

Kenji Mizuguchi

List of Publications by Citations

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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 | 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 |
| 170 | HOMSTRAD: a database of protein structure alignments for homologous families. <i>Protein Science</i> , 1998 , 7, 2469-71 | 6.3 | 421 |
| 169 | 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 |
| 168 | FlyMine: an integrated database for Drosophila and Anopheles genomics. <i>Genome Biology</i> , 2007 , 8, R12918.3 | 18.3 | 260 |
| 167 | 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 |
| 166 | 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 |
| 165 | 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 |
| 164 | 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 |
| 163 | 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 |
| 162 | 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 |
| 161 | A six-stranded double-psi beta barrel is shared by several protein superfamilies. <i>Structure</i> , 1999 , 7, 227-36 | 3.2 | 102 |
| 160 | Blockade of TLR3 protects mice from lethal radiation-induced gastrointestinal syndrome. <i>Nature Communications</i> , 2014 , 5, 3492 | 17.4 | 96 |
| 159 | TargetMine, an integrated data warehouse for candidate gene prioritisation and target discovery. <i>PLoS ONE</i> , 2011 , 6, e17844 | 3.7 | 93 |
| 158 | Getting knotted: a model for the structure and activation of SpEzle. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 239-42 | 10.3 | 90 |
| 157 | A model of globin evolution. <i>Gene</i> , 2007 , 398, 132-42 | 3.8 | 90 |
| 156 | Drosophila neurotrophins reveal a common mechanism for nervous system formation. <i>PLoS Biology</i> , 2008 , 6, e284 | 9.7 | 86 |
| 155 | HOMSTRAD: recent developments of the Homologous Protein Structure Alignment Database. <i>Nucleic Acids Research</i> , 2004 , 32, D203-7 | 20.1 | 74 |

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| 154 | Comparison of spatial arrangements of secondary structural elements in proteins. <i>Protein Engineering, Design and Selection</i> , 1995 , 8, 353-62 | 1.9 | 72 |
| 153 | A model of a transmembrane drug-efflux pump from Gram-negative bacteria. <i>FEBS Letters</i> , 2004 , 578, 5-9 | 3.8 | 69 |
| 152 | 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 |
| 151 | CAMPASS: a database of structurally aligned protein superfamilies. <i>Structure</i> , 1998 , 6, 1087-94 | 5.2 | 64 |
| 150 | A family of proteins related to SpEzle, the toll receptor ligand, are encoded in the Drosophila genome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 71-80 | 4.2 | 64 |
| 149 | Partner-aware prediction of interacting residues in protein-protein complexes from sequence data. <i>PLoS ONE</i> , 2011 , 6, e29104 | 3.7 | 55 |
| 148 | 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 |
| 147 | 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 |
| 146 | Homology-based prediction of interactions between proteins using Averaged One-Dependence Estimators. <i>BMC Bioinformatics</i> , 2014 , 15, 213 | 3.6 | 44 |
| 145 | Network based analysis of hepatitis C virus core and NS4B protein interactions. <i>Molecular BioSystems</i> , 2010 , 6, 2539-53 | | 44 |
| 144 | Seeking significance in three-dimensional protein structure comparisons. <i>Current Opinion in Structural Biology</i> , 1995 , 5, 377-82 | 8.1 | 44 |
| 143 | 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 |
| 142 | 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 |
| 141 | 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 |
| 140 | A phylogenomic profile of hemerythrins, the nonheme diiron binding respiratory proteins. <i>BMC Evolutionary Biology</i> , 2008 , 8, 244 | 3 | 41 |
| 139 | Targeting BIG3-PHB2 interaction to overcome tamoxifen resistance in breast cancer cells. <i>Nature Communications</i> , 2013 , 4, 2443 | 17.4 | 39 |
| 138 | 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 |
| 137 | Profiles of microRNA networks in intestinal epithelial cells in a mouse model of colitis. <i>Scientific Reports</i> , 2015 , 5, 18174 | 4.9 | 36 |

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| 136 | 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 |
| 135 | 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 |
| 134 | Structural genomics: an overview. <i>Progress in Biophysics and Molecular Biology</i> , 2000 , 73, 289-95 | 4.7 | 35 |
| 133 | The insulin receptor: from protein sequence to structure. <i>Biochemical Society Transactions</i> , 1999 , 27, 715-26 | 5.1 | 33 |
| 132 | Prediction of dinucleotide-specific RNA-binding sites in proteins. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 13, S5 | 3.6 | 32 |
| 131 | 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 |
| 130 | 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 |
| 129 | The SWIB and the MDM2 domains are homologous and share a common fold. <i>Bioinformatics</i> , 2002 , 18, 626-30 | 7.2 | 29 |
| 128 | An iterative structure-assisted approach to sequence alignment and comparative modeling 1999 , 37, 55-60 | | 29 |
| 127 | Collective motions in proteins investigated by X-ray diffuse scattering. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 18, 34-48 | 4.2 | 29 |
| 126 | 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 |
| 125 | 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 |
| 124 | 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 |
| 123 | Ligand-induced Ordering of the C-terminal Tail Primes STING for Phosphorylation by TBK1. <i>EBioMedicine</i> , 2016 , 9, 87-96 | 8.8 | 26 |
| 122 | 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 |
| 121 | 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 |
| 120 | Essential Role of CARD14 in Murine Experimental Psoriasis. <i>Journal of Immunology</i> , 2018 , 200, 71-81 | 5.3 | 25 |
| 119 | Crystal structure of FtsA from <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2014 , 588, 1879-85 | 3.8 | 24 |

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|-----|---|------|----|
| 118 | Functional site plasticity in domain superfamilies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 874-89 | 4 | 24 |
| 117 | Prediction of detailed enzyme functions and identification of specificity determining residues by random forests. <i>PLoS ONE</i> , 2014 , 9, e84623 | 3.7 | 24 |
| 116 | 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 |
| 115 | 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 |
| 114 | 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 |
| 113 | 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 |
| 112 | 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 |
| 111 | Systems Biology Approaches to a Rational Drug Discovery Paradigm. <i>Current Topics in Medicinal Chemistry</i> , 2016 , 16, 1009-25 | 3 | 22 |
| 110 | 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 |
| 109 | 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 |
| 108 | Toxygates: interactive toxicity analysis on a hybrid microarray and linked data platform. <i>Bioinformatics</i> , 2013 , 29, 3080-6 | 7.2 | 20 |
| 107 | Integrated pathway clusters with coherent biological themes for target prioritisation. <i>PLoS ONE</i> , 2014 , 9, e99030 | 3.7 | 19 |
| 106 | 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 |
| 105 | The chemotherapeutic agent DMXAA as a unique IRF3-dependent type-2 vaccine adjuvant. <i>PLoS ONE</i> , 2013 , 8, e60038 | 3.7 | 18 |
| 104 | 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 |
| 103 | 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 |
| 102 | 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 |
| 101 | Data Curation can Improve the Prediction Accuracy of Metabolic Intrinsic Clearance. <i>Molecular Informatics</i> , 2019 , 38, e1800086 | 3.8 | 14 |

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| 100 | 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 |
| 99 | The TargetMine Data Warehouse: Enhancement and Updates. <i>Frontiers in Genetics</i> , 2019 , 10, 934 | 4.5 | 12 |
| 98 | 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 |
| 97 | 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 |
| 96 | 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 |
| 95 | 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 |
| 94 | Characterisation of the gene for Drosophila amphiphysin. <i>Gene</i> , 2000 , 241, 167-74 | 3.8 | 12 |
| 93 | 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 |
| 92 | 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 |
| 91 | A-kinase anchoring protein BIG3 coordinates oestrogen signalling in breast cancer cells. <i>Nature Communications</i> , 2017 , 8, 15427 | 17.4 | 11 |
| 90 | 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 |
| 89 | 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 |
| 88 | Interactive Toxicogenomics: Gene set discovery, clustering and analysis in Toxygates. <i>Scientific Reports</i> , 2017 , 7, 1390 | 4.9 | 10 |
| 87 | 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 |
| 86 | CCRXP: exploring clusters of conserved residues in protein structures. <i>Nucleic Acids Research</i> , 2010 , 38, W398-401 | 20.1 | 10 |
| 85 | 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 |
| 84 | 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 |
| 83 | 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 |

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| 82 | Brefeldin A-inhibited guanine nucleotide-exchange protein 3 (BIG3) is predicted to interact with its partner through an ARM-type β -helical structure. <i>BMC Research Notes</i> , 2014 , 7, 435 | 2.3 | 9 |
| 81 | Predicting conformational ensembles and genome-wide transcription factor binding sites from DNA sequences. <i>Scientific Reports</i> , 2017 , 7, 4071 | 4.9 | 9 |
| 80 | 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 |
| 79 | Prediction of the secondary structure of short DNA aptamers. <i>Biophysics and Physicobiology</i> , 2019 , 16, 287-294 | 1.4 | 9 |
| 78 | Classification of idiopathic interstitial pneumonias using anti-myxovirus resistance-protein 1 autoantibody. <i>Scientific Reports</i> , 2017 , 7, 43201 | 4.9 | 8 |
| 77 | On nucleotide solvent accessibility in RNA structure. <i>Gene</i> , 2010 , 463, 41-8 | 3.8 | 8 |
| 76 | Fold recognition for drug discovery. <i>Drug Discovery Today: TARGETS</i> , 2004 , 3, 18-23 | | 8 |
| 75 | Distinct protein interfaces in transmembrane domains suggest an in vivo folding model. <i>Protein Science</i> , 2004 , 13, 3028-37 | 6.3 | 7 |
| 74 | Novel anti-flavivirus drugs targeting the nucleolar distribution of core protein. <i>Virology</i> , 2020 , 541, 41-53.6 | 5.6 | 7 |
| 73 | B cell-intrinsic MyD88 signaling controls IFN- β -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 |
| 72 | 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} | 7.4 | 6 |
| 71 | 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 |
| 70 | Sagace: a web-based search engine for biomedical databases in Japan. <i>BMC Research Notes</i> , 2012 , 5, 604 | 2.3 | 6 |
| 69 | Lipid recognition propensities of amino acids in membrane proteins from atomic resolution data. <i>BMC Biophysics</i> , 2011 , 4, 21 | 0 | 6 |
| 68 | 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 |
| 67 | 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, R215-26 ^{5.2} | 5.2 | 6 |
| 66 | 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 |
| 65 | 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 |

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|----|---|------|---|
| 64 | 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 |
| 63 | 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 |
| 62 | 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 |
| 61 | 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 |
| 60 | 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 |
| 59 | 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 |
| 58 | 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 |
| 57 | 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 |
| 56 | Protein three-dimensional structural databases: domains, structurally aligned homologues and superfamilies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1168-77 | | 5 |
| 55 | A prospective compound screening contest identified broader inhibitors for Sirtuin 1. <i>Scientific Reports</i> , 2019 , 9, 19585 | 4.9 | 5 |
| 54 | 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 |
| 53 | 2017 , | | 4 |
| 52 | 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 |
| 51 | 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 |
| 50 | Cylindrical channels from concave helices. <i>Science</i> , 2003 , 299, 661-2 | 33.3 | 4 |
| 49 | Relationship between Nutrient Intake and Human Gut Microbiota in Monozygotic Twins. <i>Medicina (Lithuania)</i> , 2021 , 57, | 3.1 | 4 |
| 48 | 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 |
| 47 | 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 |

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| 46 | 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 |
| 45 | 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 |
| 44 | Selective covalent targeting of SARS-CoV-2 main protease by enantiopure chlorofluoroacetamide.. <i>Chemical Science</i> , 2022 , 13, 3027-3034 | 9.4 | 3 |
| 43 | Update of the GRIP web service. <i>Journal of Receptor and Signal Transduction Research</i> , 2020 , 40, 348-356 | 2.6 | 2 |
| 42 | 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 |
| 41 | Bioinformatics Approaches for Analysis of Protein-Ligand Interactions | 267-299 | 2 |
| 40 | Amino-Acid Substitutions In Membrane Proteins: Applications To Homology Recognition And Comparative Modelling. <i>BMC Bioinformatics</i> , 2005 , 6, S9 | 3.6 | 2 |
| 39 | Group IIA secreted phospholipase A2 controls skin carcinogenesis and psoriasis by shaping the gut microbiota.. <i>JCI Insight</i> , 2022 , 7, | 9.9 | 2 |
| 38 | Assessing drug target suitability using TargetMine. <i>F1000Research</i> , 2019 , 8, 233 | 3.6 | 2 |
| 37 | MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. <i>PLoS ONE</i> , 2020 , 15, e0243609 | 3.7 | 2 |
| 36 | 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 |
| 35 | Integrative Analysis Reveals Common and Unique Roles of Tetraspanins in Fibrosis and Emphysema. <i>Frontiers in Genetics</i> , 2020 , 11, 585998 | 4.5 | 1 |
| 34 | Integrative Analysis of Multi-Omics Data | 2019, 194-199 | 1 |
| 33 | Network-Based Analysis for Biological Discovery | 2019, 283-291 | 1 |
| 32 | Network-Based Analysis of Host-Pathogen Interactions | 2019, 932-937 | 1 |
| 31 | 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 |
| 30 | 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 |
| 29 | 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 |

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|----|---|-----|---|
| 28 | Deep Learning Prediction of Adverse Drug Reactions in Drug Discovery Using Open TARGETs and FAERS Databases 2021 , 1, | | 1 |
| 27 | A Novel Superfamily that Catalyzes the Modification of Arginine. <i>Seibutsu Butsuri</i> , 2003 , 43, 97-100 | 0 | 1 |
| 26 | Assessing drug target suitability using TargetMine. <i>F1000Research</i> , 2019 , 8, 233 | 3.6 | 1 |
| 25 | Data Warehousing with TargetMine for Omics Data Analysis. <i>Methods in Molecular Biology</i> , 2019 , 1986, 35-64 | 1.4 | 1 |
| 24 | Watching the Rise of Structural Genomics.. <i>Seibutsu Butsuri</i> , 1999 , 39, 119-122 | 0 | 1 |
| 23 | 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 |
| 22 | Panomicon: A web-based environment for interactive, visual analysis of multi-omics data. <i>Heliyon</i> , 2020 , 6, e04618 | 3.6 | 1 |
| 21 | 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 |
| 20 | Clomipramine suppresses ACE2-mediated SARS-CoV-2 entry | | 1 |
| 19 | 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 |
| 18 | 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 |
| 17 | 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 |
| 16 | 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 |
| 15 | 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 |
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