

Kenji Mizuguchi

List of Publications by Year in descending order

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177
papers

7,454
citations

81743

39
h-index

62479

80
g-index

193
all docs

193
docs citations

193
times ranked

10310
citing authors

#	ARTICLE	IF	CITATIONS
1	FUGUE: sequence-structure homology recognition using environment-specific substitution tables and structure-dependent gap penalties ¹¹ Edited by B. Honig. <i>Journal of Molecular Biology</i> , 2001, 310, 243-257.	2.0	1,185
2	HOMSTRAD: A database of protein structure alignments for homologous families. <i>Protein Science</i> , 1998, 7, 2469-2471.	3.1	461
3	Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. <i>Molecular Psychiatry</i> , 2007, 12, 74-86.	4.1	386
4	FlyMine: an integrated database for <i>Drosophila</i> and <i>Anopheles</i> genomics. <i>Genome Biology</i> , 2007, 8, R129.	13.9	345
5	beta 3: An additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 2308-2313.	3.3	281
6	Applying the Naïve Bayes classifier with kernel density estimation to the prediction of protein-protein interaction sites. <i>Bioinformatics</i> , 2010, 26, 1841-1848.	1.8	244
7	The Export of Coat Protein from Enterococcal <i>Escherichia coli</i> by a Specific ATP-binding Cassette Transporter System. <i>Journal of Biological Chemistry</i> , 2003, 278, 45680-45689.	1.6	157
8	Identification and classification of bacterial Type III toxin-antitoxin systems encoded in chromosomal and plasmid genomes. <i>Nucleic Acids Research</i> , 2012, 40, 6158-6173.	6.5	129
9	Organic Anion Transporting Polypeptides of the OATP/SLCO Superfamily: Identification of New Members in Nonmammalian Species, Comparative Modeling and a Potential Transport Mode. <i>Journal of Membrane Biology</i> , 2006, 208, 213-227.	1.0	121
10	Blockade of TLR3 protects mice from lethal radiation-induced gastrointestinal syndrome. <i>Nature Communications</i> , 2014, 5, 3492.	5.8	119
11	A novel superfamily of enzymes that catalyze the modification of guanidino groups. <i>Trends in Biochemical Sciences</i> , 2001, 26, 465-468.	3.7	115
12	TargetMine, an Integrated Data Warehouse for Candidate Gene Prioritisation and Target Discovery. <i>PLoS ONE</i> , 2011, 6, e17844.	1.1	115
13	A six-stranded double-psi β^2 barrel is shared by several protein superfamilies. <i>Structure</i> , 1999, 7, 227-236.	1.6	113
14	Getting knotted: a model for the structure and activation of Sp β 1. <i>Trends in Biochemical Sciences</i> , 1998, 23, 239-242.	3.7	101
15	A model of globin evolution. <i>Gene</i> , 2007, 398, 132-142.	1.0	99
16	Predicting Fraction Unbound in Human Plasma from Chemical Structure: Improved Accuracy in the Low Value Ranges. <i>Molecular Pharmaceutics</i> , 2018, 15, 5302-5311.	2.3	95
17	<i>Drosophila</i> Neurotrophins Reveal a Common Mechanism for Nervous System Formation. <i>PLoS Biology</i> , 2008, 6, e284.	2.6	94
18	Comparison of spatial arrangements of secondary structural elements in proteins. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 353-362.	1.0	87

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19	HOMSTRAD: recent developments of the Homologous Protein Structure Alignment Database. <i>Nucleic Acids Research</i> , 2004, 32, 203D-207.	6.5	85
20	Partner-Aware Prediction of Interacting Residues in Protein-Protein Complexes from Sequence Data. <i>PLoS ONE</i> , 2011, 6, e29104.	1.1	83
21	A family of proteins related to SpÄtzle, the toll receptor ligand, are encoded in the <i>Drosophila</i> genome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 71-80.	1.5	82
22	Identification of novel functional organic anion-transporting polypeptide 1B3 polymorphisms and assessment of substrate specificity. <i>Pharmacogenetics and Genomics</i> , 2011, 21, 103-114.	0.7	79
23	Homology-based prediction of interactions between proteins using Averaged One-Dependence Estimators. <i>BMC Bioinformatics</i> , 2014, 15, 213.	1.2	77
24	Network analysis and in silico prediction of protein-protein interactions with applications in drug discovery. <i>Current Opinion in Structural Biology</i> , 2017, 44, 134-142.	2.6	76
25	CAMPASS: a database of structurally aligned protein superfamilies. <i>Structure</i> , 1998, 6, 1087-1094.	1.6	73
26	A model of a transmembrane drug-efflux pump from Gram-negative bacteria. <i>FEBS Letters</i> , 2004, 578, 5-9.	1.3	71
27	Targeting BIG3- β -PHB2 interaction to overcome tamoxifen resistance in breast cancer cells. <i>Nature Communications</i> , 2013, 4, 2443.	5.8	63
28	Method for preparing DNA from feces in guanidine thiocyanate solution affects 16S rRNA-based profiling of human microbiota diversity. <i>Scientific Reports</i> , 2017, 7, 4339.	1.6	53
29	Structure of the periplasmic domain of <i>Pseudomonas aeruginosa</i> TolA: evidence for an evolutionary relationship with the TonB transporter protein. <i>EMBO Journal</i> , 2002, 21, 4207-4218.	3.5	52
30	The diversity of H3 loops determines the antigen-binding tendencies of antibody CDR3 loops. <i>Protein Science</i> , 2016, 25, 815-825.	3.1	52
31	Impact of quality trimming on the efficiency of reads joining and diversity analysis of Illumina paired-end reads in the context of QIIME1 and QIIME2 microbiome analysis frameworks. <i>BMC Bioinformatics</i> , 2019, 20, 581.	1.2	52
32	The guanidino-group modifying enzymes: Structural basis for their diversity and commonality. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 1010-1023.	1.5	50
33	Seeking significance in three-dimensional protein structure comparisons. <i>Current Opinion in Structural Biology</i> , 1995, 5, 377-382.	2.6	49
34	Inhibitory Roles of Signal Transducer and Activator of Transcription 3 in Antitumor Immunity during Carcinogen-Induced Lung Tumorigenesis. <i>Cancer Research</i> , 2012, 72, 2990-2999.	0.4	48
35	A phylogenomic profile of hemerythrins, the nonheme diiron binding respiratory proteins. <i>BMC Evolutionary Biology</i> , 2008, 8, 244.	3.2	47
36	Ligand-induced Ordering of the C-terminal Tail Primes STING for Phosphorylation by TBK1. <i>EBioMedicine</i> , 2016, 9, 87-96.	2.7	47

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37	High-resolution modeling of antibody structures by a combination of bioinformatics, expert knowledge, and molecular simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1624-1635.	1.5	46
38	Profiles of microRNA networks in intestinal epithelial cells in a mouse model of colitis. <i>Scientific Reports</i> , 2016, 5, 18174.	1.6	46
39	Network based analysis of hepatitis C virus Core and NS4B protein interactions. <i>Molecular BioSystems</i> , 2010, 6, 2539.	2.9	44
40	Structural genomics: an overview. <i>Progress in Biophysics and Molecular Biology</i> , 2000, 73, 289-295.	1.4	42
41	Development of Simplified in Vitro P-Glycoprotein Substrate Assay and in Silico Prediction Models To Evaluate Transport Potential of P-Glycoprotein. <i>Molecular Pharmaceutics</i> , 2019, 16, 1851-1863.	2.3	41
42	Prediction of dinucleotide-specific RNA-binding sites in proteins. <i>BMC Bioinformatics</i> , 2011, 12, S5.	1.2	38
43	Integrated Pathway Clusters with Coherent Biological Themes for Target Prioritisation. <i>PLoS ONE</i> , 2014, 9, e99030.	1.1	38
44	The Insulin Receptor: from Protein Sequence to Structure. <i>Biochemical Society Transactions</i> , 1999, 27, 715-726.	1.6	36
45	Molecular Basis for SUMOylation-dependent Regulation of DNA Binding Activity of Heat Shock Factor 2. <i>Journal of Biological Chemistry</i> , 2009, 284, 2435-2447.	1.6	36
46	Prediction of mono- and di-nucleotide-specific DNA-binding sites in proteins using neural networks. <i>BMC Structural Biology</i> , 2009, 9, 30.	2.3	35
47	Double deletion of tetraspanins CD9 and CD81 in mice leads to a syndrome resembling accelerated aging. <i>Scientific Reports</i> , 2018, 8, 5145.	1.6	35
48	Collective motions in proteins investigated by X-ray diffuse scattering. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 18, 34-48.	1.5	34
49	The SWIB and the MDM2 domains are homologous and share a common fold. <i>Bioinformatics</i> , 2002, 18, 626-630.	1.8	34
50	An integrative data analysis platform for gene set analysis and knowledge discovery in a data warehouse framework. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw009.	1.4	34
51	Understanding the Biological Context of NS5A-Host Interactions in HCV Infection: A Network-Based Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2537-2551.	1.8	33
52	Identification of potential inhibitors based on compound proposal contest: Tyrosine-protein kinase Yes as a target. <i>Scientific Reports</i> , 2015, 5, 17209.	1.6	33
53	An iterative structure-assisted approach to sequence alignment and comparative modeling. , 1999, 37, 55-60.		32
54	Prediction of Detailed Enzyme Functions and Identification of Specificity Determining Residues by Random Forests. <i>PLoS ONE</i> , 2014, 9, e84623.	1.1	32

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55	Conformational changes in DNA-binding proteins: Relationships with precomplex features and contributions to specificity and stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 841-857.	1.5	32
56	Crystal structure of FtsA from <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2014, 588, 1879-1885.	1.3	32
57	Gut microbiota modification suppresses the development of pulmonary arterial hypertension in an SU5416/hypoxia rat model. <i>Pulmonary Circulation</i> , 2020, 10, 1-10.	0.8	32
58	Functional site plasticity in domain superfamilies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 874-889.	1.1	31
59	Retinoblastoma-binding Protein 4-regulated Classical Nuclear Transport Is Involved in Cellular Senescence. <i>Journal of Biological Chemistry</i> , 2015, 290, 29375-29388.	1.6	31
60	Essential Role of CARD14 in Murine Experimental Psoriasis. <i>Journal of Immunology</i> , 2018, 200, 71-81.	0.4	31
61	Gut microbial composition in patients with atrial fibrillation: effects of diet and drugs. <i>Heart and Vessels</i> , 2021, 36, 105-114.	0.5	31
62	Exploring ligand recognition and ion flow in comparative models of the human GABA type A receptor. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 26, 760-774.	1.3	30
63	Toxygates: interactive toxicity analysis on a hybrid microarray and linked data platform. <i>Bioinformatics</i> , 2013, 29, 3080-3086.	1.8	30
64	Comprehensive analysis of gut microbiota of a healthy population and covariates affecting microbial variation in two large Japanese cohorts. <i>BMC Microbiology</i> , 2021, 21, 151.	1.3	30
65	Crystal structure of glutathione synthetase at optimal pH: domain architecture and structural similarity with other proteins. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 1083-1092.	1.0	29
66	Analysis of oral microbiota in Japanese oral cancer patients using 16S rRNA sequencing. <i>Journal of Oral Biosciences</i> , 2019, 61, 120-128.	0.8	29
67	A third fibronectin type III domain in the extracellular region of the insulin receptor family. <i>FEBS Letters</i> , 1998, 441, 331-336.	1.3	28
68	The common phospholipid-binding activity of the N-terminal domains of PEX1 and VCP/p97. <i>FEBS Journal</i> , 2006, 273, 4959-4971.	2.2	27
69	PoSSuM v.2.0: data update and a new function for investigating ligand analogs and target proteins of small-molecule drugs. <i>Nucleic Acids Research</i> , 2015, 43, D392-D398.	6.5	27
70	Development of an in silico prediction system of human renal excretion and clearance from chemical structure information incorporating fraction unbound in plasma as a descriptor. <i>Scientific Reports</i> , 2019, 9, 18782.	1.6	27
71	Systems Biology Approaches to a Rational Drug Discovery Paradigm. <i>Current Topics in Medicinal Chemistry</i> , 2015, 16, 1009-1025.	1.0	25
72	The Chemotherapeutic Agent DMXAA as a Unique IRF3-Dependent Type-2 Vaccine Adjuvant. <i>PLoS ONE</i> , 2013, 8, e60038.	1.1	24

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73	Data Curation can Improve the Prediction Accuracy of Metabolic Intrinsic Clearance. <i>Molecular Informatics</i> , 2019, 38, e1800086.	1.4	24
74	Group IIA secreted phospholipase A2 controls skin carcinogenesis and psoriasis by shaping the gut microbiota. <i>JCI Insight</i> , 2022, 7, .	2.3	24
75	Integrating sequence and gene expression information predicts genome-wide DNA-binding proteins and suggests a cooperative mechanism. <i>Nucleic Acids Research</i> , 2018, 46, 54-70.	6.5	23
76	Î±-Amino acid and peptide synthesis using catalytic cross-dehydrogenative coupling. , 2022, 1, 304-312.		23
77	Conformational plasticity of JRAB/MICAL-L2 provides a slow and ordered collective cell migration. <i>Molecular Biology of the Cell</i> , 2016, 27, 3095-3108.	0.9	22
78	Development of an <i>In Silico</i> Prediction Model for P-glycoprotein Efflux Potential in Brain Capillary Endothelial Cells toward the Prediction of Brain Penetration. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 2725-2738.	2.9	22
79	The TargetMine Data Warehouse: Enhancement and Updates. <i>Frontiers in Genetics</i> , 2019, 10, 934.	1.1	21
80	Pathway-Based Analysis of Genome-Wide siRNA Screens Reveals the Regulatory Landscape of App Processing. <i>PLoS ONE</i> , 2015, 10, e0115369.	1.1	19
81	BIG3 Inhibits the Estrogen-Dependent Nuclear Translocation of PHB2 via Multiple Karyopherin-Alpha Proteins in Breast Cancer Cells. <i>PLoS ONE</i> , 2015, 10, e0127707.	1.1	19
82	Prediction of the secondary structure of short DNA aptamers. <i>Biophysics and Physicobiology</i> , 2019, 16, 287-294.	0.5	19
83	Selective covalent targeting of SARS-CoV-2 main protease by enantiopure chlorofluoroacetamide. <i>Chemical Science</i> , 2022, 13, 3027-3034.	3.7	19
84	Interactive Toxicogenomics: Gene set discovery, clustering and analysis in Toxygates. <i>Scientific Reports</i> , 2017, 7, 1390.	1.6	18
85	Constructing an In Silico Three-Class Predictor of Human Intestinal Absorption With Caco-2 Permeability and Dried-DMSO Solubility. <i>Journal of Pharmaceutical Sciences</i> , 2019, 108, 3630-3639.	1.6	17
86	Proteomics of serum extracellular vesicles identifies a novel COPD biomarker, fibulin-3 from elastic fibres. <i>ERJ Open Research</i> , 2021, 7, 00658-2020.	1.1	17
87	Prediction of the structure and function of AstA and AstB, the first two enzymes of the arginine succinyltransferase pathway of arginine catabolism. <i>FEBS Letters</i> , 2003, 555, 505-510.	1.3	16
88	Computational Model To Predict the Fraction of Unbound Drug in the Brain. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3251-3261.	2.5	16
89	Syndecan-4 as a biomarker to predict clinical outcome for glioblastoma multiforme treated with WT1 peptide vaccine. <i>Future Science OA</i> , 2016, 2, FSO96.	0.9	15
90	B cell intrinsic MyD88 signaling controls IFNÎ³-mediated early IgG2c class switching in mice in response to a particulate adjuvant. <i>European Journal of Immunology</i> , 2019, 49, 1433-1440.	1.6	15

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91	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. <i>Scientific Reports</i> , 2019, 9, 19585.	1.6	15
92	Novel anti-flavivirus drugs targeting the nucleolar distribution of core protein. <i>Virology</i> , 2020, 541, 41-51.	1.1	15
93	CCRXP: exploring clusters of conserved residues in protein structures. <i>Nucleic Acids Research</i> , 2010, 38, W398-W401.	6.5	14
94	Classification of idiopathic interstitial pneumonias using anti-“myxovirus resistance-protein 1 autoantibody. <i>Scientific Reports</i> , 2017, 7, 43201.	1.6	14
95	A-kinase anchoring protein BIG3 coordinates oestrogen signalling in breast cancer cells. <i>Nature Communications</i> , 2017, 8, 15427.	5.8	14
96	Dietary Vitamin B1 Intake Influences Gut Microbial Community and the Consequent Production of Short-Chain Fatty Acids. <i>Nutrients</i> , 2022, 14, 2078.	1.7	14
97	Characterisation of the gene for <i>Drosophila</i> amphiphysin. <i>Gene</i> , 2000, 241, 167-174.	1.0	13
98	Functional restraints on the patterns of amino acid substitutions: Application to sequence-structure homology recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 722-731.	1.5	13
99	Proteomic Analysis of Hepatitis C Virus (HCV) Core Protein Transfection and Host Regulator PA28 ³ Knockout in HCV Pathogenesis: A Network-Based Study. <i>Journal of Proteome Research</i> , 2012, 11, 3664-3679.	1.8	13
100	Actin Cytoskeletal Reorganization Function of JRAB/MICAL-L2 Is Fine-tuned by Intramolecular Interaction between First LIM Zinc Finger and C-terminal Coiled-coil Domains. <i>Scientific Reports</i> , 2019, 9, 12794.	1.6	13
101	Lipophobicity and the residue environments of the transmembrane α -helical bundle. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 32-49.	1.5	12
102	Creation of lysine-deficient mutant lymphotoxin- β with receptor selectivity by using a phage display system. <i>Biomaterials</i> , 2010, 31, 1935-1943.	5.7	12
103	Fold recognition for drug discovery. <i>Drug Discovery Today: TARGETS</i> , 2004, 3, 18-23.	0.5	11
104	A novel mechanism of allosteric regulation of archaeal phosphoenolpyruvate carboxylase: a combined approach to structure-based alignment and model assessment. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 409-419.	1.0	11
105	Integration of Ligand and Structure Based Approaches for CSAR-2014. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 974-987.	2.5	11
106	Predicting conformational ensembles and genome-wide transcription factor binding sites from DNA sequences. <i>Scientific Reports</i> , 2017, 7, 4071.	1.6	11
107	Deep Learning Prediction of Adverse Drug Reactions in Drug Discovery Using Open TG“GATEs and FAERS Databases. <i>Frontiers in Drug Discovery</i> , 2021, 1, .	1.1	11
108	On nucleotide solvent accessibility in RNA structure. <i>Gene</i> , 2010, 463, 41-48.	1.0	10

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109	A structural dissection of amino acid substitutions in helical transmembrane proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2895-2907.	1.5	9
110	Altered Actions of Memantine and NMDA-Induced Currents in a New Grid2-Deleted Mouse Line. <i>Genes</i> , 2014, 5, 1095-1114.	1.0	9
111	Brefeldin A-inhibited guanine nucleotide-exchange protein 3 (BIG3) is predicted to interact with its partner through an ARM-type α -helical structure. <i>BMC Research Notes</i> , 2014, 7, 435.	0.6	9
112	Metabolomic analysis of fibrotic mice combined with public RNA-seq human lung data reveal potential diagnostic biomarker candidates for lung fibrosis. <i>FEBS Open Bio</i> , 2020, 10, 2427-2436.	1.0	9
113	Lipid recognition propensities of amino acids in membrane proteins from atomic resolution data. <i>BMC Biophysics</i> , 2011, 4, 21.	4.4	8
114	Prediction and experimental validation of a putative non-consensus binding site for transcription factor STAT3 in serum amyloid A gene promoter. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 3650-3655.	1.1	8
115	An Antigen-Free, Plasmacytoid Dendritic Cell-Targeting Immunotherapy To Bolster Memory CD8+ T Cells in Nonhuman Primates. <i>Journal of Immunology</i> , 2018, 200, 2067-2075.	0.4	8
116	Relationship between Nutrient Intake and Human Gut Microbiota in Monozygotic Twins. <i>Medicina (Lithuania)</i> , 2021, 57, 275.	0.8	8
117	Assessing drug target suitability using TargetMine. <i>F1000Research</i> , 2019, 8, 233.	0.8	8
118	Classification of the Occurrence of Dyslipidemia Based on Gut Bacteria Related to Barley Intake. <i>Frontiers in Nutrition</i> , 2022, 9, 812469.	1.6	8
119	Altered gut microbiota and its association with inflammation in patients with chronic thromboembolic pulmonary hypertension: a single-center observational study in Japan. <i>BMC Pulmonary Medicine</i> , 2022, 22, 138.	0.8	8
120	Distinct protein interfaces in transmembrane domains suggest an in vivo folding model. <i>Protein Science</i> , 2008, 13, 3028-3037.	3.1	7
121	Dextran sulfate-resistant A/Puerto Rico/8/34 influenza virus is associated with the emergence of specific mutations in the neuraminidase glycoprotein. <i>Antiviral Research</i> , 2014, 111, 69-77.	1.9	7
122	Two distinct effector memory cell populations of WT1 (Wilms' tumor gene 1)-specific cytotoxic T lymphocytes in acute myeloid leukemia patients. <i>Cancer Immunology, Immunotherapy</i> , 2015, 64, 791-804.	2.0	7
123	PSOPIA: Toward more reliable protein-protein interaction prediction from sequence information. , 2017, , .		7
124	Distinct Age-Specific miRegulome Profiling of Isolated Small and Large Intestinal Epithelial Cells in Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3544.	1.8	7
125	A public-private partnership to enrich the development of in silico predictive models for pharmacokinetic and cardiotoxic properties. <i>Drug Discovery Today</i> , 2021, 26, 1275-1283.	3.2	7
126	Flavivirus recruits the valosin-containing protein-NPL4 complex to induce stress granule disassembly for efficient viral genome replication. <i>Journal of Biological Chemistry</i> , 2022, 298, 101597.	1.6	7

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127	Effects of Malted Rice Amazake on Constipation Symptoms and Gut Microbiota in Children and Adults with Severe Motor and Intellectual Disabilities: A Pilot Study. <i>Nutrients</i> , 2021, 13, 4466.	1.7	7
128	Co-expression analysis to identify key modules and hub genes associated with COVID-19 in platelets. <i>BMC Medical Genomics</i> , 2022, 15, 83.	0.7	7
129	Protein Three-Dimensional Structural Databases: Domains, Structurally Aligned Homologues and Superfamilies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1168-1177.	2.5	6
130	N-ethylmaleimide-sensitive fusion protein (NSF) and CDC48 confirmed as members of the double-psi β -barrel aspartate decarboxylase/formate dehydrogenase family. <i>Structure</i> , 1999, 7, R215-R216.	1.6	6
131	Integrated prediction of one-dimensional structural features and their relationships with conformational flexibility in helical membrane proteins. <i>BMC Bioinformatics</i> , 2010, 11, 533.	1.2	6
132	Relationships between functional subclasses and information contained in active site and ligand-binding residues in diverse superfamilies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2369-2384.	1.5	6
133	Sagace: A web-based search engine for biomedical databases in Japan. <i>BMC Research Notes</i> , 2012, 5, 604.	0.6	6
134	Improved pose and affinity predictions using different protocols tailored on the basis of data availability. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 817-828.	1.3	6
135	Glycan Cluster Shielding and Antibody Epitopes on Lassa Virus Envelop Protein. <i>Journal of Physical Chemistry B</i> , 2021, 125, 2089-2097.	1.2	6
136	Network modeling and inference of peroxisome proliferator-activated receptor pathway in high fat diet-linked obesity. <i>Journal of Theoretical Biology</i> , 2021, 519, 110647.	0.8	6
137	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. <i>PLoS ONE</i> , 2020, 15, e0243609.	1.1	6
138	Relationships between barley consumption and gut microbiome characteristics in a healthy Japanese population: a cross-sectional study. <i>BMC Nutrition</i> , 2022, 8, 23.	0.6	6
139	Quantifying the relative immune cell activation from whole tissue/organ-derived differentially expressed gene data. <i>Scientific Reports</i> , 2017, 7, 12847.	1.6	5
140	High-Contrast Facile Imaging with Target-Directing Fluorescent Molecular Rotors, the N3-Modified Thioflavin T Derivatives. <i>Biochemistry</i> , 2019, 58, 493-498.	1.2	5
141	Data Warehousing with TargetMine for Omics Data Analysis. <i>Methods in Molecular Biology</i> , 2019, 1986, 35-64.	0.4	5
142	The Gut Microbiome as a Biomarker of Cancer Progression Among Female Never-smokers With Lung Adenocarcinoma. <i>Anticancer Research</i> , 2022, 42, 1589-1598.	0.5	5
143	Cylindrical Channels from Concave Helices. <i>Science</i> , 2003, 299, 661-662.	6.0	4
144	Docking of cytochrome c6 and plastocyanin to the aa3-type cytochrome c oxidase in the cyanobacterium <i>Phormidium laminosum</i> . <i>Protein Engineering, Design and Selection</i> , 2008, 21, 689-698.	1.0	4

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145	Using Knowledge of Protein Structural Constraints to Predict the Evolution of HIV-1. <i>Journal of Molecular Biology</i> , 2011, 410, 1023-1034.	2.0	4
146	Computational design, construction, and characterization of a set of specificity determining residues in protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2426-2436.	1.5	4
147	Network-Based Analysis for Biological Discovery. , 2019, , 283-291.		4
148	Integrated toxicogenomics analysis with Toxygates for inferring molecular mechanisms. <i>Genomics and Computational Biology</i> , 2017, 3, 37.	0.7	4
149	Panomicon: A web-based environment for interactive, visual analysis of multi-omics data. <i>Heliyon</i> , 2020, 6, e04618.	1.4	3
150	Integrative Analysis Reveals Common and Unique Roles of Tetraspanins in Fibrosis and Emphysema. <i>Frontiers in Genetics</i> , 2020, 11, 585998.	1.1	3
151	Categorization of the Ocular Microbiome in Japanese Stevens-Johnson Syndrome Patients With Severe Ocular Complications. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 741654.	1.8	3
152	Amino-Acid Substitutions In Membrane Proteins: Applications To Homology Recognition And Comparative Modelling. <i>BMC Bioinformatics</i> , 2005, 6, S9.	1.2	2
153	Bioinformatics Approaches for Analysis of Protein-Ligand Interactions. , 0, , 267-299.		2
154	Network-Based Analysis of Host-Pathogen Interactions. , 2019, , 932-937.		2
155	Developing a Kinase-Specific Target Selection Method Using a Structure-Based Machine Learning Approach. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2020, Volume 13, 27-40.	1.6	2
156	Update of the GRIP web service. <i>Journal of Receptor and Signal Transduction Research</i> , 2020, 40, 348-356.	1.3	2
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