

Makiko Suwa

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

2,796
citations

236612

25
h-index

174990

52
g-index

65
all docs

65
docs citations

65
times ranked

3360
citing authors

#	ARTICLE	IF	CITATIONS
1	Elongation and Contraction of Scallop Sarcoplasmic Reticulum (SR): ATP Stabilizes Ca ²⁺ -ATPase Crystalline Array Elongation of SR Vesicles. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3311.	1.8	1
2	Ca ²⁺ -ATPase Molecules as a Calcium-Sensitive Membrane-Endoskeleton of Sarcoplasmic Reticulum. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2624.	1.8	4
3	SEVENS: a database for comprehensive GPCR genes obtained from genomes. <i>Biophysics and Physicobiology</i> , 2018, 15, 104-110.	0.5	5
4	Development of a Machine Learning Method to Predict Membrane Protein-Ligand Binding Residues Using Basic Sequence Information. <i>Advances in Bioinformatics</i> , 2015, 2015, 1-7.	5.7	14
5	Identification of a binding element for the cytoplasmic regulator FROUNT in the membrane-proximal C-terminal region of chemokine receptors CCR2 and CCR5. <i>Biochemical Journal</i> , 2014, 457, 313-322.	1.7	13
6	Dynamics of bovine opsin bound to G-protein fragments. <i>Journal of Structural Biology</i> , 2014, 188, 79-86.	1.3	4
7	Bioinformatics Tools for Predicting GPCR Gene Functions. <i>Advances in Experimental Medicine and Biology</i> , 2014, 796, 205-224.	0.8	5
8	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
9	Structural Elements of the Signal Propagation Pathway in Squid Rhodopsin and Bovine Rhodopsin. <i>Journal of Physical Chemistry B</i> , 2011, 115, 6172-6179.	1.2	9
10	Functional and Structural Overview of G-Protein-Coupled Receptors Comprehensively Obtained from Genome Sequences. <i>Pharmaceuticals</i> , 2011, 4, 652-664.	1.7	20
11	Highly Selective Tuning of a Silkworm Olfactory Receptor to a Key Mulberry Leaf Volatile. <i>Current Biology</i> , 2011, 21, 623.	1.8	3
12	FOLDING ELASTIC TRANSMEMBRANE HELICES TO FIT IN A LOW-RESOLUTION IMAGE BY ELECTRON MICROSCOPY. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 37-50.	0.3	3
13	1P297 Structural Classification of G-protein coupled receptors(GPCR)based on inner polarity environment of the proteins.(Bioinformatics:Structural genomics,The 48th Annual Meeting of the) Tj ETQq1 1 0.784314 rgBT/Overlock		
14	A bioinformatics strategy to produce a cyclically developing project structure. <i>Synthesiology</i> , 2010, 3, 1-12.	0.2	4
15	TMFunction: database for functional residues in membrane proteins. <i>Nucleic Acids Research</i> , 2009, 37, D201-D204.	6.5	29
16	2P-209 Molecular Dynamics Simulation of Squid Rhodopsin and Bovine Opsin(Photobiology:Vision) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 2009, 49, S140.	0.0	0
17	Computational Overview of GPCR Gene Universe to Support Reverse Chemical Genomics Study. <i>Methods in Molecular Biology</i> , 2009, 577, 41-54.	0.4	6
18	TMBETADISC-RBF: Discrimination of β -barrel membrane proteins using RBF networks and PSSM profiles. <i>Computational Biology and Chemistry</i> , 2008, 32, 227-231.	1.1	76

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19	The genome of a lepidopteran model insect, the silkworm <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1036-1045.	1.2	592
20	Neural network based prediction of protein structure and Function: Comparison with other machine learning methods. , 2008, , .		4
21	The New Paradigm of the GPCR Analysis: The Knowledge that We Obtained from Comparison of New Structures. <i>Seibutsu Butsuri</i> , 2008, 48, 335-337.	0.0	0
22	Current Developments on β -Barrel Membrane Proteins: Sequence and Structure Analysis, Discrimination and Prediction. <i>Current Protein and Peptide Science</i> , 2007, 8, 580-599.	0.7	14
23	TMBETA-GENOME: database for annotated β -barrel membrane proteins in genomic sequences. <i>Nucleic Acids Research</i> , 2007, 35, D314-D316.	6.5	17
24	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	6.5	57
25	TMB Finding Pipeline: A Novel Approach for Detecting β -Barrel Membrane Proteins in Genomic Sequences. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 2456-2461.	2.5	8
26	1P264 Comparative overview of GPCR Universe in 28 eukaryotes(Bioinformatics-structural, functional,) Tj ETQq0 0.0 rgBT /Overlock 10	0.0	0
27	Identification of Glycosyltransferases Focusing on Golgi Transmembrane Region. <i>Trends in Glycoscience and Glycotechnology</i> , 2007, 19, 41-47.	0.0	3
28	Odorant Receptor Map in the Mouse Olfactory Bulb: In Vivo Sensitivity and Specificity of Receptor-Defined Glomeruli. <i>Neuron</i> , 2006, 52, 857-869.	3.8	172
29	Discrimination of outer membrane proteins using machine learning algorithms. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 1031-1037.	1.5	53
30	Influence of amino acid properties for discriminating outer membrane proteins at better accuracy. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1493-1497.	1.1	26
31	Statistical analysis and prediction of functional residues effective for GPCR-G-protein coupling selectivity. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 277-283.	1.0	17
32	Automated classification of alternative splicing and transcriptional initiation and construction of visual database of classified patterns. <i>Bioinformatics</i> , 2006, 22, 1211-1216.	1.8	33
33	1P478 Sequence and structure features of GPCRs, which are effective to determine the GPCR and G-protein binding selectivity(23. Bioinformatics, genomics and proteomics (I),Poster) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 177		
34	Application of residue distribution along the sequence for discriminating outer membrane proteins. <i>Computational Biology and Chemistry</i> , 2005, 29, 135-142.	1.1	50
35	Pivotal function for cytoplasmic protein FROUNT in CCR2-mediated monocyte chemotaxis. <i>Nature Immunology</i> , 2005, 6, 827-835.	7.0	103
36	A simple statistical method for discriminating outer membrane proteins with better accuracy. <i>Bioinformatics</i> , 2005, 21, 961-968.	1.8	103

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37	Discrimination of outer membrane proteins using support vector machines. <i>Bioinformatics</i> , 2005, 21, 4223-4229.	1.8	75
38	TMBETA-NET: discrimination and prediction of membrane spanning α -strands in outer membrane proteins. <i>Nucleic Acids Research</i> , 2005, 33, W164-W167.	6.5	48
39	GRIFFIN: a system for predicting GPCR-G-protein coupling selectivity using a support vector machine and a hidden Markov model. <i>Nucleic Acids Research</i> , 2005, 33, W148-W153.	6.5	48
40	Large-scale analysis of human alternative protein isoforms: pattern classification and correlation with subcellular localization signals. <i>Nucleic Acids Research</i> , 2005, 33, 2355-2363.	6.5	26
41	Automatic gene collection system for genome-scale overview of G-protein coupled receptors in Eukaryotes. <i>Gene</i> , 2005, 364, 63-73.	1.0	24
42	Structural Basis for a Broad But Selective Ligand Spectrum of a Mouse Olfactory Receptor: Mapping the Odorant-Binding Site. <i>Journal of Neuroscience</i> , 2005, 25, 1806-1815.	1.7	278
43	Structural analysis of residues involving cation- π interactions in different folding types of membrane proteins. <i>International Journal of Biological Macromolecules</i> , 2005, 35, 55-62.	3.6	30
44	Species-specific variation of alternative splicing and transcriptional initiation in six eukaryotes. <i>Gene</i> , 2005, 364, 53-62.	1.0	92
45	GENIUS II: a high-throughput database system for linking ORFs in complete genomes to known protein three-dimensional structures. <i>Bioinformatics</i> , 2004, 20, 596-598.	1.8	3
46	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
47	Neural network-based prediction of transmembrane β -strand segments in outer membrane proteins. <i>Journal of Computational Chemistry</i> , 2004, 25, 762-767.	1.5	76
48	Influence of cation- π interactions in protein-DNA complexes. <i>Polymer</i> , 2004, 45, 633-639.	1.8	39
49	Role of non-covalent interactions for determining the folding rate of two-state proteins. <i>Biophysical Chemistry</i> , 2004, 107, 263-272.	1.5	19
50	Variation of amino acid properties in all- β globular and outer membrane protein structures. <i>International Journal of Biological Macromolecules</i> , 2003, 32, 93-98.	3.6	17
51	HUNT: launch of a full-length cDNA database from the Helix Research Institute. <i>Nucleic Acids Research</i> , 2001, 29, 185-188.	6.5	42
52	Using the CATH domain database to assign structures and functions to the genome sequences. <i>Biochemical Society Transactions</i> , 2000, 28, 269-275.	1.6	21
53	A novel measure characterized by a polar energy surface approximation for recognition and classification of transmembrane protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 504-517.	1.5	0
54	A triangle lattice model that predicts transmembrane helix configuration using a polar jigsaw puzzle. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 771-778.	1.0	13

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55	Combining sensitive database searches with multiple intermediates to detect distant homologues. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 95-100.	1.0	46
56	Genome analysis: Assigning protein coding regions to three-dimensional structures. <i>Protein Science</i> , 1999, 8, 771-777.	3.1	30
57	Interaction stabilizing tertiary structure of bacteriorhodopsin studied by denaturation experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 350-362.	1.5	24
58	A Continuum theory for the prediction of lateral and rotational positioning of α -helices in membrane proteins: Bacteriorhodopsin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 363-377.	1.5	25
59	Theoretical Analysis of Amino Acid Sequence of Human Dystrophin. <i>Biochemical and Biophysical Research Communications</i> , 1993, 191, 782-789.	1.0	3
60	A computer system for predicting membrane protein structure. , 1993, , 1331-1334.		0
61	Characterization of Transmembrane Helices by a Probe Helix Method of Molecular Energy Calculation. <i>Japanese Journal of Applied Physics</i> , 1992, 31, 951-956.	0.8	4
62	A computer system for predicting membrane protein structure. <i>The Protein Journal</i> , 1992, 11, 390-391.	1.1	0
63	A theoretical method for distinguishing between soluble and membrane proteins. <i>Biophysical Chemistry</i> , 1989, 34, 69-77.	1.5	21
64	Denaturation of bacteriorhodopsin by organic solvents. <i>Biophysical Chemistry</i> , 1988, 30, 69-79.	1.5	48