

# Kentaro Tomii

## List of Publications by Year in descending order

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Version: 2024-02-01

88  
papers

4,340  
citations

185998

28  
h-index

123241

61  
g-index

94  
all docs

94  
docs citations

94  
times ranked

7177  
citing authors

#	ARTICLE	IF	CITATIONS
1	Parallelization of MAFFT for large-scale multiple sequence alignments. <i>Bioinformatics</i> , 2018, 34, 2490-2492.	1.8	704
2	MitoFates: Improved Prediction of Mitochondrial Targeting Sequences and Their Cleavage Sites*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1113-1126.	2.5	470
3	Compoundâ€protein interaction prediction with end-to-end learning of neural networks for graphs and sequences. <i>Bioinformatics</i> , 2019, 35, 309-318.	1.8	377
4	Analysis of amino acid indices and mutation matrices for sequence comparison and structure prediction of proteins. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 27-36.	1.0	317
5	Application of the MAFFT sequence alignment program to large dataâ€reexamination of the usefulness of chained guide trees. <i>Bioinformatics</i> , 2016, 32, 3246-3251.	1.8	276
6	CENP-T provides a structural platform for outer kinetochore assembly. <i>EMBO Journal</i> , 2013, 32, 424-436.	3.5	181
7	Molecular architecture of the active mitochondrial protein gate. <i>Science</i> , 2015, 349, 1544-1548.	6.0	169
8	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	1.5	148
9	Tam41 Is a CDP-Diacylglycerol Synthase Required for Cardiolipin Biosynthesis in Mitochondria. <i>Cell Metabolism</i> , 2013, 17, 709-718.	7.2	135
10	A Comparative Analysis of ABC Transporters in Complete Microbial Genomes. <i>Genome Research</i> , 1998, 8, 1048-1059.	2.4	126
11	Mammalian NUMT insertion is non-random. <i>Nucleic Acids Research</i> , 2012, 40, 9073-9088.	6.5	108
12	FORTE: a profile-profile comparison tool for protein fold recognition. <i>Bioinformatics</i> , 2004, 20, 594-595.	1.8	88
13	Class of cyclic ribosomal peptide synthetic genes in filamentous fungi. <i>Fungal Genetics and Biology</i> , 2016, 86, 58-70.	0.9	84
14	Structure of the N-terminal Domain of PEX1 AAA-ATPase. <i>Journal of Biological Chemistry</i> , 2004, 279, 50060-50068.	1.6	71
15	PoSSuM: a database of similar protein-ligand binding and putative pockets. <i>Nucleic Acids Research</i> , 2012, 40, D541-D548.	6.5	62
16	Mitochondrial sorting and assembly machinery operates by Î²-barrel switching. <i>Nature</i> , 2021, 590, 163-169.	13.7	60
17	Predicting mostly disordered proteins by using structure-unknown protein data. <i>BMC Bioinformatics</i> , 2007, 8, 78.	1.2	57
18	Origin and Evolutionary Alteration of the Mitochondrial Import System in Eukaryotic Lineages. <i>Molecular Biology and Evolution</i> , 2017, 34, 1574-1586.	3.5	52

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19	Evolutionary analyses of caspase-8 and its paralogs: Deep origins of the apoptotic signaling pathways. <i>BioEssays</i> , 2015, 37, 767-776.	1.2	48
20	Tyrosine phosphorylation of the GARU E3 ubiquitin ligase promotes gibberellin signalling by preventing GID1 degradation. <i>Nature Communications</i> , 2017, 8, 1004.	5.8	47
21	Protein structure prediction using a variety of profile libraries and 3D verification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 114-121.	1.5	45
22	Functional conservation of the apoptotic machinery from coral to man: the diverse and complex Bcl-2 and caspase repertoires of <i>Acropora millepora</i> . <i>BMC Genomics</i> , 2016, 17, 62.	1.2	45
23	Revisiting amino acid substitution matrices for identifying distantly related proteins. <i>Bioinformatics</i> , 2014, 30, 317-325.	1.8	41
24	Novel Mechanism of Interaction of p85 Subunit of Phosphatidylinositol 3-Kinase and ErbB3 Receptor-derived Phosphotyrosyl Peptides. <i>Journal of Biological Chemistry</i> , 2005, 280, 1321-1326.	1.6	40
25	Identification of Cargo Proteins Specific for the Nucleocytoplasmic Transport Carrier Transportin by Combination of an in Vitro Transport System and Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)-based Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 145-157.	2.5	39
26	A Novel Antiviral Target Structure Involved in the RNA Binding, Dimerization, and Nuclear Export Functions of the Influenza A Virus Nucleoprotein. <i>PLoS Pathogens</i> , 2015, 11, e1005062.	2.1	34
27	Convergent evolution in structural elements of proteins investigated using cross profile analysis. <i>BMC Bioinformatics</i> , 2012, 13, 11.	1.2	33
28	Ligand heterogeneity of the cysteine protease binding protein family in the parasitic protist <i>Entamoeba histolytica</i> . <i>International Journal for Parasitology</i> , 2014, 44, 625-635.	1.3	32
29	DeepECA: an end-to-end learning framework for protein contact prediction from a multiple sequence alignment. <i>BMC Bioinformatics</i> , 2020, 21, 10.	1.2	31
30	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
31	The Apoptotic Initiator Caspase-8: Its Functional Ubiquity and Genetic Diversity during Animal Evolution. <i>Molecular Biology and Evolution</i> , 2014, 31, 3282-3301.	3.5	25
32	EzCatDB: the enzyme reaction database, 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D453-D458.	6.5	24
33	AIG1 affects in vitro and in vivo virulence in clinical isolates of <i>Entamoeba histolytica</i> . <i>PLoS Pathogens</i> , 2018, 14, e1006882.	2.1	24
34	PDB-scale analysis of known and putative ligand-binding sites with structural sketches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 747-763.	1.5	23
35	Identification of new abscisic acid receptor agonists using a wheat cell-free based drug screening system. <i>Scientific Reports</i> , 2018, 8, 4268.	1.6	23
36	Simple adjustment of the sequence weight algorithm remarkably enhances PSI-BLAST performance. <i>BMC Bioinformatics</i> , 2017, 18, 288.	1.2	22

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37	Distinct immune cell dynamics correlate with the immunogenicity and reactogenicity of SARS-CoV-2 mRNA vaccine. <i>Cell Reports Medicine</i> , 2022, 3, 100631.	3.3	22
38	A Novel Mitosomal Î²-Barrel Outer Membrane Protein in <i>Entamoeba</i> . <i>Scientific Reports</i> , 2015, 5, 8545.	1.6	16
39	Comprehensive analysis of PPARÎ³ agonist activities of stereo-, regio-, and enantio-isomers of hydroxyoctadecadienoic acids. <i>Bioscience Reports</i> , 2020, 40, .	1.1	16
40	<scp>Rab7D</scp> small <scp>GTPase</scp> is involved in phagoô€trogocytosis and cytoskeletal reorganization in the enteric protozoan <scp> <i>Entamoeba histolytica</i> </scp>. <i>Cellular Microbiology</i> , 2021, 23, e13267.	1.1	14
41	HMGB1 signaling phosphorylates Ku70 and impairs DNA damage repair in Alzheimerâ€™s disease pathology. <i>Communications Biology</i> , 2021, 4, 1175.	2.0	14
42	Neural networks for protein structure and function prediction and dynamic analysis. <i>Biophysical Reviews</i> , 2020, 12, 569-573.	1.5	13
43	SAHG, a comprehensive database of predicted structures of all human proteins. <i>Nucleic Acids Research</i> , 2011, 39, D487-D493.	6.5	12
44	Visualization of conformational distribution of short to medium size segments in globular proteins and identification of local structural motifs. <i>Protein Science</i> , 2005, 14, 1253-1265.	3.1	11
45	Templateâ€based quaternary structure prediction of proteins using enhanced profileâ€profile alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 274-282.	1.5	10
46	ScreenCap3: Improving prediction of caspaseâ€ cleavage sites using experimentally verified noncleavage sites. <i>Proteomics</i> , 2014, 14, 2042-2046.	1.3	9
47	Identification of hepta-histidine as a candidate drug for Huntingtonâ€™s disease by in silico-in vitro- in vivo-integrated screens of chemical libraries. <i>Scientific Reports</i> , 2016, 6, 33861.	1.6	9
48	Genome-Wide Analysis of Known and Potential Tetraspanins in <i>Entamoeba histolytica</i> . <i>Genes</i> , 2019, 10, 885.	1.0	8
49	Hinge-Deficient IgG1 Fc Fusion: Application to Human Lactoferrin. <i>Molecular Pharmaceutics</i> , 2017, 14, 3025-3035.	2.3	7
50	Discrimination of Golgi Type II Membrane Proteins Based on Their Hydropathy Profiles and the Amino Acid Propensities of Their Transmembrane Regions. <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 82-88.	0.6	6
51	Accurate Classification of Biological and non-Biological Interfaces in Protein Crystal Structures using Subtle Covariation Signals. <i>Scientific Reports</i> , 2019, 9, 12603.	1.6	6
52	Fine-tuning of protein domain boundary by minimizing potential coiled coil regions. <i>Journal of Biomolecular NMR</i> , 2006, 37, 53-63.	1.6	5
53	Protein-segment universe exhibiting transitions at intermediate segment length in conformational subspaces. <i>BMC Structural Biology</i> , 2008, 8, 37.	2.3	5
54	Conservation of structure and function in vertebrate c-FLIP proteins despite rapid evolutionary change. <i>Biochemistry and Biophysics Reports</i> , 2015, 3, 175-189.	0.7	5

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55	Effects of the difference in similarity measures on the comparison of ligand-binding pockets using a reduced vector representation of pockets. <i>Biophysics and Physicobiology</i> , 2016, 13, 139-147.	0.5	5
56	Systematic Exploration of an Efficient Amino Acid Substitution Matrix: MIQS. <i>Methods in Molecular Biology</i> , 2016, 1415, 211-223.	0.4	4
57	Protein ligand-binding site comparison by a reduced vector representation derived from multidimensional scaling of generalized description of binding sites. <i>Methods</i> , 2016, 93, 35-40.	1.9	4
58	Novel lineage-specific transmembrane $\beta$ -barrel proteins in the endoplasmic reticulum of <i>Entamoeba histolytica</i> . <i>FEBS Journal</i> , 2019, 286, 3416-3432.	2.2	4
59	Localization Prediction and Structure-Based In Silico Analysis of Bacterial Proteins: With Emphasis on Outer Membrane Proteins. <i>Methods in Molecular Biology</i> , 2013, 939, 115-140.	0.4	3
60	Crim1C140S mutant mice reveal the importance of cysteine 140 in the internal region 1 of CRIM1 for its physiological functions. <i>Mammalian Genome</i> , 2019, 30, 329-338.	1.0	3
61	A New Variational Framework for Rigid-Body Alignment. <i>Lecture Notes in Computer Science</i> , 2004, , 171-179.	1.0	3
62	Identification of Glycosyltransferases Focusing on Golgi Transmembrane Region. <i>Trends in Glycoscience and Glycotechnology</i> , 2007, 19, 41-47.	0.0	3
63	Crystallographic characterization of the N-terminal domain of PEX1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2098-2099.	2.5	2
64	Import of <i>Entamoeba histolytica</i> Mitosomal ATP Sulfurylase Relies on Internal Targeting Sequences. <i>Microorganisms</i> , 2020, 8, 1229.	1.6	2
65	CASP6 Meeting Report "Japanese Predictors Achieved Good Scores". <i>Seibutsu Butsuri</i> , 2005, 45, 165-167.	0.0	2
66	Structural Modeling and Ligand-Binding Prediction for Analysis of Structure-Unknown and Function-Unknown Proteins Using FORTE Alignment and PoSSuM Pocket Search. <i>Methods in Molecular Biology</i> , 2020, 2165, 1-11.	0.4	2
67	1P267 Application of novel amino acid substitution matrix, MIQS, to the MAFFT multiple sequence aligner(22C. <i>Bioinformatics:Comparative genomics,Poster,The 52nd Annual Meeting of the Biophysical</i> ) Tj ETQq1 100784314 rgBT /O		
68	Protein sequence-similarity search acceleration using a heuristic algorithm with a sensitive matrix. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 147-154.	1.2	1
69	Designing better diffracting crystals of biotin carboxyl carrier protein from <i>Pyrococcus horikoshii</i> by a mutation based on the crystal-packing propensity of amino acids. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 757-766.	1.1	1
70	Protein Properties. , 2019, , 28-33.		1
71	An ensemble reweighting method for combining the information of experiments and simulations. <i>Chemical Physics Letters</i> , 2021, 779, 138821.	1.2	1
72	Protein Structure Prediction Using a Profile-Profile Comparison Method: FORTE. <i>Seibutsu Butsuri</i> , 2006, 46, 106-110.	0.0	1

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73	Application of Homology Modeling by Enhanced Profile-Profile Alignment and Flexible-Fitting Simulation to Cryo-EM Based Structure Determination. International Journal of Molecular Sciences, 2022, 23, 1977.	1.8	1
74	PreBINDS: An Interactive Web Tool to Create Appropriate Datasets for Predicting Compound-Protein Interactions. Frontiers in Molecular Biosciences, 2021, 8, 758480.	1.6	1
75	Crystal structure of Tam41 cytidine diphosphate diacylglycerol synthase from a Firmicutes bacterium. Journal of Biochemistry, 2022, 171, 429-441.	0.9	1
76	1P323 Molecular basis of microtubule disassembly mechanism regulated by katanin p60(10.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 2006, 46, S227.	0.0	0
77	2P450 Correlation between sequence profiles and profiles derived from local structural classifications(48. Bioinformatics, genomics and proteomics (II),Poster Session,Abstract,Meeting) Tj ETQq1 1 0.784304 rgBTφOverlock	0.0	0
78	1P241 An exhaustive modeling and evaluation system in protein 3D structure prediction pipeline FORTE-SUITE(Bioinformatics-structural genomics,Poster Presentations). Seibutsu Butsuri, 2007, 47, S83.	0.0	0
79	2P-009 Identification of essential structural variables for medium-size protein-segment and application to structural class assignment(The 46th Annual Meeting of the Biophysical Society of) Tj ETQq1 1 0.784304 rgBTφOverlock	0.0	0
80	2P-034 Two types universality of a fold universe of 50-residue segments(The 46th Annual Meeting of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.0	0
81	Universal partitioning of the hierarchical fold network of 50-residue segments in proteins. BMC Structural Biology, 2009, 9, 34.	2.3	0
82	2P029 An Exhaustive Search of Known and Unknown Protein-Ligand Binding Sites with A Fast Alignment-Free Method(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S87.	0.0	0
83	2PT005 PoSSuM : a database for searching similar pairs of known and potential ligand-binding sites in proteins(The 50th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2012, 52, S120.	0.0	0
84	1P266 Improved prediction of mitochondrial presequence for detecting undiscovered mitochondrial proteins(22B. Bioinformatics:Functional genomics,Poster,The 52nd Annual Meeting of the Biophysical) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.0	0
85	Refinement of Amino Acid Substitution Matrix for Detecting Distant Relationships of Proteins. Seibutsu Butsuri, 2015, 55, 133-136.	0.0	0
86	The Structure of N-terminal Domain from PEX1 Reveals Its Evolutionary Relationship to Type II AAA-ATPases. Seibutsu Butsuri, 2006, 46, 159-163.	0.0	0
87	Convergent Evolution of Protein Segments Detected in Cross Profile Analysis. Seibutsu Butsuri, 2013, 53, 101-102.	0.0	0
88	Prediction of Structures and Functions of Proteins by Database Searching.. Japanese Journal of Thrombosis and Hemostasis, 1999, 10, 285-289.	0.1	0