutsu Butsuri</i> , 2006, 46, 257-262.	0.0	0