Kentaro Tomii

List of Publications by Year
in descending order

88	4,340	186265 28	123424 61
papers	citations	h-index	g-index

94	94	94	7177
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Application of Homology Modeling by Enhanced Profileâ€“Profile Alignment and Flexible-Fitting Simulation to Cryo-EM Based Structure Determination. International Journal of Molecular Sciences, 2022, 23, 1977.	4.1	1
2	Crystal structure of Tam41 cytidine diphosphate diacylglycerol synthase from a Firmicutes bacterium. Journal of Biochemistry, 2022, 171, 429-441.	1.7	1
3	Distinct immune cell dynamics correlate with the immunogenicity and reactogenicity of SARS-CoV-2 mRNA vaccine. Cell Reports Medicine, 2022, 3, 100631.	6.5	22
4	Mitochondrial sorting and assembly machinery operates by Î²-barrel switching. Nature, 2021, 590, 163-169.	27.8	60
5	An ensemble reweighting method for combining the information of experiments and simulations. Chemical Physics Letters, 2021, 779, 138821.	2.6	1
6	<scp>Rab7D</scp> small <scp>GTPase</scp> is involved in phagoâ€trogocytosis and cytoskeletal reorganization in the enteric protozoan <scp> Entamoeba histolytica </scp>. Cellular Microbiology, 2021, 23, e13267.	2.1	14
7	HMGB1 signaling phosphorylates Ku70 and impairs DNA damage repair in Alzheimerâ€™s disease pathology. Communications Biology, 2021, 4, 1175.	4.4	14
8	PreBINDS: An Interactive Web Tool to Create Appropriate Datasets for Predicting Compoundâ€“Protein Interactions. Frontiers in Molecular Biosciences, 2021, 8, 758480.	3.5	1
9	Import of Entamoeba histolytica Mitosomal ATP Sulfurylase Relies on Internal Targeting Sequences. Microorganisms, 2020, 8, 1229.	3.6	2
10	Neural networks for protein structure and function prediction and dynamic analysis. Biophysical Reviews, 2020, 12, 569-573.	3.2	13
11	DeepECA: an end-to-end learning framework for protein contact prediction from a multiple sequence alignment. BMC Bioinformatics, 2020, 21, 10.	2.6	31
12	Comprehensive analysis of PPARÎ³ agonist activities of stereo-, regio-, and enantio-isomers of hydroxyoctadecadienoic acids. Bioscience Reports, 2020, 40, .	2.4	16
13	Structural Modeling and Ligand-Binding Prediction for Analysis of Structure-Unknown and Function-Unknown Proteins Using FORTE Alignment and PoSSuM Pocket Search. Methods in Molecular Biology, 2020, 2165, 1-11.	0.9	2
14	Protein Properties. , 2019, , 28-33.		1
15	Compoundâ€“protein interaction prediction with end-to-end learning of neural networks for graphs and sequences. Bioinformatics, 2019, 35, 309-318.	4.1	377
16	Accurate Classification of Biological and non-Biological Interfaces in Protein Crystal Structures using Subtle Covariation Signals. Scientific Reports, 2019, 9, 12603.	3.3	6
17	Novel lineageâ€specific transmembrane Î²â€barrel proteins in the endoplasmic reticulum of EntamoebaÂhistolytica. FEBS Journal, 2019, 286, 3416-3432.	4.7	4
18	Genome-Wide Analysis of Known and Potential Tetraspanins in Entamoeba histolytica. Genes, 2019, 10, 885.	2.4	8

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19	Crim1C140S mutant mice reveal the importance of cysteine 140 in the internal region 1 of CRIM1 for its physiological functions. Mammalian Genome, 2019, 30, 329-338.	2.2	3
20	Parallelization of MAFFT for large-scale multiple sequence alignments. Bioinformatics, 2018, 34, 2490-2492.	4.1	704
21	Identification of new abscisic acid receptor agonists using a wheat cell-free based drug screening system. Scientific Reports, 2018, 8, 4268.	3.3	23
22	Templateâ€based quaternary structure prediction of proteins using enhanced profileâ€“profile alignments. Proteins: Structure, Function and Bioinformatics, 2018, 86, 274-282.	2.6	10
23	AIG1 affects in vitro and in vivo virulence in clinical isolates of Entamoeba histolytica. PLoS Pathogens, 2018, 14, e1006882.	4.7	24
24	Origin and Evolutionary Alteration of the Mitochondrial Import System in Eukaryotic Lineages. Molecular Biology and Evolution, 2017, 34, 1574-1586.	8.9	52
25	Designing better diffracting crystals of biotin carboxyl carrier protein fromPyrococcus horikoshiiby a mutation based on the crystal-packing propensity of amino acids. Acta Crystallographica Section D: Structural Biology, 2017, 73, 757-766.	2.3	1
26	Tyrosine phosphorylation of the GARU E3 ubiquitin ligase promotes gibberellin signalling by preventing GID1 degradation. Nature Communications, 2017, 8, 1004.	12.8	47
27	Hinge-Deficient IgG1 Fc Fusion: Application to Human Lactoferrin. Molecular Pharmaceutics, 2017, 14, 3025-3035.	4.6	7
28	Simple adjustment of the sequence weight algorithm remarkably enhances PSI-BLAST performance. BMC Bioinformatics, 2017, 18, 288.	2.6	22
29	Application of the MAFFT sequence alignment program to large dataâ€”reexamination of the usefulness of chained guide trees. Bioinformatics, 2016, 32, 3246-3251.	4.1	276
30	Effects of the difference in similarity measures on the comparison of ligand-binding pockets using a reduced vector representation of pockets. Biophysics and Physicobiology, 2016, 13, 139-147.	1.0	5
31	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
32	Protein sequence-similarity search acceleration using a heuristic algorithm with a sensitive matrix. Journal of Structural and Functional Genomics, 2016, 17, 147-154.	1.2	1
33	Systematic Exploration of an Efficient Amino Acid Substitution Matrix: MIQS. Methods in Molecular Biology, 2016, 1415, 211-223.	0.9	4
34	Class of cyclic ribosomal peptide synthetic genes in filamentous fungi. Fungal Genetics and Biology, 2016, 86, 58-70.	2.1	84
35	Identification of hepta-histidine as a candidate drug for Huntingtonâ€™s disease by in silico-in vitro- in vivo-integrated screens of chemical libraries. Scientific Reports, 2016, 6, 33861.	3.3	9
36	Functional conservation of the apoptotic machinery from coral to man: the diverse and complex Bcl-2 and caspase repertoires of Acropora millepora. BMC Genomics, 2016, 17, 62.	2.8	45

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37	Protein ligand-binding site comparison by a reduced vector representation derived from multidimensional scaling of generalized description of binding sites. Methods, 2016, 93, 35-40.	3.8	4
38	A Novel Mitosomal Î²-Barrel Outer Membrane Protein in Entamoeba. Scientific Reports, 2015, 5, 8545.	3.3	16
39	Conservation of structure and function in vertebrate c-FLIP proteins despite rapid evolutionary change. Biochemistry and Biophysics Reports, 2015, 3, 175-189.	1.3	5
40	Evolutionary analyses of caspaseâ€8 and its paralogs: Deep origins of the apoptotic signaling pathways. BioEssays, 2015, 37, 767-776.	2.5	48
41	Refinement of Amino Acid Substitution Matrix for Detecting Distant Relationships of Proteins. Seibutsu Butsuri, 2015, 55, 133-136.	0.1	0
42	EzCatDB: the enzyme reaction database, 2015 update. Nucleic Acids Research, 2015, 43, D453-D458.	14.5	24
43	MitoFates: Improved Prediction of Mitochondrial Targeting Sequences and Their Cleavage Sites*. Molecular and Cellular Proteomics, 2015, 14, 1113-1126.	3.8	470
44	PoSSuM v.2.0: data update and a new function for investigating ligand analogs and target proteins of small-molecule drugs. Nucleic Acids Research, 2015, 43, D392-D398.	14.5	27
45	Molecular architecture of the active mitochondrial protein gate. Science, 2015, 349, 1544-1548.	12.6	169
46	A Novel Antiviral Target Structure Involved in the RNA Binding, Dimerization, and Nuclear Export Functions of the Influenza A Virus Nucleoprotein. PLoS Pathogens, 2015, 11, e1005062.	4.7	34
47	Revisiting amino acid substitution matrices for identifying distantly related proteins. Bioinformatics, 2014, 30, 317-325.	4.1	41
48	ScreenCap3: Improving prediction of caspaseâ€3 cleavage sites using experimentally verified noncleavage sites. Proteomics, 2014, 14, 2042-2046.	2.2	9
49	The Apoptotic Initiator Caspase-8: Its Functional Ubiquity and Genetic Diversity during Animal Evolution. Molecular Biology and Evolution, 2014, 31, 3282-3301.	8.9	25
50	Ligand heterogeneity of the cysteine protease binding protein family in the parasitic protist Entamoeba histolytica. International Journal for Parasitology, 2014, 44, 625-635.	3.1	32
51	1P266 Improved prediction of mitochondrial presequence for detecting undiscovered mitochondrial proteins(22B. Bioinformatics:Functional genomics,Poster,The 52nd Annual Meeting of the Biophysical) Tj ETQq1 1 0.784314 rgBT /Over		
52	1P267 Application of novel amino acid substitution matrix, MIQS, to the MAFFT multiple sequence aligner(22C. Bioinformatics:Comparative genomics,Poster,The 52nd Annual Meeting of the Biophysical) Tj ETQq0 0 0 rgBT /Overlock 10		
53	Tam41 Is a CDP-Diacylglycerol Synthase Required for Cardiolipin Biosynthesis in Mitochondria. Cell Metabolism, 2013, 17, 709-718.	16.2	135
54	Localization Prediction and Structure-Based In Silico Analysis of Bacterial Proteins: With Emphasis on Outer Membrane Proteins. Methods in Molecular Biology, 2013, 939, 115-140.	0.9	3

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55	CENP-T provides a structural platform for outer kinetochore assembly. EMBO Journal, 2013, 32, 424-436.	7.8	181
56	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. Molecular and Cellular Proteomics, 2013, 12, 145-157.	3.8	39
57	Convergent Evolution of Protein Segments Detected in Cross Profile Analysis. Seibutsu Butsuri, 2013, 53, 101-102.	0.1	0
58	PoSSuM: a database of similar protein-ligand binding and putative pockets. Nucleic Acids Research, 2012, 40, D541-D548.	14.5	62
59	Mammalian NUMT insertion is non-random. Nucleic Acids Research, 2012, 40, 9073-9088.	14.5	108
60	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.	0.1	0
61	Convergent evolution in structural elements of proteins investigated using cross profile analysis. BMC Bioinformatics, 2012, 13, 11.	2.6	33
62	PDBâ€scale analysis of known and putative ligandâ€binding sites with structural sketches. Proteins: Structure, Function and Bioinformatics, 2012, 80, 747-763.	2.6	23
63	Discrimination of Golgi Type II Membrane Proteins Based on Their Hydropathy Profiles and the Amino Acid Propensities of Their Transmembrane Regions. Bioscience, Biotechnology and Biochemistry, 2011, 75, 82-88.	1.3	6
64	SAHG, a comprehensive database of predicted structures of all human proteins. Nucleic Acids Research, 2011, 39, D487-D493.	14.5	12
65	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.	0.1	0
66	Universal partitioning of the hierarchical fold network of 50-residue segments in proteins. BMC Structural Biology, 2009, 9, 34.	2.3	0
67	Protein-segment universe exhibiting transitions at intermediate segment length in conformational subspaces. BMC Structural Biology, 2008, 8, 37.	2.3	5
68	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 ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
69	2P-034 Two types universality of a fold universe of 50-residue segments(The 46th Annual Meeting of) Tj ETQq1 1 0.784314 rgBT /Ove	0.1	0
70	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.	0.1	0
71	Predicting mostly disordered proteins by using structure-unknown protein data. BMC Bioinformatics, 2007, 8, 78.	2.6	57
72	Identification of Glycosyltransferases Focusing on Golgi Transmembrane Region. Trends in Glycoscience and Glycotechnology, 2007, 19, 41-47.	0.1	3

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73	1P323 Molecular basis of microtubule disassembly mechanism regulated by katanin p60(10.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 2006, 46, S227.	0.1	0
74	2P450 Correlation between sequence profiles and profiles derived from local structural classifications(48. Bioinformatics, genomics and proteomics (II),Poster Session,Abstract,Meeting) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
75	Fine-tuning of protein domain boundary by minimizing potential coiled coil regions. Journal of Biomolecular NMR, 2006, 37, 53-63.	2.8	5
76	The Structure of N-terminal Domain from PEX1 Reveals Its Evolutionary Relationship to Type II AAA-ATPases. Seibutsu Butsuri, 2006, 46, 159-163.	0.1	0
77	Protein Structure Prediction Using a Profile-Profile Comparison Method: FORTE. Seibutsu Butsuri, 2006, 46, 106-110.	0.1	1
78	Protein structure prediction using a variety of profile libraries and 3D verification. Proteins: Structure, Function and Bioinformatics, 2005, 61, 114-121.	2.6	45
79	Novel Mechanism of Interaction of p85 Subunit of Phosphatidylinositol 3-Kinase and ErbB3 Receptor-derived Phosphotyrosyl Peptides. Journal of Biological Chemistry, 2005, 280, 1321-1326.	3.4	40
80	Visualization of conformational distribution of short to medium size segments in globular proteins and identification of local structural motifs. Protein Science, 2005, 14, 1253-1265.	7.6	11
81	CASP6 Meeting Reportâ€"Japanese Predictors Achieved Good Scoresâ€". Seibutsu Butsuri, 2005, 45, 165-167.	0.1	2
82	FORTE: a profile-profile comparison tool for protein fold recognition. Bioinformatics, 2004, 20, 594-595.	4.1	88
83	Structure of the N-terminal Domain of PEX1 AAA-ATPase. Journal of Biological Chemistry, 2004, 279, 50060-50068.	3.4	71
84	Crystallographic characterization of the N-terminal domain of PEX1. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2098-2099.	2.5	2
85	A New Variational Framework for Rigid-Body Alignment. Lecture Notes in Computer Science, 2004, , 171-179.	1.3	3
86	Prediction of Structures and Functions of Proteins by Database Searching.. Japanese Journal of Thrombosis and Hemostasis, 1999, 10, 285-289.	0.1	0
87	A Comparative Analysis of ABC Transporters in Complete Microbial Genomes. Genome Research, 1998, 8, 1048-1059.	5.5	126
88	Analysis of amino acid indices and mutation matrices for sequence comparison and structure prediction of proteins. Protein Engineering, Design and Selection, 1996, 9, 27-36.	2.1	317