

Shin-ichiro Kawano

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

3,453
citations

257450

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330143

37
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41
all docs

41
docs citations

41
times ranked

6661
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidofoms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.	3.7	14
2	A Light-Harvesting/Charge-Separation Model with Energy Gradient Made of Assemblies of <i>meta</i> -Pyridyl Zinc Porphyrins. <i>Chemistry - A European Journal</i> , 2021, 27, 4053-4063.	3.3	1
3	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021, 18, 768-770.	19.0	47
4	The ProteomeXchange consortium in 2020: enabling "big data" approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	14.5	491
5	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , 2020, 9, 136.	1.6	5
6	Role of the membrane potential in mitochondrial protein unfolding and import. <i>Scientific Reports</i> , 2019, 9, 7637.	3.3	23
7	The jPOST environment: an integrated proteomics data repository and database. <i>Nucleic Acids Research</i> , 2019, 47, D1218-D1224.	14.5	94
8	jPOSTrepo: an international standard data repository for proteomes. <i>Nucleic Acids Research</i> , 2017, 45, D1107-D1111.	14.5	451
9	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	3.7	87
10	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	14.5	860
11	Glycobiology Meets the Semantic Web. , 2017, , 351-370.		1
12	In Vivo Curdlan/Cellulose Bionanocomposite Synthesis by Genetically Modified <i>Gluconacetobacter xylinus</i> . <i>Biomacromolecules</i> , 2015, 16, 3154-3160.	5.4	45
13	Structural and mechanistic insights into phospholipid transfer by Ups1-Mdm35 in mitochondria. <i>Nature Communications</i> , 2015, 6, 7922.	12.8	75
14	GlycoRDF: an ontology to standardize glycomics data in RDF. <i>Bioinformatics</i> , 2015, 31, 919-925.	4.1	51
15	TogoTable: cross-database annotation system using the Resource Description Framework (RDF) data model. <i>Nucleic Acids Research</i> , 2014, 42, W442-W448.	14.5	7
16	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , 2014, 5, 5.	1.6	47
17	NMR analyses on the interactions of the yeast Tim50 C-terminal region with the presequence and Tim50 core domain. <i>FEBS Letters</i> , 2014, 588, 678-684.	2.8	20
18	WURCS: The Web3 Unique Representation of Carbohydrate Structures. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 1558-1566.	5.4	61

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19	Introducing glycomics data into the Semantic Web. <i>Journal of Biomedical Semantics</i> , 2013, 4, 39.	1.6	46
20	Cellulose complementing factor (Ccp) is a new member of the cellulose synthase complex (terminal) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.2	71
21	Double Helices of a Pyridine-Appended Zinc Chlorophyll Derivative. <i>Journal of the American Chemical Society</i> , 2013, 135, 5262-5265.	13.7	33
22	Integrated Proteomics Identified Novel Activation of Dynein IC2-GR-COX-1 Signaling in Neurofibromatosis Type I (NF1) Disease Model Cells. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1377-1394.	3.8	24
23	Cellulose production by <i>Enterobacter</i> sp. CJF-002 and identification of genes for cellulose biosynthesis. <i>Cellulose</i> , 2012, 19, 1989-2001.	4.9	35
24	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , 2011, 2, 4.	1.6	19
25	Structure of bacterial cellulose synthase subunit D octamer with four inner passageways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17957-17961.	7.1	118
26	Structural basis of yeast Tim40/Mia40 as an oxidative translocator in the mitochondrial intermembrane space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14403-14407.	7.1	90
27	Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. <i>Carbohydrate Research</i> , 2009, 344, 881-887.	2.3	37
28	3P-030 Structural analysis of mitochondrial thiol oxidase Tim40(Protein:Structure & Function,The) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
29	Regulation of endoglucanase gene (cmcaX) expression in <i>Acetobacter xylinum</i> . <i>Journal of Bioscience and Bioengineering</i> , 2008, 106, 88-94.	2.2	25
30	Purification, Crystallization and Preliminary X-Ray Studies of AxcesD Required for Efficient Cellulose Biosynthesis in <i>Acetobacter xylinum</i> . <i>Protein and Peptide Letters</i> , 2008, 15, 115-117.	0.9	4
31	Structural characterization of the <i>Acetobacter xylinum</i> endo- β -1,4-glucanase CMcaX required for cellulose biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 1069-1077.	2.6	47
32	KEGG as a glycome informatics resource. <i>Glycobiology</i> , 2006, 16, 63R-70R.	2.5	279
33	Crystallization and preliminary crystallographic analysis of the cellulose biosynthesis-related protein CMcaX from <i>Acetobacter xylinum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 252-254.	0.7	5
34	Prediction of glycan structures from gene expression data based on glycosyltransferase reactions. <i>Bioinformatics</i> , 2005, 21, 3976-3982.	4.1	78
35	Cloning of Cellulose Synthesis Related Genes from <i>Acetobacter xylinum</i> ATCC23769 and ATCC53582: Comparison of Cellulose Synthetic Ability Between Strains. <i>DNA Research</i> , 2002, 9, 149-156.	3.4	59
36	Effects of endogenous endo- β -1,4-glucanase on cellulose biosynthesis in <i>Acetobacter xylinum</i> ATCC23769. <i>Journal of Bioscience and Bioengineering</i> , 2002, 94, 275-281.	2.2	42

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37	Effects of Endogenous Endo- β -1,4-Glucanase on Cellulose Biosynthesis in <i>Acetobacter xylinum</i> ATCC23769. <i>Journal of Bioscience and Bioengineering</i> , 2002, 94, 275-281.	2.2	23
38	Structural analyses of new tri- and tetrasaccharides produced from disaccharides by transglycosylation of purified <i>Trichoderma viride</i> beta-glucosidase. <i>Glycoconjugate Journal</i> , 1999, 16, 415-423.	2.7	27
39	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 0, 8, 1677.	1.6	0