

Shinya Honda

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

1,789
citations

361413

20
h-index

302126

39
g-index

83
all docs

83
docs citations

83
times ranked

1738
citing authors

#	ARTICLE	IF	CITATIONS
1	of Therapeutic in Solution. <i>Methods in Molecular Biology</i> , 2022, 2313, 219-239.	0.9	0
2	Local disorder of the C-terminal segment of the heavy chain as a common sign of stressed antibodies evidenced with a peptide affinity probe specific to non-native IgG. <i>International Journal of Biological Macromolecules</i> , 2021, 182, 1697-1703.	7.5	4
3	Effect of backbone circularization on colloidal stability: Compaction of unfolded structures improves aggregation resistance of granulocyte colony-stimulating factor. <i>International Journal of Pharmaceutics</i> , 2021, 605, 120774.	5.2	3
4	Polyploid engineering by increasing mutant gene dosage in yeasts. <i>Microbial Biotechnology</i> , 2021, 14, 979-992.	4.2	4
5	Live-cell imaging to analyze intracellular aggregation of recombinant IgG in CHO cells. <i>Cell Chemical Biology</i> , 2021, , .	5.2	4
6	Stabilization of backbone-circularized protein is attained by synergistic gains in enthalpy of folded structure and entropy of unfolded structure. <i>FEBS Journal</i> , 2020, 287, 1554-1575.	4.7	5
7	Wipi3 is essential for alternative autophagy and its loss causes neurodegeneration. <i>Nature Communications</i> , 2020, 11, 5311.	12.8	30
8	Histidine-Mediated Intramolecular Electrostatic Repulsion for Controlling pH-Dependent Protein-Protein Interaction. <i>ACS Chemical Biology</i> , 2019, 14, 2729-2736.	3.4	13
9	Synthetic gene expression circuits regulating sexual reproduction. <i>Methods in Enzymology</i> , 2019, 621, 17-30.	1.0	4
10	In-Solution Microscopic Imaging of Fractal Aggregates of a Stressed Therapeutic Antibody. <i>Analytical Chemistry</i> , 2019, 91, 4640-4648.	6.5	11
11	pH-shift stress on antibodies. <i>Methods in Enzymology</i> , 2019, 622, 329-345.	1.0	9
12	<i>Anxa2</i> and <i>Ctsd</i> knockout CHO cell lines to diminish the risk of contamination with host cell proteins. <i>Biotechnology Progress</i> , 2019, 35, e2820.	2.6	16
13	C _H 2 domain orientation of human immunoglobulin G in solution: Structural comparison of glycosylated and aglycosylated Fc regions using small-angle X-ray scattering. <i>MAbs</i> , 2019, 11, 453-462.	5.2	7
14	Artificial Mating-Type Conversion and Repetitive Mating for Polyploid Generation. <i>ACS Synthetic Biology</i> , 2018, 7, 1413-1423.	3.8	9
15	Suppression of Aggregation of Therapeutic Monoclonal Antibodies during Storage by Removal of Aggregation Precursors Using a Specific Adsorbent of Non-Native IgG Conformers. <i>Bioconjugate Chemistry</i> , 2018, 29, 3250-3261.	3.6	7
16	Generation of ubiquitin-based binder with an inserted active peptide. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 3162-3166.	2.1	1
17	Structural insights into the backbone-circularized granulocyte colony-stimulating factor containing a short connector. <i>Biochemical and Biophysical Research Communications</i> , 2018, 500, 224-228.	2.1	4
18	Calibration-free concentration analysis for an analyte prone to self-association. <i>Analytical Biochemistry</i> , 2017, 516, 61-64.	2.4	4

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19	Conformational and Colloidal Stabilities of Human Immunoglobulin G Fc and Its Cyclized Variant: Independent and Compensatory Participation of Domains in Aggregation of Multidomain Proteins. <i>Molecular Pharmaceutics</i> , 2017, 14, 699-711.	4.6	9
20	Positive Detection of GPCR Antagonists Using a System for Inverted Expression of a Fluorescent Reporter Gene. <i>ACS Synthetic Biology</i> , 2017, 6, 1554-1562.	3.8	6
21	Friability Testing as a New Stress-Stability Assay for Biopharmaceuticals. <i>Journal of Pharmaceutical Sciences</i> , 2017, 106, 2966-2978.	3.3	27
22	AlphaScreen-based homogeneous assay using a pair of 25-residue artificial proteins for high-throughput analysis of non-native IgG. <i>Scientific Reports</i> , 2017, 7, 12466.	3.3	8
23	Backbone Circularization Coupled with Optimization of Connecting Segment in Effectively Improving the Stability of Granulocyte-Colony Stimulating Factor. <i>ACS Chemical Biology</i> , 2017, 12, 2690-2696.	3.4	17
24	Fate of a Stressed Therapeutic Antibody Tracked by Fluorescence Correlation Spectroscopy: Folded Monomers Survive Aggregation. <i>Journal of Physical Chemistry B</i> , 2017, 121, 8085-8093.	2.6	21
25	Surface plasmon resonance biosensing of the monomer and the linked dimer of the variants of protein G under mass transport limitation. <i>Data in Brief</i> , 2016, 9, 917-921.	1.0	1
26	Biosensing Probe for Quality Control Monitoring of the Structural Integrity of Therapeutic Antibodies. <i>Analytical Chemistry</i> , 2016, 88, 10095-10101.	6.5	17
27	Continuous crossbreeding of sake yeasts using growth selection systems for a-type and $\hat{\iota}$ -type cells. <i>AMB Express</i> , 2016, 6, 45.	3.0	17
28	Kinetics of Antibody Aggregation at Neutral pH and Ambient Temperatures Triggered by Temporal Exposure to Acid. <i>Journal of Physical Chemistry B</i> , 2016, 120, 9581-9589.	2.6	35
29	Adaptive Assembly: Maximizing the Potential of a Given Functional Peptide with a Tailor-Made Protein Scaffold. <i>Chemistry and Biology</i> , 2015, 22, 1165-1173.	6.0	4
30	Rapid Evaluation of Tyrosine Kinase Activity of Membrane-Integrated Human Epidermal Growth Factor Receptor Using the Yeast Gl^3 Recruitment System. <i>ACS Synthetic Biology</i> , 2015, 4, 421-429.	3.8	6
31	Conformational and Colloidal Stabilities of Isolated Constant Domains of Human Immunoglobulin G and Their Impact on Antibody Aggregation under Acidic Conditions. <i>Molecular Pharmaceutics</i> , 2015, 12, 1443-1455.	4.6	35
32	3SEA-04 The approach to the function-stability tradeoff: A case of the design of a humanized protein mimicking the albumin-binding protein(Frontiers in physical properties of proteins: challenges by) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50.1 <i>Seibutsu Butsuri</i> , 2014, 54, S140.	0.1	6
33	3P086 Design of an Albumin-Binding Humanized Protein by Mimicking the Contact Surface of a Bacterial Albumin-Binding Domain(01F. Protein: Engineering,Poster,The 52nd Annual Meeting of the) Tj ETQq1 1 0.084314 rgBT /Overlock 10 Tf 50.1	0.1	6
34	Tracing Primordial Protein Evolution through Structurally Guided Stepwise Segment Elongation. <i>Journal of Biological Chemistry</i> , 2014, 289, 3394-3404.	3.4	14
35	Structure of the Microtubule-Binding Domain of Flagellar Dynein. <i>Structure</i> , 2014, 22, 1628-1638.	3.3	18
36	Engineered protein A ligands, derived from a histidine-scanning library, facilitate the affinity purification of IgG under mild acidic conditions. <i>Journal of Biological Engineering</i> , 2014, 8, 15.	4.7	21

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37	Imparting Albumin-Binding Affinity to a Human Protein by Mimicking the Contact Surface of a Bacterial Binding Protein. <i>ACS Chemical Biology</i> , 2014, 9, 1052-1060.	3.4	2
38	Structure-based histidine substitution for optimizing pH-sensitive Staphylococcus protein A. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2013, 929, 155-160.	2.3	17
39	Artificial Conversion of the Mating-Type of <i>Saccharomyces cerevisiae</i> without Autopolyploidization. <i>ACS Synthetic Biology</i> , 2013, 2, 697-704.	3.8	12
40	Construction of new cloning vectors that employ the phytoene synthase encoding gene for color screening of cloned DNA inserts in <i>Thermus thermophilus</i> . <i>Gene</i> , 2013, 527, 655-662.	2.2	12
41	Directed Evolution for Thermostabilization of a Hygromycin B Phosphotransferase from <i>Streptomyces hygrosopicus</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2234-2241.	1.3	10
42	Development of growth selection systems to isolate a-type or Δ -type of yeast cells spontaneously emerging from MATa/ Δ diploids. <i>Journal of Biological Engineering</i> , 2013, 7, 27.	4.7	11
43	Yeast One-Hybrid $G\beta^3$ Recruitment System for Identification of Protein Lipidation Motifs. <i>PLoS ONE</i> , 2013, 8, e70100.	2.5	5
44	Convergent evolution in structural elements of proteins investigated using cross profile analysis. <i>BMC Bioinformatics</i> , 2012, 13, 11.	2.6	33
45	Aggregation factor analysis for protein formulation by a systematic approach using FTIR, SEC and design of experiments techniques. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2012, 57, 143-152.	2.8	9
46	Thermostability of <i>Rhodospseudomonas viridis</i> and <i>Rhodospirillum rubrum</i> chromatophores reflecting physiological conditions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 1645-1653.	2.6	9
47	Improved isolation and purification of functional human Fas receptor extracellular domain using baculovirus α silkworm expression system. <i>Protein Expression and Purification</i> , 2011, 80, 102-109.	1.3	5
48	Conserved amino acid residues in C-terminus of PERIOD 2 are involved in interaction with CRYPTOCHROME 1. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2010, 1803, 492-498.	4.1	10
49	Efficient production of human Fas receptor extracellular domain α human IgG1 heavy chain Fc domain fusion protein using baculovirus/silkworm expression system. <i>Protein Expression and Purification</i> , 2010, 73, 209-216.	1.3	11
50	Optimizing pH Response of Affinity between Protein G and IgG Fc. <i>Journal of Biological Chemistry</i> , 2009, 284, 12373-12383.	3.4	44
51	ProSeg: a database of local structures of protein segments. <i>Journal of Computer-Aided Molecular Design</i> , 2009, 23, 163-169.	2.9	2
52	Crystal Structure of a Ten-Amino Acid Protein. <i>Journal of the American Chemical Society</i> , 2008, 130, 15327-15331.	18.7	151
53	Free Energy Landscape Analysis System Based on Parallel Molecular Dynamics Simulation. <i>IPSIJ Digital Courier</i> , 2007, 3, 757-766.	0.3	0
54	Structural Diversity of Protein Segments Follows a Power-Law Distribution. <i>Biophysical Journal</i> , 2006, 91, 1213-1223.	0.5	18

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55	Higher-order Molecular Packing in Amyloid-like Fibrils Constructed with Linear Arrangements of Hydrophobic and Hydrogen-bonding Side-chains. <i>Journal of Molecular Biology</i> , 2005, 348, 983-998.	4.2	55
56	10 Residue Folded Peptide Designed by Segment Statistics. <i>Structure</i> , 2004, 12, 1507-1518.	3.3	278
57	Thermodynamics of a β^2 -hairpin structure: evidence for cooperative formation of folding nucleus. <i>Journal of Molecular Biology</i> , 2000, 295, 269-278.	4.2	163
58	Role of Side-chains in the Cooperative β^2 -Hairpin Folding of the Short C-terminal Fragment Derived from Streptococcal Protein G. <i>Biochemistry</i> , 2000, 39, 6564-6571.	2.5	97
59	Fragment Reconstitution of a Small Protein: A Disulfide Mutant of a Short C-Terminal Fragment Derived from Streptococcal Protein G. <i>Biochemistry</i> , 1999, 38, 3228-3234.	2.5	21
60	Fragment Reconstitution of a Small Protein: Folding Energetics of the Reconstituted Immunoglobulin Binding Domain B1 of Streptococcal Protein G. <i>Biochemistry</i> , 1999, 38, 1203-1213.	2.5	49
61	Folding energetics of a multidomain protein, flagellin 1. Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 293, 719-732.	4.2	17
62	Stability and Reversibility of Thermal Denaturation Are Greatly Improved by Limiting Terminal Flexibility of Escherichia coli Dihydrofolate Reductase. <i>Journal of Biochemistry</i> , 1996, 119, 414-420.	1.7	22
63	Thermal denaturation of photosynthetic membrane proteins from Rhodospirillum rubrum. <i>Thermochimica Acta</i> , 1995, 266, 355-364.	2.7	11
64	Complement assembly of two fragments of the streptococcal protein G B1 domain in aqueous solution. <i>FEBS Letters</i> , 1995, 366, 99-103.	2.8	57
65	β -Helical assembly of biologically active peptides and designed helix bundle protein. <i>Biopolymers</i> , 1994, 34, 481-488.	2.4	13
66	Fluctuation and rotation of human growth hormone-releasing factor in the presence and the absence of phospholipid bilayer analyzed by time-resolved fluorescence depolarization. <i>Biochimica et Biophysica Acta - Biomembranes</i> , 1991, 1068, 81-86.	2.6	2
67	Design for the Peptide Analog of Calcium Binding Loops by Considering the Steric Restriction Effect of Incorporated Nonprotein Amino Acids. <i>Chemistry Letters</i> , 1991, 20, 757-760.	1.3	0
68	Association Characteristics of Amphiphilic β -Helices Connected by Flexible Links. <i>Bulletin of the Chemical Society of Japan</i> , 1991, 64, 396-402.	3.2	15
69	Role of Negative Charge on Acidic Lipids in the Interaction with Human Growth Hormone-Releasing Factor. <i>Chemistry Letters</i> , 1991, 20, 73-76.	1.3	2
70	Solution structure of human growth hormone-releasing factor fragment (1-29) by CD: Characteristic conformational change on phospholipid membrane. <i>Biopolymers</i> , 1991, 31, 869-876.	2.4	16
71	Thermal transition of a mutated dihydrofolate reductase. <i>Thermochimica Acta</i> , 1990, 163, 123-128.	2.7	5
72	Thermal Stability of Dihydrofolate Reductase and Its Fused Proteins with Oligopeptides. <i>Annals of the New York Academy of Sciences</i> , 1990, 613, 352-357.	3.8	5

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73	Fibrous Support Module Composed of Braided Poly(Vinyl Alcohol) Superfine Fibers. <i>Annals of the New York Academy of Sciences</i> , 1990, 613, 858-862.	3.8	1
74	The β -Sheet Structure-Disrupting Potential of Electron-Donor and -Acceptor Solvents and Role of Mixed Solvents in Solvation of Peptides. <i>Bulletin of the Chemical Society of Japan</i> , 1989, 62, 342-344.	3.2	24
75	Individuality of Amino Acid Residues in Protected Peptides. Conformational and β -Sheet Structure-Disrupted Behaviors of Resin-Bound Peptides. <i>Bulletin of the Chemical Society of Japan</i> , 1989, 62, 773-779.	3.2	21
76	The Electron Donor–Acceptor Interaction between Mixed Solvents and Its Influence on Their β -Sheet Structure-Disrupting Potential. <i>Bulletin of the Chemical Society of Japan</i> , 1989, 62, 780-785.	3.2	20
77	Infrared Spectroscopic Conformational Analysis of Polystyrene Resin-Bound Human Proinsulin C-Peptide Fragments. β -Sheet Aggregation of Peptide Chains during Solid-Phase Peptide Synthesis. <i>Bulletin of the Chemical Society of Japan</i> , 1988, 61, 1201-1206.	3.2	13
78	The Solubility of Peptide Intermediates in Organic Solvents. Solubilizing Potential of Hexafluoro-2-propanol. <i>Bulletin of the Chemical Society of Japan</i> , 1988, 61, 281-284.	3.2	53
79	The Study on Peptide and Protein Syntheses. Infrared Spectroscopic Conformational Analysis of Oligo-L-leucines Containing Only One D-Amino Acid Residue. <i>Bulletin of the Chemical Society of Japan</i> , 1987, 60, 4127-4131.	3.2	10
80	Design of the Synthetic Route for Peptides and Proteins Based on the Solubility Prediction Method. I. Synthesis and Solubility Properties of Human Proinsulin C-Peptide Fragments. <i>Bulletin of the Chemical Society of Japan</i> , 1986, 59, 2433-2438.	3.2	28
81	Infrared Absorption Study of Human Proinsulin C-Peptide Fragments in the Solid State. <i>Bulletin of the Chemical Society of Japan</i> , 1986, 59, 2439-2443.	3.2	19
82	Infrared Absorption Study of Human Proinsulin C-Peptide Fragments in Dichloromethane. <i>Bulletin of the Chemical Society of Japan</i> , 1986, 59, 2445-2449.	3.2	20