

Yutaka Kuroda

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3937997/publications.pdf>

Version: 2024-02-01

104
papers

2,729
citations

218677

26
h-index

197818

49
g-index

112
all docs

112
docs citations

112
times ranked

2339
citing authors

#	ARTICLE	IF	CITATIONS
1	Blocking PSD95&PDZ3's amyloidogenesis through point mutations that inhibit high&temperature reversible oligomerization (RO). FEBS Journal, 2022, 289, 3205-3216.	4.7	2
2	A Multi-Disulfide Receptor-Binding Domain (RBD) of the SARS-CoV-2 Spike Protein Expressed in E. coli Using a SEP-Tag Produces Antisera Interacting with the Mammalian Cell Expressed Spike (S1) Protein. International Journal of Molecular Sciences, 2022, 23, 1703.	4.1	15
3	Reverse Engineering Analysis of the High-Temperature Reversible Oligomerization and Amyloidogenicity of PSD95-PDZ3. Molecules, 2022, 27, 2813.	3.8	2
4	Lattice-model analysis of the effect of protein surface charge distribution on amorphous aggregation and condensation. Chemical Physics Letters, 2022, 802, 139767.	2.6	0
5	Stochastic modelling of the effects of human-mobility restriction and viral infection characteristics on the spread of COVID-19. Scientific Reports, 2021, 11, 6856.	3.3	10
6	EGFR extracellular domain III expressed in Escherichia coli with SEP tag shows improved biophysical and functional properties and generate anti-sera inhibiting cancer cell growth. Biochemical and Biophysical Research Communications, 2021, 555, 121-127.	2.1	8
7	Anti-EGFR VHH Antibody under Thermal Stress Is Better Solubilized with a Lysine than with an Arginine SEP Tag. Biomolecules, 2021, 11, 810.	4.0	4
8	Solubility Controlling Peptide Tags of Opposite Charges Generate a Bivalent Immune Response Against Dengue ED3 Serotypes 3 and 4. Frontiers in Immunology, 2021, 12, 671590.	4.8	3
9	Immune response with long-term memory triggered by amorphous aggregates of misfolded anti-EGFR VHH-7D12 is directed against the native VHH-7D12 as well as the framework of the analogous VHH-9G8. European Journal of Pharmaceutics and Biopharmaceutics, 2021, 165, 13-21.	4.3	6
10	Assessment of prediction methods for protein structures determined by <sc>NMR</sc> in <sc>CASP14</sc>: Impact of <sc>AlphaFold2</sc>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1959-1976.	2.6	30
11	A novel caged Cookson&type reagent toward a practical vitamin D derivatization method for mass spectrometric analyses. Rapid Communications in Mass Spectrometry, 2020, 34, e8648.	1.5	7
12	A systematic mutational analysis identifies a 5&residue proline tag that enhances the <i>in Vivo</i> immunogenicity of a non&immunogenic model protein. FEBS Open Bio, 2020, 10, 1947-1956.	2.3	9
13	Reversible Oligomerization and Reverse Hydrophobic Effect Induced by Isoleucine Tags Attached at the C-Terminus of a Simplified BPTI Variant. Biochemistry, 2020, 59, 3660-3668.	2.5	9
14	Solution structure of Gaussia Luciferase with five disulfide bonds and identification of a putative coelenterazine binding cavity by heteronuclear NMR. Scientific Reports, 2020, 10, 20069.	3.3	34
15	Thermodynamic Analysis of Point Mutations Inhibiting High-Temperature Reversible Oligomerization of PDZ3. Biophysical Journal, 2020, 119, 1391-1401.	0.5	6
16	How A Novel Scientific Concept Was Coined the "Molten Globule State". Biomolecules, 2020, 10, 269.	4.0	13
17	Nanometer-Sized Aggregates Generated Using Short Solubility Controlling Peptide Tags Do Increase the In Vivo Immunogenicity of a Nonimmunogenic Protein. Molecular Pharmaceutics, 2020, 17, 1629-1637.	4.6	11
18	Anti-Dengue ED3 Long-Term Immune Response With T-Cell Memory Generated Using Solubility Controlling Peptide Tags. Frontiers in Immunology, 2020, 11, 333.	4.8	16

#	ARTICLE	IF	CITATIONS
19	The immunogenicity of an anti-EGFR single domain antibody (VHH) is enhanced by misfolded amorphous aggregation but not by heat-induced aggregation. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2020, 152, 164-174.	4.3	16
20	Folding of the Ig-Like Domain of the Dengue Virus Envelope Protein Analyzed by High-Hydrostatic-Pressure NMR at a Residue-Level Resolution. <i>Biomolecules</i> , 2019, 9, 309.	4.0	9
21	Misfolding of a Single Disulfide Bonded Globular Protein into a Low-Solubility Species Conformationally and Biophysically Distinct from the Native One. <i>Biomolecules</i> , 2019, 9, 250.	4.0	7
22	Hydrophobic surface residues can stabilize a protein through improved water-protein interactions. <i>FEBS Journal</i> , 2019, 286, 4122-4134.	4.7	30
23	Large-scale all-atom molecular dynamics alanine-scanning of IAPP octapeptides provides insights into the molecular determinants of amyloidogenicity. <i>Scientific Reports</i> , 2019, 9, 2530.	3.3	4
24	Design and assessment of an active anti-epidermal growth factor receptor (EGFR) single chain variable fragment (ScFv) with improved solubility. <i>Biochemical and Biophysical Research Communications</i> , 2019, 508, 1043-1049.	2.1	17
25	A SEP tag enhances the expression, solubility and yield of recombinant TEV protease without altering its activity. <i>New Biotechnology</i> , 2018, 42, 77-84.	4.4	30
26	Biophysical studies of protein solubility and amorphous aggregation by systematic mutational analysis and a helical polymerization model. <i>Biophysical Reviews</i> , 2018, 10, 473-480.	3.2	21
27	Reversible association of proteins into sub-visible amorphous aggregates using short solubility controlling peptide tags. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 366-372.	2.3	17
28	Crystal structures of highly simplified BPTIs provide insights into hydration-driven increase of unfolding enthalpy. <i>Scientific Reports</i> , 2017, 7, 41205.	3.3	5
29	Thermodynamics of the Thermal Denaturation of Acid Molten Globule State of Cytochrome <i>c</i> Indicate a Reversible High-Temperature Oligomerization Process. <i>Biochemistry</i> , 2017, 56, 2372-2378.	2.5	8
30	Fast H-DROP: A thirty times accelerated version of H-DROP for interactive SVM-based prediction of helical domain linkers. <i>Journal of Computer-Aided Molecular Design</i> , 2017, 31, 237-244.	2.9	2
31	A hetero-micro-seeding strategy for readily crystallizing closely related protein variants. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 504-508.	2.1	3
32	Crystallographic studies of sero-specific dengue ED3 immune response. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a404-a404.	0.1	0
33	Crystal structures of dengue virus protein revealed ED3 sero-specificity. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C394-C394.	0.1	0
34	A novel screening system based on VanX-mediated autolysis Application to <i>Gaussia</i> luciferase. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1413-1420.	3.3	7
35	Amorphous protein aggregation monitored using fluorescence self-quenching. <i>FEBS Letters</i> , 2016, 590, 3501-3509.	2.8	15
36	Unusual Reversible Oligomerization of Unfolded Dengue Envelope Protein Domain 3 at High Temperatures and Its Abolition by a Point Mutation. <i>Biochemistry</i> , 2016, 55, 4469-4475.	2.5	20

#	ARTICLE	IF	CITATIONS
37	All-atom molecular dynamics analysis of multi-peptide systems reproduces peptide solubility in line with experimental observations. <i>Scientific Reports</i> , 2016, 6, 19479.	3.3	33
38	Modeling and experimental assessment of a buried Leu→Ile mutation in dengue envelope domain III. <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 163-168.	2.1	7
39	Plant-PrAS: A Database of Physicochemical and Structural Properties and Novel Functional Regions in Plant Proteomes. <i>Plant and Cell Physiology</i> , 2015, 56, e11-e11.	3.1	15
40	Bacterial expression and re-engineering of <i>Gaussia princeps</i> luciferase and its use as a reporter protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1392-1399.	2.3	32
41	Analysis and Control of Protein Crystallization Using Short Peptide Tags That Change Solubility without Affecting Structure, Thermal Stability, and Function. <i>Crystal Growth and Design</i> , 2015, 15, 2703-2711.	3.0	22
42	Structural and biophysical analysis of sero-specific immune responses using epitope grafted Dengue ED3 mutants. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1438-1443.	2.3	11
43	Biochemical and Biophysical Characterization of an Unexpected Bacteriolytic Activity of VanX, a Member of the Vancomycin-resistance vanA Gene Cluster. <i>Journal of Biological Chemistry</i> , 2014, 289, 35686-35694.	3.4	4
44	Correlations between predicted protein disorder and post-translational modifications in plants. <i>Bioinformatics</i> , 2014, 30, 1095-1103.	4.1	36
45	Computational prediction and experimental characterization of a "size switch type repacking" during the evolution of dengue envelope protein domain III (ED3). <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 585-592.	2.3	17
46	H-DROP: an SVM based helical domain linker predictor trained with features optimized by combining random forest and stepwise selection. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 831-839.	2.9	5
47	3P048 Analysis of protein crystallization using short Solubility Controlling Peptide tags(01C. Protein:) Tj ETQq1 1 0.784314 rgBT /Overle Butsuri, 2014, 54, S256.	0.1	0
48	Analysis of protein aggregation kinetics using short amino acid peptide tags. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2107-2115.	2.3	30
49	IS-Dom: a dataset of independent structural domains automatically delineated from protein structures. <i>Journal of Computer-Aided Molecular Design</i> , 2013, 27, 419-426.	2.9	2
50	High resolution crystal structure of dengue envelope protein domain III suggests possible molecular mechanisms for serospecific antibody recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1090-1095.	2.6	21
51	Extraction of recombinant protein from <i>Escherichia coli</i> by using a novel cell autolysis activity of VanX. <i>Analytical Biochemistry</i> , 2013, 439, 212-217.	2.4	4
52	Probing the Physical Determinants of Thermal Expansion of Folded Proteins. <i>Journal of Physical Chemistry B</i> , 2013, 117, 12742-12749.	2.6	25
53	1P071 All atom molecular dynamics simulation of short tetra-peptides shed insights into amino acid's amorphous aggregation propensities(01C. Protein:Property,Poster). <i>Seibutsu Butsuri</i> , 2013, 53, S117.	0.1	0
54	2P063 Thermodynamic characterization of a reversible oligomerization process in the thermal transition of a BPTI variant tagged with isoleucines(01C. Protein: Property). <i>Seibutsu Butsuri</i> , 2013, 53, S169.	0.1	0

#	ARTICLE	IF	CITATIONS
55	1C1412 Toward a simplified screening method using a novel VanX cell lysis activity(Proteins: Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF 5	0.1	0
56	Experimental Identification and Theoretical Analysis of a Thermally Stabilized Green Fluorescent Protein Variant. <i>Biochemistry</i> , 2012, 51, 7974-7982.	2.5	11
57	Analysis of amino acid contributions to protein solubility using short peptide tags fused to a simplified BPTI variant. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1144-1150.	2.3	36
58	2E1546 Protein Aggregation Kinetics Using Short Amino acid Peptide Tags(Proteins:Property II,Oral) Tj ETQq0 0 0 rgBT /Overlock 10 TF 5 S47.	0.1	0
59	Solubilization and folding of a fully active recombinant Gaussia luciferase with native disulfide bonds by using a SEP-Tag. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1775-1778.	2.3	35
60	DROP: an SVM domain linker predictor trained with optimal features selected by random forest. <i>Bioinformatics</i> , 2011, 27, 487-494.	4.1	60
61	3P055 EXPERIMENTAL ANALYSIS OF BPTI VARIANTS STABILIZED BY SINGLE AND DOUBLE MUTATIONS.(Protein: Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF 5	0.1	0
62	2P294 ANALYSIS OF THREE-RESIDUE FRAGMENT'S CONFORMATIONAL SPACE(The 48th Annual Meeting of) Tj ETQq0 0 0 rgBT /Overlock 10 TF 5	0.1	0
63	1P055 DEVELOPMENT OF NOVEL ANALYTICAL METHODS FOR MEASURING SHORT PEPTIDE SOLUBILITIES(Protein:Property,The 48th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2010, 50, S28-S29.	0.1	0
64	1P292 Influence of Domain Linker Sequence and Structure on the Definition of Structural Domains.(Bioinformatics:Structural genomics,The 48th Annual Meeting of the Biophysical Society of) Tj ETQq0 0 0 rgBT /Overlock 10 TF 5	0.1	0
65	2P005 1F1505 A hetero-seeding strategy for crystallizing protein variants difficult to crystallize(The Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF 5	0.1	0
66	Mathematical model for empirically optimizing large scale production of soluble protein domains. <i>BMC Bioinformatics</i> , 2010, 11, 113.	2.6	7
67	Biophysical characterization of highly active recombinant Gaussia luciferase expressed in <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1902-1907.	2.3	31
68	Prediction of protein motions from amino acid sequence and its application to protein-protein interaction. <i>BMC Structural Biology</i> , 2010, 10, 20.	2.3	14
69	1P016 Biophysical characterization of highly active recombinant Gaussia luciferase expressed in <i>Escherichia coli</i> (Protein:Structure,The 48th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2010, 50, S21.	0.1	0
70	Loop Length-Dependent SVM prediction of domain linkers for high-throughput structural proteomics. <i>Biopolymers</i> , 2009, 92, 1-8.	2.4	49
71	Improved protein splicing reaction for low solubility protein fragments without insertion of native extein residues. <i>Biopolymers</i> , 2009, 92, 465-470.	2.4	2
72	Thermodynamic and structural analysis of highly stabilized BPTIs by single and double mutations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 962-970.	2.6	22

#	ARTICLE	IF	CITATIONS
73	Crystal structure of an extensively simplified variant of bovine pancreatic trypsin inhibitor in which over one-third of the residues are alanines. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15334-15339.	7.1	31
74	Methods for Enhancing Protein Solubility and the Effect of SEP-Tags on Protein Solubility. Seibutsu Butsurei, 2008, 48, 185-189.	0.1	0
75	POODLE-L: a two-level SVM prediction system for reliably predicting long disordered regions. Bioinformatics, 2007, 23, 2046-2053.	4.1	132
76	Dynamic Viscoelastic Measurement of E. coli Giant DNA Solutions. Kobunshi Ronbunshu, 2007, 64, 458-463.	0.2	0
77	Thermodynamic Properties of BPTI Variants with Highly Simplified Amino Acid Sequences. Journal of Molecular Biology, 2007, 372, 737-746.	4.2	27
78	Mutational analysis of protein solubility enhancement using short peptide tags. Biopolymers, 2007, 85, 12-18.	2.4	88
79	Identification of putative domain linkers by a neural network - application to a large sequence database. BMC Bioinformatics, 2006, 7, 323.	2.6	16
80	Computer-aided NMR assay for detecting natively folded structural domains. Protein Science, 2006, 15, 871-883.	7.6	27
81	1P472 Domain linker prediction using a Support Vector Machine(SVM)(23. Bioinformatics, genomics and) Tj ETQq1 1 0.784314 rgBT S264.	0.1	0
82	Improvement of domain linker prediction by incorporating loop-length-dependent characteristics. Biopolymers, 2006, 84, 161-168.	2.4	30
83	Structural and Functional Characterization of a Mutant of Pseudocerastes persicus Natriuretic Peptide. Protein and Peptide Letters, 2006, 13, 295-300.	0.9	2
84	ProteoMix: an integrated and flexible system for interactively analyzing large numbers of protein sequences. Bioinformatics, 2004, 20, 2836-2838.	4.1	8
85	Characteristics and prediction of domain linker sequences in multi-domain proteins. Journal of Structural and Functional Genomics, 2003, 4, 79-85.	1.2	27
86	Solution Structure of the DFF-C Domain of DFF45/ICAD. A Structural Basis for the Regulation of Apoptotic DNA Fragmentation. Journal of Molecular Biology, 2002, 321, 317-327.	4.2	40
87	Characterization and prediction of linker sequences of multi-domain proteins by a neural network. Journal of Structural and Functional Genomics, 2002, 2, 37-51.	1.2	45
88	Structural genomics projects in Japan. Nature Structural Biology, 2000, 7, 943-945.	9.7	316
89	Structural genomics projects in Japan. Progress in Biophysics and Molecular Biology, 2000, 73, 363-376.	2.9	49
90	Automated search of natively folded protein fragments for high-throughput structure determination in structural genomics. Protein Science, 2000, 9, 2313-2321.	7.6	31

#	ARTICLE	IF	CITATIONS
91	Folding of bovine pancreatic trypsin inhibitor (BPTI) variants in which almost half the residues are alanine. <i>Journal of Molecular Biology</i> , 2000, 298, 493-501.	4.2	53
92	Role of Heme Axial Ligands in the Conformational Stability of the Native and Molten Globule States of Horse Cytochrome c. <i>Journal of Molecular Biology</i> , 1996, 256, 172-186.	4.2	86
93	High helicity of peptide fragments corresponding to β^2 -strand regions of β^2 -lactoglobulin observed by 2D-NMR spectroscopy. <i>Folding & Design</i> , 1996, 1, 255-263.	4.5	78
94	A strategy for the de novo design of helical proteins with stable folds. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 97-101.	2.1	15
95	High Helical Propensity of the Peptide Fragments Derived from β^2 -Lactoglobulin, a Predominantly β^2 -sheet Protein. <i>Journal of Molecular Biology</i> , 1995, 254, 737-746.	4.2	176
96	Stability of β -helices in a molten globule state of cytochrome c by hydrogen-deuterium exchange and two-dimensional NMR spectroscopy. <i>Journal of Molecular Biology</i> , 1995, 247, 682-688.	4.2	13
97	Cooperative deformation of a de novo designed protein. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 969-976.	2.1	27
98	Thermodynamic characterization of an artificially designed amphiphilic β -helical peptide containing periodic prolines: Observations of high thermal stability and cold denaturation. <i>Protein Science</i> , 1994, 3, 831-837.	7.6	21
99	Individual Ionization Constants of All the Carboxyl Groups in Ribonuclease HI from <i>Escherichia coli</i> Determined by NMR. <i>Biochemistry</i> , 1994, 33, 5275-5284.	2.5	147
100	Solution Structure of a de Novo Helical Protein by 2D-NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 1994, 236, 862-868.	4.2	54
101	Residual helical structure in the C-terminal fragment of cytochrome c. <i>Biochemistry</i> , 1993, 32, 1219-1224.	2.5	86
102	Thermodynamic characterization of cytochrome c at low pH. <i>Journal of Molecular Biology</i> , 1992, 223, 1139-1153.	4.2	157
103	Postacquisition data processing method for suppression of the solvent signal. II. The weighted first derivative. <i>Journal of Magnetic Resonance</i> , 1990, 88, 141-145.	0.5	4
104	Postacquisition data processing method for suppression of the solvent signal. <i>Journal of Magnetic Resonance</i> , 1989, 84, 604-610.	0.5	15