

Kouhei Tsumoto

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

199
papers

4,321
citations

33
h-index

59
g-index

220
ext. papers

5,074
ext. citations

5.5
avg. IF

5.5
L-index

#	Paper	IF	Citations
199	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics.. <i>MABs</i> , 2022 , 14, 2020082	6.6	6
198	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 , 106075	2	0
197	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	5.4	0
196	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 , 101995	5.4	
195	Development of a high-throughput method to screen novel antiviral materials.. <i>PLoS ONE</i> , 2022 , 17, e0266474	5.4	0
194	Experimental Comparison of Bond Lifetime and Viscoelastic Relaxation in Transient Networks with Well-Controlled Structures.. <i>ACS Macro Letters</i> , 2022 , 753-759	6.6	1
193	The transcriptional corepressor CtBP2 serves as a metabolite sensor orchestrating hepatic glucose and lipid homeostasis. <i>Nature Communications</i> , 2021 , 12, 6315	17.4	1
192	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	3.4	3
191	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	5.4	4
190	Delicate balance among thermal stability, binding affinity, and conformational space explored by single-domain VH antibodies. <i>Scientific Reports</i> , 2021 , 11, 20624	4.9	3
189	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	4.9	2
188	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
187	A new twist of rubredoxin function in <i>M. tuberculosis</i> . <i>Bioorganic Chemistry</i> , 2021 , 109, 104721	5.1	4
186	Heme controls the structural rearrangement of its sensor protein mediating the hemolytic bacterial survival. <i>Communications Biology</i> , 2021 , 4, 467	6.7	3
185	A Novel Cell-Based Intracellular Protein-Protein Interaction Detection Platform (SOLIS) for Multimodality Screening. <i>ACS Synthetic Biology</i> , 2021 , 10, 990-999	5.7	2
184	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	3.1	0
183	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	3.4	1

182	Structural basis for antigen recognition by methylated lysine-specific antibodies. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100176	5.4	5
181	Peptoid-based reprogrammable template for cell-permeable inhibitors of protein-protein interactions. <i>Chemical Science</i> , 2021 , 12, 13292-13300	9.4	3
180	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	5.4	1
179	Elaboration of Non-naturally Occurring Helical Tripeptides as p53-MDM2/MDMX Interaction Inhibitors. <i>Chemical and Pharmaceutical Bulletin</i> , 2021 , 69, 681-692	1.9	4
178	Structural basis for selective inhibition of human serine hydroxymethyltransferase by secondary bile acid conjugate. <i>IScience</i> , 2021 , 24, 102036	6.1	
177	Thermodynamic Dissection of Potency and Selectivity of Cytosolic Hsp90 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 2669-2677	8.3	0
176	Single-chain variable fragment (scFv) targeting streptolysin O controls group A Streptococcus infection. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 566, 177-183	3.4	
175	Electrostatic-triggered exothermic antibody adsorption to the cellulose nanoparticles. <i>Analytical Biochemistry</i> , 2021 , 632, 114337	3.1	
174	An integrated computational pipeline for designing high-affinity nanobodies with expanded genetic codes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	1
173	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	3.4	0
172	Mechanism of dimerization and structural features of human LI-cadherin. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101054	5.4	0
171	Regulation of cadherin dimerization by chemical fragments as a trigger to inhibit cell adhesion. <i>Communications Biology</i> , 2021 , 4, 1041	6.7	0
170	A glutamine sensor that directly activates TORC1. <i>Communications Biology</i> , 2021 , 4, 1093	6.7	3
169	Molecular basis for the activation of actinoporins by lipids. <i>Methods in Enzymology</i> , 2021 , 649, 277-306	1.7	1
168	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	1.4	0
167	Dual-Sensitive Nanomicelles Enhancing Systemic Delivery of Therapeutically Active Antibodies Specifically into the Brain. <i>ACS Nano</i> , 2020 , 14, 6729-6742	16.7	33
166	Highly sensitive HPLC analysis and biophysical characterization of N-glycans of IgG-Fc domain in comparison between CHO and 293 cells using FcB11a ligand. <i>Biotechnology Progress</i> , 2020 , 36, e3016	2.8	2
165	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	6.1	2

164	System-Wide Analysis of Protein Acetylation and Ubiquitination Reveals a Diversified Regulation in Human Cancer Cells. <i>Biomolecules</i> , 2020 , 10,	5.9	6
163	Engineering Stability, Viscosity, and Immunogenicity of Antibodies by Computational Design. <i>Journal of Pharmaceutical Sciences</i> , 2020 , 109, 1631-1651	3.9	19
162	Polymeric Nanocarriers with Controlled Chain Flexibility Boost mRNA Delivery In Vivo through Enhanced Structural Fastening. <i>Advanced Healthcare Materials</i> , 2020 , 9, e2000538	10.1	17
161	Discovery of chemical probes that suppress Wnt/ β -catenin signaling through high-throughput screening. <i>Cancer Science</i> , 2020 , 111, 783-794	6.9	7
160	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	5.3	5
159	Development and activities, including immunocomplex formation, of biparatopic antibodies and alternative scaffold proteins. <i>Translational and Regulatory Sciences</i> , 2020 , 2, 1-6	0.3	1
158	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	3.9	2
157	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	3.8	5
156	Per-Residue Program of Multiple Backbone Dihedral Angles of β -Peptoids via Backbone Substitutions. <i>Journal of the American Chemical Society</i> , 2020 , 142, 2277-2284	16.4	7
155	Unique Electronic Structures of the Highly Ruffled Hemes in Heme-Degrading Enzymes of β -IsdG and IsdI, by Resonance Raman and Electron Paramagnetic Resonance Spectroscopies. <i>Biochemistry</i> , 2020 , 59, 3918-3928	3.2	2
154	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	8.3	6
153	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	4.9	5
152	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	2.5	4
151	Site-specific Manipulation of Mitochondrial DNA by Artificial Restriction DNA Cutter. <i>Chemistry Letters</i> , 2019 , 48, 1332-1335	1.7	1
150	Apoptotic Cell-Inspired Polymeric Particles for Controlling Microglial Inflammation toward Neurodegenerative Disease Treatment. <i>ACS Biomaterials Science and Engineering</i> , 2019 , 5, 5705-5713	5.5	4
149	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 , 618, 71-80	4.1	7
148	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	3.7	16
147	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	4.9	18

146	Control of Protein Adsorption to Cyclo Olefin Polymer by the Hofmeister Effect. <i>Journal of Pharmaceutical Sciences</i> , 2019 , 108, 1686-1691	3.9	2
145	An epitope-directed antibody affinity maturation system utilizing mammalian cell survival as readout. <i>Biotechnology and Bioengineering</i> , 2019 , 116, 1742-1751	4.9	5
144	Design strategy for serine hydroxymethyltransferase probes based on retro-aldol-type reaction. <i>Nature Communications</i> , 2019 , 10, 876	17.4	17
143	A Peptoid with Extended Shape in Water. <i>Journal of the American Chemical Society</i> , 2019 , 141, 14612-14624	6.4	15
142	The Isolation of New Pore-Forming Toxins from the Sea Anemone Provides Insights into the Mechanisms of Actinoporin Evolution. <i>Toxins</i> , 2019 , 11,	4.9	7
141	Structural features of methionine aminopeptidase2-active core peptide essential for binding with S100A4. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 516, 1123-1129	3.4	1
140	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	5.8	1
139	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	3.4	1
138	Computer-guided library generation applied to the optimization of single-domain antibodies. <i>Protein Engineering, Design and Selection</i> , 2019 , 32, 423-431	1.9	2
137	Modified AMBER force-field (FUJI) parameters for sulfated and phosphorylated tyrosine residues: Development and application to CCR5-derived peptide systems 2019 ,		1
136	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	4.9	3
135	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	4.9	14
134	Affinity Improvement of a Cancer-Targeted Antibody through Alanine-Induced Adjustment of Antigen-Antibody Interface. <i>Structure</i> , 2019 , 27, 519-527.e5	5.2	17
133	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	3.2	18
132	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	11.5	38
131	Characterization of glycoengineered anti-HER2 monoclonal antibodies produced by using a silkworm-baculovirus expression system. <i>Journal of Biochemistry</i> , 2018 , 163, 481-488	3.1	5
130	Intramolecular H-bonds govern the recognition of a flexible peptide by an antibody. <i>Journal of Biochemistry</i> , 2018 , 164, 65-76	3.1	7
129	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	1.9	4

128	A combination of 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	3.4	7
127	Molecular basis for governing the morphology of type-I collagen fibrils by Osteomodulin. <i>Communications Biology</i> , 2018 , 1, 33	6.7	11
126	Development of drug discovery screening system by molecular interaction kinetics-mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2018 , 32, 665-671	2.2	2
125	A secondary RET mutation in the activation loop conferring resistance to vandetanib. <i>Nature Communications</i> , 2018 , 9, 625	17.4	52
124	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	3.4	2
123	PRDM14 directly interacts with heat shock proteins HSP90 and glucose-regulated protein 78. <i>Cancer Science</i> , 2018 , 109, 373-383	6.9	13
122	Assessing the Heterogeneity of the Fc-Glycan of a Therapeutic Antibody Using an engineered Fc Receptor IIIa-Immobilized Column. <i>Scientific Reports</i> , 2018 , 8, 3955	4.9	27
121	Discovery and Optimization of Inhibitors of the Parkinson Disease Associated Protein DJ-1. <i>ACS Chemical Biology</i> , 2018 , 13, 2783-2793	4.9	18
120	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	2.2	15
119	Repertoire Analysis of Antibody CDR-H3 Loops Suggests Affinity Maturation Does Not Typically Result in Rigidification. <i>Frontiers in Immunology</i> , 2018 , 9, 413	8.4	26
118	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	5.8	4
117	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	3.9	2
116	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	3.4	2
115	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	1.9	3
114	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	3.7	13
113	Antibody Affinity Maturation by Computational Design. <i>Methods in Molecular Biology</i> , 2018 , 1827, 15-34	1.4	14
112	Tyrosine Sulfation Restricts the Conformational Ensemble of a Flexible Peptide, Strengthening the Binding Affinity for an Antibody. <i>Biochemistry</i> , 2018 , 57, 4177-4185	3.2	7
111	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	4.9	12

110	Peripheral Membrane Interactions Boost the Engagement by an Anti-HIV-1 Broadly Neutralizing Antibody. <i>Journal of Biological Chemistry</i> , 2017 , 292, 5571-5583	5.4	9
109	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	3.1	16
108	Haemolytic actinoporins interact with carbohydrates using their lipid-binding module. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	7
107	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	6.5	11
106	Polymeric SpyCatcher Scaffold Enables Bioconjugation in a Ratio-Controllable Manner. <i>Biotechnology Journal</i> , 2017 , 12, 1700195	5.6	18
105	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. <i>Nature Plants</i> , 2017 , 3, 825-832	11.5	31
104	Analysis of Pore Formation and Protein Translocation Using Large Biological Nanopores. <i>Analytical Chemistry</i> , 2017 , 89, 11269-11277	7.8	29
103	Through-bond effects in the ternary complexes of thrombin sandwiched by two DNA aptamers. <i>Nucleic Acids Research</i> , 2017 , 45, 461-469	20.1	37
102	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	3.4	3
101	Structural basis for binding and transfer of heme in bacterial heme-acquisition systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 2217-2230	4.2	4
100	Elucidation of potential sites for antibody engineering by fluctuation editing. <i>Scientific Reports</i> , 2017 , 7, 9597	4.9	12
99	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	3.1	1
98	Glycosylation of IgG-Fc: a molecular perspective. <i>International Immunology</i> , 2017 , 29, 311-317	4.9	34
97	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, 269-277	3.1	7
96	Production and characterization of genetically modified human IL-11 variants. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 205-217	4	2
95	Formulation and Stability 2016 , 105-129		
94	Differential Effect of Membrane Composition on the Pore-Forming Ability of Four Different Sea Anemone Actinoporins. <i>Biochemistry</i> , 2016 , 55, 6630-6641	3.2	21
93	Structural basis for amino acid export by DMT superfamily transporter YddG. <i>Nature</i> , 2016 , 534, 417-20	50.4	38

92	Integrative Network Analysis Combined with Quantitative Phosphoproteomics Reveals Transforming Growth Factor-beta Receptor type-2 (TGFB2) as a Novel Regulator of Glioblastoma Stem Cell Properties. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1017-31	7.6	13
91	Epiregulin Recognition Mechanisms by Anti-epiregulin Antibody 9E5: STRUCTURAL, FUNCTIONAL, AND MOLECULAR DYNAMICS SIMULATION ANALYSES. <i>Journal of Biological Chemistry</i> , 2016 , 291, 2319-301	5.4	9
90	Reply to "The Broadly Neutralizing, Anti-HIV Antibody 4E10: an Open and Shut Case?". <i>Journal of Virology</i> , 2016 , 90, 3276-7	6.6	2
89	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	4.9	25
88	Assessment of the Protein-Protein Interactions in a Highly Concentrated Antibody Solution by Using Raman Spectroscopy. <i>Pharmaceutical Research</i> , 2016 , 33, 956-69	4.5	13
87	Quantitative phosphoproteomics-based molecular network description for high-resolution kinase-substrate interactome analysis. <i>Bioinformatics</i> , 2016 , 32, 2083-8	7.2	15
86	Adhesive Dimerization of Human P-Cadherin Catalyzed by a Chaperone-like Mechanism. <i>Structure</i> , 2016 , 24, 1523-36	5.2	8
85	Identification of a Membrane-bound Prepore Species Clarifies the Lytic Mechanism of Actinoporins. <i>Journal of Biological Chemistry</i> , 2016 , 291, 19210-19219	5.4	20
84	In-Cell Enzymology To Probe His-Heme Ligation in Heme Oxygenase Catalysis. <i>Biochemistry</i> , 2016 , 55, 4836-49	3.2	3
83	Structural basis for self-assembly of a cytolytic pore lined by protein and lipid. <i>Nature Communications</i> , 2015 , 6, 6337	17.4	142
82	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, 1840-6	3.8	16
81	Crystal structure of streptavidin mutant with low immunogenicity. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 119, 642-7	3.3	11
80	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, 10850-61	5.4	29
79	Thermodynamics of antibody-antigen interaction revealed by mutation analysis of antibody variable regions. <i>Journal of Biochemistry</i> , 2015 , 158, 1-13	3.1	29
78	Click conjugation of a binuclear terbium(III) complex for real-time detection of tyrosine phosphorylation. <i>Analytical Chemistry</i> , 2015 , 87, 3834-40	7.8	14
77	Differential Effects of IFN- β on the Survival and Growth of Human Vascular Smooth Muscle and Endothelial Cells. <i>BioResearch Open Access</i> , 2015 , 4, 1-15	2.4	5
76	Structural basis for binding of human IgG1 to its high-affinity human receptor Fc γ R1. <i>Nature Communications</i> , 2015 , 6, 6866	17.4	87
75	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	4.9	18

74	Structural basis for inhibition of the Tob-CNOT7 interaction by a fragment screening approach. <i>Protein and Cell</i> , 2015 , 6, 924-8	7.2	1
73	Revealing the peptide presenting process of human leukocyte antigen through the analysis of fluctuation. <i>Biophysics (Nagoya-shi, Japan)</i> , 2015 , 11, 103-6		
72	Structural analysis of Fc/Fc β complexes: a blueprint for antibody design. <i>Immunological Reviews</i> , 2015 , 268, 201-21	11.3	43
71	Rapid Heme Transfer Reactions between NEAr Transporter Domains of Staphylococcus aureus: A Theoretical Study Using QM/MM and MD Simulations. <i>PLoS ONE</i> , 2015 , 10, e0145125	3.7	9
70	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, 12999-30154	5.4	34
69	Osteomodulin regulates diameter and alters shape of collagen fibrils. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 463, 292-6	3.4	36
68	Differential binding of prohibitin-2 to estrogen receptor α and to drug-resistant ER α mutants. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 463, 726-31	3.4	6
67	Bidirectional Transformation of a Metamorphic Protein between the Water-Soluble and Transmembrane Native States. <i>Biochemistry</i> , 2015 , 54, 6863-6	3.2	14
66	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, 11975-89	6.6	20
65	Identification and characterization of the X-dimer of human P-cadherin: implications for homophilic cell adhesion. <i>Biochemistry</i> , 2014 , 53, 1742-52	3.2	12
64	Next generation drying technologies for pharmaceutical applications. <i>Journal of Pharmaceutical Sciences</i> , 2014 , 103, 2673-2695	3.9	118
63	Alternative downstream processes for production of antibodies and antibody fragments. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 2032-2040	4	14
62	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	3.7	65
61	Protective effect of the long pentraxin PTX3 against histone-mediated endothelial cell cytotoxicity in sepsis. <i>Science Signaling</i> , 2014 , 7, ra88	8.8	27
60	Efficacy of ribavirin against malignant glioma cell lines. <i>Oncology Letters</i> , 2014 , 8, 2469-2474	2.6	13
59	The staphylococcal elastin-binding protein regulates zinc-dependent growth/biofilm formation. <i>Journal of Biochemistry</i> , 2014 , 156, 155-62	3.1	12
58	Peptide-dependent conformational fluctuation determines the stability of the human leukocyte antigen class I complex. <i>Journal of Biological Chemistry</i> , 2014 , 289, 24680-90	5.4	27
57	Effects of subclass change on the structural stability of chimeric, humanized, and human antibodies under thermal stress. <i>Protein Science</i> , 2013 , 22, 1542-51	6.3	40

56	Dynamic elements govern the catalytic activity of CapE, a capsular polysaccharide-synthesizing enzyme from <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2013 , 587, 3824-30	3.8	15
55	Mutations for decreasing the immunogenicity and maintaining the function of core streptavidin. <i>Protein Science</i> , 2013 , 22, 213-21	6.3	35
54	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	3.4	37
53	Improving the affinity of an antibody for its antigen via long-range electrostatic interactions. <i>Protein Engineering, Design and Selection</i> , 2013 , 26, 773-80	1.9	24
52	Incorporation of rapid thermodynamic data in fragment-based drug discovery. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 2155-9	8.3	14
51	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, 8866-77	3.2	16
50	Heme degradation by <i>Staphylococcus aureus</i> IsdG and IsdI liberates formaldehyde rather than carbon monoxide. <i>Biochemistry</i> , 2013 , 52, 3025-7	3.2	64
49	Crystal structure of the capsular polysaccharide synthesizing protein CapE of <i>Staphylococcus aureus</i> . <i>Bioscience Reports</i> , 2013 , 33,	4.1	15
48	Selective binding of antimicrobial porphyrins to the heme-receptor IsdH-NEAT3 of <i>Staphylococcus aureus</i> . <i>Protein Science</i> , 2013 , 22, 942-53	6.3	17
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