

Kenji Mizuguchi

List of Publications by Year in Descending Order

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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.

171
papers

5,869
citations

36
h-index

74
g-index

193
ext. papers

6,755
ext. citations

5.7
avg. IF

5.6
L-index

#	Paper	IF	Citations
171	Group IIA secreted phospholipase A2 controls skin carcinogenesis and psoriasis by shaping the gut microbiota.. <i>JCI Insight</i> , 2022 , 7,	9.9	2
170	Flavivirus recruits the valosin-containing protein (VCP)/NPL4 complex to induce stress granule disassembly for efficient viral genome replication.. <i>Journal of Biological Chemistry</i> , 2022 , 101597	5.4	0
169	Selective covalent targeting of SARS-CoV-2 main protease by enantiopure chlorofluoroacetamide.. <i>Chemical Science</i> , 2022 , 13, 3027-3034	9.4	3
168	Relationships between barley consumption and gut microbiome characteristics in a healthy Japanese population: a cross-sectional study.. <i>BMC Nutrition</i> , 2022 , 8, 23	2.5	1
167	Classification of the Occurrence of Dyslipidemia Based on Gut Bacteria Related to Barley Intake.. <i>Frontiers in Nutrition</i> , 2022 , 9, 812469	6.2	1
166	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	3.5	1
165	The Gut Microbiome as a Biomarker of Cancer Progression Among Female Never-smokers With Lung Adenocarcinoma.. <i>Anticancer Research</i> , 2022 , 42, 1589-1598	2.3	1
164	Co-expression analysis to identify key modules and hub genes associated with COVID-19 in platelets.. <i>BMC Medical Genomics</i> , 2022 , 15, 83	3.7	0
163	Dietary Vitamin B1 Intake Influences Gut Microbial Community and the Consequent Production of Short-Chain Fatty Acids. <i>Nutrients</i> , 2022 , 14, 2078	6.7	1
162	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	5.9	0
161	Deep Learning Prediction of Adverse Drug Reactions in Drug Discovery Using Open TGATES and FAERS Databases 2021 , 1,		1
160	Distinct Age-Specific miRegulome Profiling of Isolated Small and Large Intestinal Epithelial Cells in Mice. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
159	Relationship between Nutrient Intake and Human Gut Microbiota in Monozygotic Twins. <i>Medicina (Lithuania)</i> , 2021 , 57,	3.1	4
158	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	4.5	10
157	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	8.8	1
156	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	2.3	1
155	Gut microbial composition in patients with atrial fibrillation: effects of diet and drugs. <i>Heart and Vessels</i> , 2021 , 36, 105-114	2.1	12

154	Development of an 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	8.3	3
153	Glycan Cluster Shielding and Antibody Epitopes on Lassa Virus Envelop Protein. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 2089-2097	3.4	1
152	Proteomics of serum extracellular vesicles identifies a novel COPD biomarker, fibulin-3 from elastic fibres. <i>ERJ Open Research</i> , 2021 , 7,	3.5	3
151	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,	6.7	2
150	Integrative Analysis Reveals Common and Unique Roles of Tetraspanins in Fibrosis and Emphysema. <i>Frontiers in Genetics</i> , 2020 , 11, 585998	4.5	1
149	Update of the GRIP web service. <i>Journal of Receptor and Signal Transduction Research</i> , 2020 , 40, 348-356	2.6	2
148	Docking algorithms and scoring functions 2020 , 257-269		
147	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. <i>PLoS ONE</i> , 2020 , 15, e0243609	3.7	2
146	Novel anti-flavivirus drugs targeting the nucleolar distribution of core protein. <i>Virology</i> , 2020 , 541, 41-51	3.6	7
145	Panomicon: A web-based environment for interactive, visual analysis of multi-omics data. <i>Heliyon</i> , 2020 , 6, e04618	3.6	1
144	Developing a Kinase-Specific Target Selection Method Using a Structure-Based Machine Learning Approach. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2020 , 13, 27-40	1.5	1
143	Gut microbiota modification suppresses the development of pulmonary arterial hypertension in an SU5416/hypoxia rat model. <i>Pulmonary Circulation</i> , 2020 , 10, 2045894020929147	2.7	10
142	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	2.7	6
141	The TargetMine Data Warehouse: Enhancement and Updates. <i>Frontiers in Genetics</i> , 2019 , 10, 934	4.5	12
140	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	4.9	5
139	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	3.9	5
138	Analysis of oral microbiota in Japanese oral cancer patients using 16S rRNA sequencing. <i>Journal of Oral Biosciences</i> , 2019 , 61, 120-128	2.5	12
137	B cell-intrinsic MyD88 signaling controls IFN- γ -mediated early IgG2c class switching in mice in response to a particulate adjuvant. <i>European Journal of Immunology</i> , 2019 , 49, 1433-1440	6.1	6

136	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	5.6	21
135	Integrative Analysis of Multi-Omics Data 2019 , 194-199		1
134	Network-Based Analysis for Biological Discovery 2019 , 283-291		1
133	Network-Based Analysis of Host-Pathogen Interactions 2019 , 932-937		1
132	Computational Model To Predict the Fraction of Unbound Drug in the Brain. <i>Journal of Chemical Information and Modeling</i> , 2019 , 59, 3251-3261	6.1	5
131	CLINE: a web-tool for the comparison of biological dendrogram structures. <i>BMC Bioinformatics</i> , 2019 , 20, 528	3.6	
130	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	3.6	26
129	Assessing drug target suitability using TargetMine. <i>F1000Research</i> , 2019 , 8, 233	3.6	2
128	Assessing drug target suitability using TargetMine. <i>F1000Research</i> , 2019 , 8, 233	3.6	1
127	Data Warehousing with TargetMine for Omics Data Analysis. <i>Methods in Molecular Biology</i> , 2019 , 1986, 35-64	1.4	1
126	Prediction of the secondary structure of short DNA aptamers. <i>Biophysics and Physicobiology</i> , 2019 , 16, 287-294	1.4	9
125	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. <i>Scientific Reports</i> , 2019 , 9, 19585	4.9	5
124	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	4.9	15
123	High-Contrast Facile Imaging with Target-Directing Fluorescent Molecular Rotors, the N-Modified Thioflavin T Derivatives. <i>Biochemistry</i> , 2019 , 58, 493-498	3.2	5
122	Data Curation can Improve the Prediction Accuracy of Metabolic Intrinsic Clearance. <i>Molecular Informatics</i> , 2019 , 38, e1800086	3.8	14
121	Double deletion of tetraspanins CD9 and CD81 in mice leads to a syndrome resembling accelerated aging. <i>Scientific Reports</i> , 2018 , 8, 5145	4.9	26
120	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	5.3	6
119	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	20.1	5

118	Essential Role of CARD14 in Murine Experimental Psoriasis. <i>Journal of Immunology</i> , 2018 , 200, 71-81	5.3	25
117	Predicting Fraction Unbound in Human Plasma from Chemical Structure: Improved Accuracy in the Low Value Ranges. <i>Molecular Pharmaceutics</i> , 2018 , 15, 5302-5311	5.6	43
116	Classification of idiopathic interstitial pneumonias using anti-myxovirus resistance-protein 1 autoantibody. <i>Scientific Reports</i> , 2017 , 7, 43201	4.9	8
115	Interactive Toxicogenomics: Gene set discovery, clustering and analysis in Toxygates. <i>Scientific Reports</i> , 2017 , 7, 1390	4.9	10
114	A-kinase anchoring protein BIG3 coordinates oestrogen signalling in breast cancer cells. <i>Nature Communications</i> , 2017 , 8, 15427	17.4	11
113	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	8.1	52
112	Quantifying the relative immune cell activation from whole tissue/organ-derived differentially expressed gene data. <i>Scientific Reports</i> , 2017 , 7, 12847	4.9	5
111	Database Development and Computational Modelling in Early-Stage Drug Discovery. <i>Trends in the Sciences</i> , 2017 , 22, 7_62-7_65	0	
110	Predicting conformational ensembles and genome-wide transcription factor binding sites from DNA sequences. <i>Scientific Reports</i> , 2017 , 7, 4071	4.9	9
109	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	4.9	37
108	2017 ,		4
107	Ligand-induced Ordering of the C-terminal Tail Primes STING for Phosphorylation by TBK1. <i>EBioMedicine</i> , 2016 , 9, 87-96	8.8	26
106	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,	5	25
105	Integration of Ligand and Structure Based Approaches for CSAR-2014. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 974-87	6.1	10
104	Systems Biology Approaches to a Rational Drug Discovery Paradigm. <i>Current Topics in Medicinal Chemistry</i> , 2016 , 16, 1009-25	3	22
103	The diversity of H3 loops determines the antigen-binding tendencies of antibody CDR loops. <i>Protein Science</i> , 2016 , 25, 815-25	6.3	29
102	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	2.7	12
101	Conformational plasticity of JRAB/MICAL-L2 provides "law and order" in collective cell migration. <i>Molecular Biology of the Cell</i> , 2016 , 27, 3095-3108	3.5	17

100	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	4.2	3
99	Two distinct effector memory cell populations of WT1 (WilmsTumor gene 1)-specific cytotoxic T lymphocytes in acute myeloid leukemia patients. <i>Cancer Immunology, Immunotherapy</i> , 2015 , 64, 791-804	7.4	6
98	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, D392-8	20.1	18
97	Profiles of microRNA networks in intestinal epithelial cells in a mouse model of colitis. <i>Scientific Reports</i> , 2015 , 5, 18174	4.9	36
96	Identification of potential inhibitors based on compound proposal contest: Tyrosine-protein kinase Yes as a target. <i>Scientific Reports</i> , 2015 , 5, 17209	4.9	27
95	Pathway-based analysis of genome-wide siRNA screens reveals the regulatory landscape of APP processing. <i>PLoS ONE</i> , 2015 , 10, e0115369	3.7	14
94	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	3.7	12
93	Retinoblastoma-binding Protein 4-regulated Classical Nuclear Transport Is Involved in Cellular Senescence. <i>Journal of Biological Chemistry</i> , 2015 , 290, 29375-88	5.4	21
92	Integration of Disease Entries Across OMIM, Orphanet, and a Proprietary Knowledge Base. <i>Lecture Notes in Computer Science</i> , 2015 , 120-130	0.9	1
91	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	10.8	5
90	Homology-based prediction of interactions between proteins using Averaged One-Dependence Estimators. <i>BMC Bioinformatics</i> , 2014 , 15, 213	3.6	44
89	Brefeldin A-inhibited guanine nucleotide-exchange protein 3 (BIG3) is predicted to interact with its partner through an ARM-type Helical structure. <i>BMC Research Notes</i> , 2014 , 7, 435	2.3	9
88	Crystal structure of FtsA from Staphylococcus aureus. <i>FEBS Letters</i> , 2014 , 588, 1879-85	3.8	24
87	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, 1624-35	4.2	36
86	Prediction of detailed enzyme functions and identification of specificity determining residues by random forests. <i>PLoS ONE</i> , 2014 , 9, e84623	3.7	24
85	Integrated pathway clusters with coherent biological themes for target prioritisation. <i>PLoS ONE</i> , 2014 , 9, e99030	3.7	19
84	Altered Actions of Memantine and NMDA-Induced Currents in a New Grid2-Deleted Mouse Line. <i>Genes</i> , 2014 , 5, 1095-114	4.2	5
83	Blockade of TLR3 protects mice from lethal radiation-induced gastrointestinal syndrome. <i>Nature Communications</i> , 2014 , 5, 3492	17.4	96

82	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, 841-57	4.2	23
81	Functional site plasticity in domain superfamilies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 874-89	4	24
80	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, 3650-5	4	5
79	Understanding the biological context of NS5A-host interactions in HCV infection: a network-based approach. <i>Journal of Proteome Research</i> , 2013 , 12, 2537-51	5.6	22
78	Targeting BIG3-PHB2 interaction to overcome tamoxifen resistance in breast cancer cells. <i>Nature Communications</i> , 2013 , 4, 2443	17.4	39
77	Toxygates: interactive toxicity analysis on a hybrid microarray and linked data platform. <i>Bioinformatics</i> , 2013 , 29, 3080-6	7.2	20
76	Expression, purification, crystallization and preliminary crystallographic study of FtsA from methicillin-resistant <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 895-8		1
75	The chemotherapeutic agent DMXAA as a unique IRF3-dependent type-2 vaccine adjuvant. <i>PLoS ONE</i> , 2013 , 8, e60038	3.7	18
74	1P114 DNA-binding-induced conformational changes in proteins(04. Nucleic acid binding proteins,Poster,The 51st Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2013 , 53, S124	0	
73	A combined proteomics and computational approach provides a better understanding of HCV-induced liver disease. <i>Expert Review of Proteomics</i> , 2012 , 9, 493-6	4.2	1
72	Proteomic analysis of hepatitis C virus (HCV) core protein transfection and host regulator PA28 \square knockout in HCV pathogenesis: a network-based study. <i>Journal of Proteome Research</i> , 2012 , 11, 3664-79	5.6	12
71	Sagace: a web-based search engine for biomedical databases in Japan. <i>BMC Research Notes</i> , 2012 , 5, 604	2.3	6
70	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, 2426-36	4.2	2
69	Inhibitory roles of signal transducer and activator of transcription 3 in antitumor immunity during carcinogen-induced lung tumorigenesis. <i>Cancer Research</i> , 2012 , 72, 2990-9	10.1	43
68	Identification and classification of bacterial Type III toxin-antitoxin systems encoded in chromosomal and plasmid genomes. <i>Nucleic Acids Research</i> , 2012 , 40, 6158-73	20.1	107
67	An Open Framework for Extensible Multi-stage Bioinformatics Software. <i>Lecture Notes in Computer Science</i> , 2012 , 106-117	0.9	
66	Lipid recognition propensities of amino acids in membrane proteins from atomic resolution data. <i>BMC Biophysics</i> , 2011 , 4, 21	0	6
65	Using knowledge of protein structural constraints to predict the evolution of HIV-1. <i>Journal of Molecular Biology</i> , 2011 , 410, 1023-34	6.5	4

64	Partner-aware prediction of interacting residues in protein-protein complexes from sequence data. <i>PLoS ONE</i> , 2011 , 6, e29104	3.7	55
63	Prediction of dinucleotide-specific RNA-binding sites in proteins. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 13, S5	3.6	32
62	Identification of novel functional organic anion-transporting polypeptide 1B3 polymorphisms and assessment of substrate specificity. <i>Pharmacogenetics and Genomics</i> , 2011 , 21, 103-14	1.9	66
61	TargetMine, an integrated data warehouse for candidate gene prioritisation and target discovery. <i>PLoS ONE</i> , 2011 , 6, e17844	3.7	93
60	CCRXP: exploring clusters of conserved residues in protein structures. <i>Nucleic Acids Research</i> , 2010 , 38, W398-401	20.1	10
59	Applying the Naïve Bayes classifier with kernel density estimation to the prediction of protein-protein interaction sites. <i>Bioinformatics</i> , 2010 , 26, 1841-8	7.2	144
58	Detecting subtle functional differences in ketopantoate reductase and related enzymes using a rule-based approach with sequence-structure homology recognition scores. <i>Protein Engineering, Design and Selection</i> , 2010 , 23, 859-69	1.9	1
57	On nucleotide solvent accessibility in RNA structure. <i>Gene</i> , 2010 , 463, 41-8	3.8	8
56	Network based analysis of hepatitis C virus core and NS4B protein interactions. <i>Molecular BioSystems</i> , 2010 , 6, 2539-53		44
55	Integrated prediction of one-dimensional structural features and their relationships with conformational flexibility in helical membrane proteins. <i>BMC Bioinformatics</i> , 2010 , 11, 533	3.6	5
54	Creation of lysine-deficient mutant lymphotoxin-alpha with receptor selectivity by using a phage display system. <i>Biomaterials</i> , 2010 , 31, 1935-43	15.6	11
53	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, 2369-84	4.2	6
52	A structural dissection of amino acid substitutions in helical transmembrane proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 2895-907	4.2	9
51	Molecular basis for SUMOylation-dependent regulation of DNA binding activity of heat shock factor 2. <i>Journal of Biological Chemistry</i> , 2009 , 284, 2435-47	5.4	35
50	Lipophobicity and the residue environments of the transmembrane alpha-helical bundle. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 32-49	4.2	12
49	Prediction of mono- and di-nucleotide-specific DNA-binding sites in proteins using neural networks. <i>BMC Structural Biology</i> , 2009 , 9, 30	2.7	32
48	2P-238 Functional classification of enzymes by clustering of subsequences consisting of active sites and ligand interaction sites(Bioinformatics:Functional genomics,The 47th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2009 , 49, S144	0	
47	2P-243 The prediction of protein-protein interaction sites in sequences using a naive bayes classifier with a kernel density estimation(Bioinformatics:Functional genomics,The 47th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2009 , 49, S145	0	

46	A phylogenomic profile of hemerythrins, the nonheme diiron binding respiratory proteins. <i>BMC Evolutionary Biology</i> , 2008 , 8, 244	3	41
45	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, 689-98	1.9	4
44	<i>Drosophila</i> neurotrophins reveal a common mechanism for nervous system formation. <i>PLoS Biology</i> , 2008 , 6, e284	9.7	86
43	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, 760-74	2.8	29
42	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	15.1	349
41	A model of globin evolution. <i>Gene</i> , 2007 , 398, 132-42	3.8	90
40	FlyMine: an integrated database for <i>Drosophila</i> and <i>Anopheles</i> genomics. <i>Genome Biology</i> , 2007 , 8, R12918.3	18.3	260
39	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, 409-19	1.9	10
38	The guanidino-group modifying enzymes: structural basis for their diversity and commonality. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 1010-23	4.2	42
37	The common phospholipid-binding activity of the N-terminal domains of PEX1 and VCP/p97. <i>FEBS Journal</i> , 2006 , 273, 4959-71	5.7	24
36	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> , 2005 , 208, 213-27	2.3	107
35	Amino-Acid Substitutions In Membrane Proteins: Applications To Homology Recognition And Comparative Modelling. <i>BMC Bioinformatics</i> , 2005 , 6, S9	3.6	2
34	Functional restraints on the patterns of amino acid substitutions: application to sequence-structure homology recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 722-31	4.2	13
33	Distinct protein interfaces in transmembrane domains suggest an in vivo folding model. <i>Protein Science</i> , 2004 , 13, 3028-37	6.3	7
32	HOMSTRAD: recent developments of the Homologous Protein Structure Alignment Database. <i>Nucleic Acids Research</i> , 2004 , 32, D203-7	20.1	74
31	A model of a transmembrane drug-efflux pump from Gram-negative bacteria. <i>FEBS Letters</i> , 2004 , 578, 5-9	3.8	69
30	Fold recognition for drug discovery. <i>Drug Discovery Today: TARGETS</i> , 2004 , 3, 18-23		8
29	Cylindrical channels from concave helices. <i>Science</i> , 2003 , 299, 661-2	33.3	4

28	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, 505-10	3.8	11
27	The export of coat protein from enteroaggregative Escherichia coli by a specific ATP-binding cassette transporter system. <i>Journal of Biological Chemistry</i> , 2003 , 278, 45680-9	5.4	125
26	A Novel Superfamily that Catalyzes the Modification of Arginine. <i>Seibutsu Butsuri</i> , 2003 , 43, 97-100	0	1
25	Structure of the periplasmic domain of Pseudomonas aeruginosa TolA: evidence for an evolutionary relationship with the TonB transporter protein. <i>EMBO Journal</i> , 2002 , 21, 4207-18	13	45
24	The SWIB and the MDM2 domains are homologous and share a common fold. <i>Bioinformatics</i> , 2002 , 18, 626-30	7.2	29
23	A family of proteins related to Spätzle, the toll receptor ligand, are encoded in the Drosophila genome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 71-80	4.2	64
22	A novel superfamily of enzymes that catalyze the modification of guanidino groups. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 465-8	10.3	104
21	FUGUE: sequence-structure homology recognition using environment-specific substitution tables and structure-dependent gap penalties. <i>Journal of Molecular Biology</i> , 2001 , 310, 243-57	6.5	1102
20	Crystallographer's Challenge in the 21st Century. 3. Frontier of Protein Crystallography. From Genome to Structure: Challenges in Structural Bioinformatics.. <i>Nihon Kessho Gakkaishi</i> , 2001 , 43, 55-62	0	
19	Structural genomics: an overview. <i>Progress in Biophysics and Molecular Biology</i> , 2000 , 73, 289-95	4.7	35
18	Characterisation of the gene for Drosophila amphiphysin. <i>Gene</i> , 2000 , 241, 167-74	3.8	12
17	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, 2308-13	11.5	259
16	A six-stranded double-psi beta barrel is shared by several protein superfamilies. <i>Structure</i> , 1999 , 7, 227-36	3.2	102
15	N-ethylmaleimide-sensitive fusion protein (NSF) and CDC48 confirmed as members of the double-psi beta-barrel aspartate decarboxylase/formate dehydrogenase family. <i>Structure</i> , 1999 , 7, R215-6	5.2	6
14	An iterative structure-assisted approach to sequence alignment and comparative modeling 1999 , 37, 55-60		29
13	The insulin receptor: from protein sequence to structure. <i>Biochemical Society Transactions</i> , 1999 , 27, 715-26	5.1	33
12	Watching the Rise of Structural Genomics.. <i>Seibutsu Butsuri</i> , 1999 , 39, 119-122	0	1
11	Getting knotted: a model for the structure and activation of Spätzle. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 239-42	10.3	90

10	CAMPASS: a database of structurally aligned protein superfamilies. <i>Structure</i> , 1998 , 6, 1087-94	5.2	64
9	HOMSTRAD: a database of protein structure alignments for homologous families. <i>Protein Science</i> , 1998 , 7, 2469-71	6.3	421
8	Protein three-dimensional structural databases: domains, structurally aligned homologues and superfamilies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1168-77		5
7	A third fibronectin type III domain in the extracellular region of the insulin receptor family. <i>FEBS Letters</i> , 1998 , 441, 331-6	3.8	24
6	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, 1083-92	1.9	24
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