

Kouhei Tsumoto

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1265650/publications.pdf>

Version: 2024-02-01

206
papers

5,726
citations

94269

37
h-index

102304

66
g-index

220
all docs

220
docs citations

220
times ranked

7263
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of Arginine in Protein Refolding, Solubilization, and Purification. <i>Biotechnology Progress</i> , 2004, 20, 1301-1308.	1.3	378
2	Practical considerations in refolding proteins from inclusion bodies. <i>Protein Expression and Purification</i> , 2003, 28, 1-8.	0.6	366
3	Fucose Depletion from Human IgG1 Oligosaccharide Enhances Binding Enthalpy and Association Rate Between IgG1 and Fc γ 3RIIIa. <i>Journal of Molecular Biology</i> , 2004, 336, 1239-1249.	2.0	330
4	Highly efficient recovery of functional single-chain Fv fragments from inclusion bodies overexpressed in <i>Escherichia coli</i> by controlled introduction of oxidizing reagent—application to a human single-chain Fv fragment. <i>Journal of Immunological Methods</i> , 1998, 219, 119-129.	0.6	190
5	Structural basis for self-assembly of a cytolytic pore lined by protein and lipid. <i>Nature Communications</i> , 2015, 6, 6337.	5.8	185
6	Effects of acid exposure on the conformation, stability, and aggregation of monoclonal antibodies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 954-962.	1.5	176
7	Next Generation Drying Technologies for Pharmaceutical Applications. <i>Journal of Pharmaceutical Sciences</i> , 2014, 103, 2673-2695.	1.6	162
8	Open sandwich ELISA: A novel immunoassay based on the interchain interaction of antibody variable region. <i>Nature Biotechnology</i> , 1996, 14, 1714-1718.	9.4	159
9	Arginine as an effective additive in gel permeation chromatography. <i>Journal of Chromatography A</i> , 2005, 1094, 49-55.	1.8	138
10	Solubilization of active green fluorescent protein from insoluble particles by guanidine and arginine. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 1383-1386.	1.0	134
11	Structural basis for binding of human IgG1 to its high-affinity human receptor Fc γ 3RI. <i>Nature Communications</i> , 2015, 6, 6866.	5.8	109
12	Effects of salts on protein—surface interactions: applications for column chromatography. <i>Journal of Pharmaceutical Sciences</i> , 2007, 96, 1677-1690.	1.6	95
13	Heme Degradation by <i>Staphylococcus aureus</i> IsdG and IsdI Liberates Formaldehyde Rather Than Carbon Monoxide. <i>Biochemistry</i> , 2013, 52, 3025-3027.	1.2	79
14	Affinity Improvement of a Therapeutic Antibody by Structure-Based Computational Design: Generation of Electrostatic Interactions in the Transition State Stabilizes the Antibody-Antigen Complex. <i>PLoS ONE</i> , 2014, 9, e87099.	1.1	78
15	Structural Basis for Multimeric Heme Complexation through a Specific Protein-Heme Interaction. <i>Journal of Biological Chemistry</i> , 2008, 283, 28649-28659.	1.6	75
16	A secondary RET mutation in the activation loop conferring resistance to vandetanib. <i>Nature Communications</i> , 2018, 9, 625.	5.8	75
17	Structural analysis of Fc/Fc γ 3R complexes: a blueprint for antibody design. <i>Immunological Reviews</i> , 2015, 268, 201-221.	2.8	68
18	Dual-Sensitive Nanomicelles Enhancing Systemic Delivery of Therapeutically Active Antibodies Specifically into the Brain. <i>ACS Nano</i> , 2020, 14, 6729-6742.	7.3	65

#	ARTICLE	IF	CITATIONS
19	Structural basis for amino acid export by DMT superfamily transporter YddG. <i>Nature</i> , 2016, 534, 417-420.	13.7	60
20	Glycosylation of IgG-Fc: a molecular perspective. <i>International Immunology</i> , 2017, 29, 311-317.	1.8	57
21	Structures of the prefusion form of measles virus fusion protein in complex with inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2496-2501.	3.3	56
22	Catalytic activity of MsbA reconstituted in nanodisc particles is modulated by remote interactions with the bilayer. <i>FEBS Letters</i> , 2011, 585, 3533-3537.	1.3	54
23	Through-bond effects in the ternary complexes of thrombin sandwiched by two DNA aptamers. <i>Nucleic Acids Research</i> , 2017, 45, 461-469.	6.5	53
24	Signal peptide design for improving recombinant protein secretion in the baculovirus expression vector system. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 931-935.	1.0	51
25	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. <i>Nature Plants</i> , 2017, 3, 825-832.	4.7	51
26	Effects of subclass change on the structural stability of chimeric, humanized, and human antibodies under thermal stress. <i>Protein Science</i> , 2013, 22, 1542-1551.	3.1	50
27	Arginine improves protein elution in hydrophobic interaction chromatography. <i>Journal of Chromatography A</i> , 2007, 1154, 81-86.	1.8	49
28	Assessing the Heterogeneity of the Fc-Glycan of a Therapeutic Antibody Using an engineered Fcγ3 Receptor IIIa-Immobilized Column. <i>Scientific Reports</i> , 2018, 8, 3955.	1.6	48
29	Bidirectional binding property of high glycine-tyrosine keratin-associated protein contributes to the mechanical strength and shape of hair. <i>Journal of Structural Biology</i> , 2013, 183, 484-494.	1.3	46
30	Expression of a model peptide of a marine mussel adhesive protein in <i>Escherichia coli</i> and characterization of its structural and functional properties. <i>Journal of Polymer Science Part A</i> , 1999, 37, 729-736.	2.5	45
31	Molecular Basis of Recognition of Antibacterial Porphyrins by Heme-Transporter IsdH-NEAT3 of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2011, 50, 7311-7320.	1.2	44
32	Mutations for decreasing the immunogenicity and maintaining the function of core streptavidin. <i>Protein Science</i> , 2013, 22, 213-221.	3.1	44
33	Mapping Ultra-weak Protein-Protein Interactions between Heme Transporters of <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 16477-16487.	1.6	43
34	Osteomodulin regulates diameter and alters shape of collagen fibrils. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 292-296.	1.0	43
35	Analysis of Pore Formation and Protein Translocation Using Large Biological Nanopores. <i>Analytical Chemistry</i> , 2017, 89, 11269-11277.	3.2	43
36	Protective effect of the long pentraxin PTX3 against histone-mediated endothelial cell cytotoxicity in sepsis. <i>Science Signaling</i> , 2014, 7, ra88.	1.6	42

#	ARTICLE	IF	CITATIONS
37	Thermodynamics of antibody-antigen interaction revealed by mutation analysis of antibody variable regions. <i>Journal of Biochemistry</i> , 2015, 158, 1-13.	0.9	40
38	Repertoire Analysis of Antibody CDR-H3 Loops Suggests Affinity Maturation Does Not Typically Result in Rigidification. <i>Frontiers in Immunology</i> , 2018, 9, 413.	2.2	39
39	Engineering Stability, Viscosity, and Immunogenicity of Antibodies by Computational Design. <i>Journal of Pharmaceutical Sciences</i> , 2020, 109, 1631-1651.	1.6	38
40	Peptide-dependent Conformational Fluctuation Determines the Stability of the Human Leukocyte Antigen Class I Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 24680-24690.	1.6	37
41	The Atomic Structure of the HIV-1 gp41 Transmembrane Domain and Its Connection to the Immunogenic Membrane-proximal External Region. <i>Journal of Biological Chemistry</i> , 2015, 290, 12999-13015.	1.6	37
42	Structural and thermodynamic basis for the recognition of the substrate-binding cleft on hen egg lysozyme by a single-domain antibody. <i>Scientific Reports</i> , 2019, 9, 15481.	1.6	36
43	A Stable Phage-Display System Using a Phagemid Vector: Phage Display of Hen Egg-White Lysozyme (HEL), <i>Escherichia coli</i> Alkaline Phosphatase, and Anti-HEL Monoclonal Antibody, HyHEL10. <i>Biochemical and Biophysical Research Communications</i> , 1996, 218, 682-687.	1.0	35
44	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. <i>MAbs</i> , 2022, 14, 2020082.	2.6	35
45	Structural basis for broad neutralization of HIV-1 through the molecular recognition of 10E8 helical epitope at the membrane interface. <i>Scientific Reports</i> , 2016, 6, 38177.	1.6	34
46	Polymeric Nanocarriers with Controlled Chain Flexibility Boost mRNA Delivery In Vivo through Enhanced Structural Fastening. <i>Advanced Healthcare Materials</i> , 2020, 9, e2000538.	3.9	33
47	A Pore-Forming Toxin Requires a Specific Residue for Its Activity in Membranes with Particular Physicochemical Properties. <i>Journal of Biological Chemistry</i> , 2015, 290, 10850-10861.	1.6	31
48	A Peptoid with Extended Shape in Water. <i>Journal of the American Chemical Society</i> , 2019, 141, 14612-14623.	6.6	31
49	Exploring designability of electrostatic complementarity at an antigen-antibody interface directed by mutagenesis, biophysical analysis, and molecular dynamics simulations. <i>Scientific Reports</i> , 2019, 9, 4482.	1.6	31
50	Design strategy for serine hydroxymethyltransferase probes based on retro-aldol-type reaction. <i>Nature Communications</i> , 2019, 10, 876.	5.8	31
51	Affinity Improvement of a Cancer-Targeted Antibody through Alanine-Induced Adjustment of Antigen-Antibody Interface. <i>Structure</i> , 2019, 27, 519-527.e5.	1.6	31
52	Tumor-directed lymphocyte-activating cytokines: refolding-based preparation of recombinant human interleukin-12 and an antibody variable domain-fused protein by additive-introduced stepwise dialysis. <i>Biochemical and Biophysical Research Communications</i> , 2005, 328, 98-105.	1.0	29
53	Phospholipid Membrane Fluidity Alters Ligand Binding Activity of a G Protein-Coupled Receptor by Shifting the Conformational Equilibrium. <i>Biochemistry</i> , 2019, 58, 504-508.	1.2	29
54	Discovery and Optimization of Inhibitors of the Parkinson's Disease Associated Protein DJ-1. <i>ACS Chemical Biology</i> , 2018, 13, 2783-2793.	1.6	27

#	ARTICLE	IF	CITATIONS
55	Improving the affinity of an antibody for its antigen via long-range electrostatic interactions. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 773-780.	1.0	26
56	Differential Effect of Membrane Composition on the Pore-Forming Ability of Four Different Sea Anemone Actinoporins. <i>Biochemistry</i> , 2016, 55, 6630-6641.	1.2	26
57	Polymeric SpyCatcher Scaffold Enables Bioconjugation in a Ratio-Controllable Manner. <i>Biotechnology Journal</i> , 2017, 12, 1700195.	1.8	26
58	Immobilized oxidoreductase as an additive for refolding inclusion bodies: application to antibody fragments. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 535-541.	1.0	25
59	Dynamic elements govern the catalytic activity of CapE, a capsular polysaccharide-synthesizing enzyme from <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2013, 587, 3824-3830.	1.3	24
60	Identification of key modules and hub genes for small-cell lung carcinoma and large-cell neuroendocrine lung carcinoma by weighted gene co-expression network analysis of clinical tissue-proteomes. <i>PLoS ONE</i> , 2019, 14, e0217105.	1.1	24
61	Assessment of the Protein-Protein Interactions in a Highly Concentrated Antibody Solution by Using Raman Spectroscopy. <i>Pharmaceutical Research</i> , 2016, 33, 956-969.	1.7	23
62	Identification of a Membrane-bound Prepore Species Clarifies the Lytic Mechanism of Actinoporins. <i>Journal of Biological Chemistry</i> , 2016, 291, 19210-19219.	1.6	23
63	Discovery and characterization of natural tropolones as inhibitors of the antibacterial target CapF from <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2015, 5, 15337.	1.6	22
64	Structural and Thermodynamic Basis of Epitope Binding by Neutralizing and Nonneutralizing Forms of the Anti-HIV-1 Antibody 4E10. <i>Journal of Virology</i> , 2015, 89, 11975-11989.	1.5	22
65	A glutamine sensor that directly activates TORC1. <i>Communications Biology</i> , 2021, 4, 1093.	2.0	22
66	Use of SpyTag/SpyCatcher to construct bispecific antibodies that target two epitopes of a single antigen. <i>Journal of Biochemistry</i> , 2017, 162, 203-210.	0.9	21
67	Selective binding of antimicrobial porphyrins to the heme-receptor IsdH-NEAT3 of <i>Staphylococcus aureus</i> . <i>Protein Science</i> , 2013, 22, 942-953.	3.1	20
68	Functional characterization of Val60, a key residue involved in the membrane-oligomerization of fragaceatoxin C, an actinoporin from <i>Actinia fragacea</i> . <i>FEBS Letters</i> , 2015, 589, 1840-1846.	1.3	20
69	Adhesive Dimerization of Human P-Cadherin Catalyzed by a Chaperone-like Mechanism. <i>Structure</i> , 2016, 24, 1523-1536.	1.6	20
70	Contributions of Interfacial Residues of Human Interleukin15 to the Specificity and Affinity for Its Private β -Receptor. <i>Journal of Molecular Biology</i> , 2009, 389, 880-894.	2.0	19
71	Heme Binding Mechanism of Structurally Similar Iron-Regulated Surface Determinant Near Transporter Domains of <i>Staphylococcus aureus</i> Exhibiting Different Affinities for Heme. <i>Biochemistry</i> , 2013, 52, 8866-8877.	1.2	19
72	Antibody Affinity Maturation by Computational Design. <i>Methods in Molecular Biology</i> , 2018, 1827, 15-34.	0.4	19

#	ARTICLE	IF	CITATIONS
73	Folding-unfolding of goat γ -lactalbumin studied by stopped-flow circular dichroism and molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 49-65.	1.5	18
74	Incorporation of Rapid Thermodynamic Data in Fragment-Based Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 2155-2159.	2.9	18
75	The staphylococcal elastin-binding protein regulates zinc-dependent growth/biofilm formation. <i>Journal of Biochemistry</i> , 2014, 156, 155-162.	0.9	18
76	Quantitative phosphoproteomics-based molecular network description for high-resolution kinase-substrate interactome analysis. <i>Bioinformatics</i> , 2016, 32, 2083-2088.	1.8	18
77	Disruption of cell adhesion by an antibody targeting the cell-adhesive intermediate (X-dimer) of human P-cadherin. <i>Scientific Reports</i> , 2017, 7, 39518.	1.6	18
78	Molecular basis for governing the morphology of type-I collagen fibrils by Osteomodulin. <i>Communications Biology</i> , 2018, 1, 33.	2.0	18
79	Identification and Characterization of the X-Dimer of Human P-Cadherin: Implications for Homophilic Cell Adhesion. <i>Biochemistry</i> , 2014, 53, 1742-1752.	1.2	17
80	Alternative downstream processes for production of antibodies and antibody fragments. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 2032-2040.	1.1	17
81	Critical Contribution of Aromatic Rings to Specific Recognition of Polyether Rings. <i>Journal of Biological Chemistry</i> , 2008, 283, 12259-12266.	1.6	16
82	Crystal structure of the capsular polysaccharide synthesizing protein CapE of <i>Staphylococcus aureus</i> . <i>Bioscience Reports</i> , 2013, 33, .	1.1	16
83	Efficacy of ribavirin against malignant glioma cell lines. <i>Oncology Letters</i> , 2014, 8, 2469-2474.	0.8	16
84	Click Conjugation of a Binuclear Terbium(III) Complex for Real-Time Detection of Tyrosine Phosphorylation. <i>Analytical Chemistry</i> , 2015, 87, 3834-3840.	3.2	16
85	Integrative Network Analysis Combined with Quantitative Phosphoproteomics Reveals Transforming Growth Factor-beta Receptor type-2 (TGFBR2) as a Novel Regulator of Glioblastoma Stem Cell Properties. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1017-1031.	2.5	16
86	Improvement of antibody affinity by introduction of basic amino acid residues into the framework region. <i>Biochemistry and Biophysics Reports</i> , 2018, 15, 81-85.	0.7	16
87	Generation and characterization of antagonistic anti-human interleukin (IL)-18 monoclonal antibodies with high affinity: Two types of monoclonal antibodies against full-length IL-18 and the neoepitope of inflammatory caspase-cleaved active IL-18. <i>Archives of Biochemistry and Biophysics</i> , 2019, 663, 71-82.	1.4	16
88	Replacing factor-dependency with that for lysozyme: Affordable culture of IL-6-dependent hybridoma by transfecting artificial cell surface receptor. <i>Biotechnology and Bioengineering</i> , 2001, 74, 416-423.	1.7	15
89	Bidirectional Transformation of a Metamorphic Protein between the Water-Soluble and Transmembrane Native States. <i>Biochemistry</i> , 2015, 54, 6863-6866.	1.2	15
90	Crystal structure of streptavidin mutant with low immunogenicity. <i>Journal of Bioscience and Bioengineering</i> , 2015, 119, 642-647.	1.1	15

#	ARTICLE	IF	CITATIONS
91	Elucidation of potential sites for antibody engineering by fluctuation editing. <i>Scientific Reports</i> , 2017, 7, 9597.	1.6	15
92	PRDM14 directly interacts with heat shock proteins HSP90 α and glucose-regulated protein 78. <i>Cancer Science</i> , 2018, 109, 373-383.	1.7	15
93	Thermodynamic and computational analyses reveal the functional roles of the galloyl group of tea catechins in molecular recognition. <i>PLoS ONE</i> , 2018, 13, e0204856.	1.1	15
94	Functional Contacts between MPER and the Anti-HIV-1 Broadly Neutralizing Antibody 4E10 Extend into the Core of the Membrane. <i>Journal of Molecular Biology</i> , 2017, 429, 1213-1226.	2.0	14
95	The Isolation of New Pore-Forming Toxins from the Sea Anemone <i>Actinia fragacea</i> Provides Insights into the Mechanisms of Actinoporin Evolution. <i>Toxins</i> , 2019, 11, 401.	1.5	14
96	Tyrosine Sulfation Restricts the Conformational Ensemble of a Flexible Peptide, Strengthening the Binding Affinity for an Antibody. <i>Biochemistry</i> , 2018, 57, 4177-4185.	1.2	13
97	Structural Basis for the Binding Mechanism of Human Serum Albumin Complexed with Cyclic Peptide Dalbavancin. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 14045-14053.	2.9	13
98	Generation of biparatopic antibody through two-step targeting of fragment antibodies on antigen using SpyTag and SpyCatcher. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2020, 25, e00418.	2.1	13
99	Non-core Region Modulates Interleukin-11 Signaling Activity. <i>Journal of Biological Chemistry</i> , 2011, 286, 8085-8093.	1.6	12
100	Crystal structure of the enzyme CapF of <i>Staphylococcus aureus</i> reveals a unique architecture composed of two functional domains. <i>Biochemical Journal</i> , 2012, 443, 671-680.	1.7	12
101	Intramolecular H-bonds govern the recognition of a flexible peptide by an antibody. <i>Journal of Biochemistry</i> , 2018, 164, 65-76.	0.9	12
102	Per-Residue Program of Multiple Backbone Dihedral Angles of β^2 -Peptoids via Backbone Substitutions. <i>Journal of the American Chemical Society</i> , 2020, 142, 2277-2284.	6.6	12
103	The transcriptional corepressor CtBP2 serves as a metabolite sensor orchestrating hepatic glucose and lipid homeostasis. <i>Nature Communications</i> , 2021, 12, 6315.	5.8	12
104	Contribution of Thr29 to the thermodynamic stability of goat γ -lactalbumin as determined by experimental and theoretical approaches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 16-29.	1.5	11
105	Epiregulin Recognition Mechanisms by Anti-epiregulin Antibody 9E5. <i>Journal of Biological Chemistry</i> , 2016, 291, 2319-2330.	1.6	11
106	Discovery of chemical probes that suppress Wnt/ β -catenin signaling through high-throughput screening. <i>Cancer Science</i> , 2020, 111, 783-794.	1.7	11
107	Peptoid-based reprogrammable template for cell-permeable inhibitors of protein-protein interactions. <i>Chemical Science</i> , 2021, 12, 13292-13300.	3.7	11
108	A new twist of rubredoxin function in <i>M. tuberculosis</i> . <i>Bioorganic Chemistry</i> , 2021, 109, 104721.	2.0	11

#	ARTICLE	IF	CITATIONS
109	Delicate balance among thermal stability, binding affinity, and conformational space explored by single-domain VHH antibodies. <i>Scientific Reports</i> , 2021, 11, 20624.	1.6	11
110	Rapid Heme Transfer Reactions between NEAr Transporter Domains of <i>Staphylococcus aureus</i> : A Theoretical Study Using QM/MM and MD Simulations. <i>PLoS ONE</i> , 2015, 10, e0145125.	1.1	10
111	Thermodynamic Dissection of Potency and Selectivity of Cytosolic Hsp90 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 2669-2677.	2.9	10
112	Stepwise Characterization of the Thermodynamics of Trichocyte Intermediate Filament Protein Supramolecular Assembly. <i>Journal of Molecular Biology</i> , 2011, 408, 832-838.	2.0	9
113	Structural and thermodynamic characterization of the self-adhesive properties of human P-cadherin. <i>Molecular BioSystems</i> , 2012, 8, 2050.	2.9	9
114	Differential binding of prohibitin-2 to estrogen receptor $\hat{1}\pm$ and to drug-resistant ER $\hat{1}\pm$ mutants. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 726-731.	1.0	9
115	Peripheral Membrane Interactions Boost the Engagement by an Anti-HIV-1 Broadly Neutralizing Antibody. <i>Journal of Biological Chemistry</i> , 2017, 292, 5571-5583.	1.6	9
116	Haemolytic actinoporins interact with carbohydrates using their lipid-binding module. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160216.	1.8	9
117	Modified AMBER force-field (FUJI) parameters for sulfated and phosphorylated tyrosine residues: Development and application to CCR5-derived peptide systems. <i>AIP Conference Proceedings</i> , 2019, , .	0.3	9
118	^{111}In -labeled anti-cadherin17 antibody D2101 has potential as a noninvasive imaging probe for diagnosing gastric cancer and lymph-node metastasis. <i>Annals of Nuclear Medicine</i> , 2020, 34, 13-23.	1.2	9
119	Proteomic identification and validation of novel interactions of the putative tumor suppressor PRELP with membrane proteins including IGF1-R and p75NTR. <i>Journal of Biological Chemistry</i> , 2021, 296, 100278.	1.6	9
120	A DNA Aptamer That Inhibits the Aberrant Signaling of Fibroblast Growth Factor Receptor in Cancer Cells. <i>Jacs Au</i> , 2021, 1, 578-585.	3.6	9
121	Step-Wise Refolding of Recombinant Proteins. <i>Current Pharmaceutical Biotechnology</i> , 2010, 11, 285-288.	0.9	9
122	Structural and thermodynamical insights into the binding and inhibition of FIH-1 by the N-terminal disordered region of Mint3. <i>Journal of Biological Chemistry</i> , 2021, 297, 101304.	1.6	9
123	Inhibition of hepatitis C virus NS3 protease by peptides derived from complementarity-determining regions (CDRs) of the monoclonal antibody 8D4: tolerance of a CDR peptide to conformational changes of a target. <i>FEBS Letters</i> , 2002, 525, 77-82.	1.3	8
124	The carboxyl-terminal region of Dok-7 plays a key, but not essential, role in activation of muscle-specific receptor kinase MuSK and neuromuscular synapse formation. <i>Journal of Biochemistry</i> , 2017, 161, mvw073.	0.9	8
125	A combination of ^{19}F NMR and surface plasmon resonance for site-specific hit selection and validation of fragment molecules that bind to the ATP-binding site of a kinase. <i>Bioorganic and Medicinal Chemistry</i> , 2018, 26, 1929-1938.	1.4	8
126	Apoptotic Cell-Inspired Polymeric Particles for Controlling Microglial Inflammation toward Neurodegenerative Disease Treatment. <i>ACS Biomaterials Science and Engineering</i> , 2019, 5, 5705-5713.	2.6	8

#	ARTICLE	IF	CITATIONS
127	Computer-guided library generation applied to the optimization of single-domain antibodies. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 423-431.	1.0	8
128	System-Wide Analysis of Protein Acetylation and Ubiquitination Reveals a Diversified Regulation in Human Cancer Cells. <i>Biomolecules</i> , 2020, 10, 411.	1.8	8
129	Heme controls the structural rearrangement of its sensor protein mediating the hemolytic bacterial survival. <i>Communications Biology</i> , 2021, 4, 467.	2.0	8
130	Structure-based screening combined with computational and biochemical analyses identified the inhibitor targeting the binding of DNA Ligase 1 to UHRF1. <i>Bioorganic and Medicinal Chemistry</i> , 2021, 52, 116500.	1.4	8
131	B cell intrinsic TBK1 is essential for germinal center formation during infection and vaccination in mice. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	8
132	Experimental Comparison of Bond Lifetime and Viscoelastic Relaxation in Transient Networks with Well-Controlled Structures. <i>ACS Macro Letters</i> , 2022, 11, 753-759.	2.3	8
133	Functional Fv fragment of an antibody specific for CD28: Fv-mediated co-stimulation of T cells. <i>FEBS Letters</i> , 2000, 476, 266-271.	1.3	7
134	How the protonation state of a phosphorylated amino acid governs molecular recognition: insights from classical molecular dynamics simulations. <i>FEBS Letters</i> , 2020, 594, 903-912.	1.3	7
135	Structure-based design and discovery of novel anti-tissue factor antibodies with cooperative double-point mutations, using interaction analysis. <i>Scientific Reports</i> , 2020, 10, 17590.	1.6	7
136	Anti-EGFR antibody 528 binds to domain III of EGFR at a site shifted from the cetuximab epitope. <i>Scientific Reports</i> , 2021, 11, 5790.	1.6	7
137	A Novel Cell-Based Intracellular Protein-Protein Interaction Detection Platform (SOLIS) for Multimodality Screening. <i>ACS Synthetic Biology</i> , 2021, 10, 990-999.	1.9	7
138	Development of an Outward Proton Pumping Rhodopsin with a New Record in Thermostability by Means of Amino Acid Mutations. <i>Journal of Physical Chemistry B</i> , 2022, 126, 1004-1015.	1.2	7
139	Differential Effects of IFN- γ on the Survival and Growth of Human Vascular Smooth Muscle and Endothelial Cells. <i>BioResearch Open Access</i> , 2015, 4, 1-15.	2.6	6
140	Structural basis for binding and transfer of heme in bacterial heme-acquisition systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2217-2230.	1.5	6
141	Synergistic Cytotoxic Effect on Gastric Cancer Cells of an Immunotoxin Cocktail in Which Antibodies Recognize Different Epitopes on CDH17. <i>Monoclonal Antibodies in Immunodiagnosis and Immunotherapy</i> , 2018, 37, 1-11.	0.8	6
142	Inhibition of homophilic dimerization and disruption of cell adhesion by P-cadherin-specific small molecules from SPR-based assays. <i>Chemical Communications</i> , 2018, 54, 5350-5353.	2.2	6
143	Long-Term Stability and Reversible Thermal Unfolding of Antibody Structure at Low pH: Case Study. <i>Journal of Pharmaceutical Sciences</i> , 2018, 107, 2965-2967.	1.6	6
144	Roles of the disulfide bond between the variable and the constant domains of rabbit immunoglobulin kappa chains in thermal stability and affinity. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 243-247.	1.0	6

#	ARTICLE	IF	CITATIONS
145	Control of Protein Adsorption to Cyclo Olefin Polymer by the Hofmeister Effect. <i>Journal of Pharmaceutical Sciences</i> , 2019, 108, 1686-1691.	1.6	6
146	An epitope-directed antibody affinity maturation system utilizing mammalian cell survival as readout. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1742-1751.	1.7	6
147	Structural basis for antigen recognition by methylated lysine-specific antibodies. <i>Journal of Biological Chemistry</i> , 2021, 296, 100176.	1.6	6
148	Elaboration of non-naturally occurring helical tripeptides as p53-MDM2/MDMX interaction inhibitors. <i>Chemical and Pharmaceutical Bulletin</i> , 2021, 69, 681-692.	0.6	6
149	Biophysical characterization of the interaction between heme and proteins responsible for heme transfer in <i>Streptococcus pyogenes</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 1109-1114.	1.0	5
150	Characterization of glycoengineered anti-HER2 monoclonal antibodies produced by using a silkworm baculovirus expression system. <i>Journal of Biochemistry</i> , 2018, 163, 481-488.	0.9	5
151	Unique Electronic Structures of the Highly Ruffled Hemes in Heme-Degrading Enzymes of <i>Staphylococcus aureus</i> , IsdG and IsdI, by Resonance Raman and Electron Paramagnetic Resonance Spectroscopies. <i>Biochemistry</i> , 2020, 59, 3918-3928.	1.2	5
152	Highly sensitive HPLC analysis and biophysical characterization of N-glycans of IgG ₁ domain in comparison between CHO and 293 cells using Fc ³ R1IIa ligand. <i>Biotechnology Progress</i> , 2020, 36, e3016.	1.3	5
153	Methodology for Further Thermostabilization of an Intrinsically Thermostable Membrane Protein Using Amino Acid Mutations with Its Original Function Being Retained. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1709-1716.	2.5	5
154	Addition of arginine hydrochloride and proline to the culture medium enhances recombinant protein expression in <i>Brevibacillus choshinensis</i> : The case of RBD of SARS-CoV-2 spike protein and its antibody. <i>Protein Expression and Purification</i> , 2022, 194, 106075.	0.6	5
155	Expression, purification, crystallization and preliminary diffraction analysis of CapF, a capsular polysaccharide-synthesis enzyme from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 512-515.	0.7	4
156	Manipulation of protein-complex function by using an engineered heterotrimeric coiled-coil switch. <i>Organic and Biomolecular Chemistry</i> , 2009, 7, 3102.	1.5	4
157	Thermodynamic analyses of amino acid residues at the interface of an antibody B2212A and its antigen roundabout homolog 1. <i>Journal of Biochemistry</i> , 2017, 162, 255-258.	0.9	4
158	Production and characterization of genetically modified human IL-11 variants. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 205-217.	1.1	4
159	Effects of a remote mutation from the contact paratope on the structure of CDR-H3 in the anti-HIV neutralizing antibody PG16. <i>Scientific Reports</i> , 2019, 9, 19840.	1.6	4
160	Technical Capabilities and Limitations of Optical Spectroscopy and Calorimetry Using Water-Miscible Solvents: The Case of Dimethyl Sulfoxide, Acetonitrile, and 1,4-Dioxane. <i>Journal of Pharmaceutical Sciences</i> , 2020, 109, 524-531.	1.6	4
161	Anion solvation enhanced by positive supercharging mutations preserves thermal stability of an antibody in a wide pH range. <i>Biochemical and Biophysical Research Communications</i> , 2021, 563, 54-59.	1.0	4
162	An integrated computational pipeline for designing high-affinity nanobodies with expanded genetic codes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4

#	ARTICLE	IF	CITATIONS
163	Mechanism of dimerization and structural features of human LI-cadherin. <i>Journal of Biological Chemistry</i> , 2021, 297, 101054.	1.6	4
164	Regulation of cadherin dimerization by chemical fragments as a trigger to inhibit cell adhesion. <i>Communications Biology</i> , 2021, 4, 1041.	2.0	4
165	Structure and role of the linker domain of the iron surface-determinant protein IsdH in heme transportation in <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2022, 298, 101995.	1.6	4
166	Relationship between Fluorescence Intensity of GFP and the Expression Level of Prestin in a Prestin-Expressing Chinese Hamster Ovary Cell Line. <i>JSME International Journal Series C-Mechanical Systems Machine Elements and Manufacturing</i> , 2004, 47, 970-976.	0.3	3
167	In-Cell Enzymology To Probe His ⁶⁴ -Heme Ligation in Heme Oxygenase Catalysis. <i>Biochemistry</i> , 2016, 55, 4836-4849.	1.2	3
168	Development of drug discovery screening system by molecular interaction kinetics ⁶⁴ mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2018, 32, 665-671.	0.7	3
169	Production and characterization of a novel site-specific-modifiable anti-OX40-receptor single-chain variable fragment for targeted drug delivery. <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 614-620.	1.0	3
170	Biophysical characterization of the breast cancer-related BIG3-PHB2 interaction: Effect of non-conserved loop region of BIG3 on the structure and the interaction. <i>Biochemical and Biophysical Research Communications</i> , 2019, 518, 183-189.	1.0	3
171	Development of biparatopic bispecific antibody possessing tetravalent scFv-Fc capable of binding to ROBO1 expressed in hepatocellular carcinoma cells. <i>Journal of Biochemistry</i> , 2021, 170, 307-315.	0.9	3
172	Microsecond molecular dynamics suggest that a non-synonymous mutation, frequently observed in patients with mild symptoms in Tokyo, alters dynamics of the SARS-CoV-2 main protease. <i>Biophysics and Physicobiology</i> , 2021, 18, 215-222.	0.5	3
173	Antigen-Mediated Genetically Modified Cell Amplification (AMEGA) with Single Vector Transduction. <i>Journal of Chemical Engineering of Japan</i> , 2004, 37, 1259-1264.	0.3	3
174	Unfolding is the driving force for mitochondrial import and degradation of the Parkinson's disease-related protein DJ-1. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	3
175	Effects of Mutation in the Conserved GTSRH Sequence of the Motor Protein Prestin on Its Characteristics. <i>JSME International Journal Series C-Mechanical Systems Machine Elements and Manufacturing</i> , 2005, 48, 403-410.	0.3	2
176	Purification of the Motor Protein Prestin from Chinese Hamster Ovary Cells Stably Expressing Prestin. <i>Journal of Biomechanical Science and Engineering</i> , 2008, 3, 221-234.	0.1	2
177	Structural basis for inhibition of the Tob-CNOT7 interaction by a fragment screening approach. <i>Protein and Cell</i> , 2015, 6, 924-928.	4.8	2
178	Reply to "The Broadly Neutralizing, Anti-HIV Antibody 4E10: an Open and Shut Case?" <i>Journal of Virology</i> , 2016, 90, 3276-3277.	1.5	2
179	Structural behavior of keratin-associated protein 8.1 in human hair as revealed by a monoclonal antibody. <i>Journal of Structural Biology</i> , 2018, 204, 207-214.	1.3	2
180	Structural features of methionine aminopeptidase2-active core peptide essential for binding with S100A4. <i>Biochemical and Biophysical Research Communications</i> , 2019, 516, 1123-1129.	1.0	2

#	ARTICLE	IF	CITATIONS
181	Effect of allotypic variation of human IgG1 on the thermal stability of disulfide-linked knobs-into-holes mutants of the Fc for stable bispecific antibody design. <i>Antibody Therapeutics</i> , 2019, 2, 65-69.	1.2	2
182	Site-specific Manipulation of Mitochondrial DNA by Artificial Restriction DNA Cutter. <i>Chemistry Letters</i> , 2019, 48, 1332-1335.	0.7	2
183	Structural basis for selective inhibition of human serine hydroxymethyltransferase by secondary bile acid conjugate. <i>IScience</i> , 2021, 24, 102036.	1.9	2
184	Electrostatic-triggered exothermic antibody adsorption to the cellulose nanoparticles. <i>Analytical Biochemistry</i> , 2021, 632, 114337.	1.1	2
185	Epitope-dependent thermodynamic signature of single-domain antibodies against hen egg lysozyme. <i>Journal of Biochemistry</i> , 2021, 170, 623-629.	0.9	2
186	Molecular basis for the activation of actinoporins by lipids. <i>Methods in Enzymology</i> , 2021, 649, 277-306.	0.4	2
187	Oligo (N-methylalanine) as a Peptide-Based Molecular Scaffold with a Minimal Structure and High Density of Functionalizable Sites. <i>Angewandte Chemie - International Edition</i> , 2022, , .	7.2	2
188	Antibody recognition of complement Factor H reveals a flexible loop involved in Atypical Hemolytic Uremic Syndrome pathogenesis. <i>Journal of Biological Chemistry</i> , 2022, , 101962.	1.6	2
189	Development of a high-throughput method to screen novel antiviral materials. <i>PLoS ONE</i> , 2022, 17, e0266474.	1.1	2
190	Functional Expression of Prestin, the Outer Hair Cell Motor Protein, Using the Baculovirus/Insect Cell System. <i>Journal of Biomechanical Science and Engineering</i> , 2008, 3, 287-298.	0.1	1
191	Characterization of a putative maltodextrin-binding protein of <i>Streptococcus pyogenes</i> , SPs0871 and the development of a VHH inhibitor. <i>Biochemical and Biophysical Research Communications</i> , 2021, 565, 1-7.	1.0	1
192	Development and activities, including immunocomplex formation, of biparatopic antibodies and alternative scaffold proteins. <i>Translational and Regulatory Sciences</i> , 2020, 2, 1-6.	0.2	1
193	Biophysical Characterization of the Contribution of the Fab Region to the IgG-FcγR3a Interaction. <i>Biochemistry</i> , 2023, 62, 262-269.	1.2	1
194	Open Sandwich Selection: Selection of Human Antibody Fragments Using the Mechanism of Fv Fragment Stabilization in the Presence of Antigen. <i>ACS Symposium Series</i> , 2002, , 285-295.	0.5	0
195	2P019 The solubility of amino acids, diglycine, triglycine in aqueous L-Arginine hydrochloride solution(29. Protein structure and dynamics (II),Poster Session,Abstract,Meeting Program of EABS & Tj ETQq1 1 0784314 rgBT /Overlock 10	0.0	0
196	1P125 Thermodynamic profiles of the interaction between hyperthermostable TATA-box binding protein and a double-stranded DNA at high temperature(Protein engineering, evolutionary engineering, nucleic) Tj ETQq0 0 00rgBT /Overlock 10	0.0	0
197	2P-120 SELEX experiments of a hyperthermostable TATA-box-binding protein at different temperatures(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S93.	0.0	0
198	INCREASE IN THE ACTIVITY BY MUTATIONS OF THE MOTOR PROTEIN PRESTIN. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
199	Recent advances in antibody engineering. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1889-1890.	1.1	0
200	Revealing the peptide presenting process of human leukocyte antigen through the analysis of fluctuation. <i>Biophysics (Nagoya-shi, Japan)</i> , 2015, 11, 103-106.	0.4	0
201	Single-chain variable fragment (scFv) targeting streptolysin O controls group A <i>Streptococcus</i> infection. <i>Biochemical and Biophysical Research Communications</i> , 2021, 566, 177-183.	1.0	0
202	A Method for Efficient Refolding of Antibody Domains. <i>Seibutsu Butsuri</i> , 2000, 40, 274-276.	0.0	0
203	Application of Spectroscopic Folding Study to Highly Efficient Refolding Systems-With a Focus on Antibody Molecules-. <i>Seibutsu Butsuri</i> , 2004, 44, 102-107.	0.0	0
204	INTERACTION OF THE INNER EAR MOTOR PROTEIN PRESTIN WITH CHLORIDE STUDIED BY ISOTHERMAL TITRATION CALORIMETRY(2A1 Micro & Nano Biomechanics IV). <i>The Proceedings of the Asian Pacific Conference on Biomechanics Emerging Science and Technology in Biomechanics</i> , 2007, 2007.3, S137.	0.0	0
205	MISFOLDING AND MISLOCALIZATION BY MUTATIONS OF THE MOTOR PROTEIN PRESTIN(2A1 Micro & Nano) <i>Tj ETQq1 1 0.784314 rgBT and Technology in Biomechanics</i> , 2007, 2007.3, S136.	0.0	0
206	Oligo(N -methylalanine) as a Peptide-Based Molecular Scaffold with a Minimal Structure and High Density of Functionalizable Sites. <i>Angewandte Chemie</i> , 0, , .	1.6	0