

Jimin Pei

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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.

55
papers

3,298
citations

26
h-index

57
g-index

60
ext. papers

4,164
ext. citations

9.4
avg, IF

5.55
L-index

#	Paper	IF	Citations
55	PROMALS3D: a tool for multiple protein sequence and structure alignments. <i>Nucleic Acids Research</i> , 2008 , 36, 2295-300	20.1	919
54	PROMALS: towards accurate multiple sequence alignments of distantly related proteins. <i>Bioinformatics</i> , 2007 , 23, 802-8	7.2	262
53	ECOD: an evolutionary classification of protein domains. <i>PLoS Computational Biology</i> , 2014 , 10, e1003926	9.9	184
52	PCMA: fast and accurate multiple sequence alignment based on profile consistency. <i>Bioinformatics</i> , 2003 , 19, 427-8	7.2	173
51	Large-scale determination of previously unsolved protein structures using evolutionary information. <i>ELife</i> , 2015 , 4, e09248	8.9	173
50	PROMALS3D: multiple protein sequence alignment enhanced with evolutionary and three-dimensional structural information. <i>Methods in Molecular Biology</i> , 2014 , 1079, 263-71	1.4	158
49	GGDEF domain is homologous to adenylyl cyclase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 42, 210-6	4.2	128
48	PROMALS3D web server for accurate multiple protein sequence and structure alignments. <i>Nucleic Acids Research</i> , 2008 , 36, W30-4	20.1	119
47	The Ancient Gamete Fusogen HAP2 Is a Eukaryotic Class II Fusion Protein. <i>Cell</i> , 2017 , 168, 904-915.e10	56.2	109
46	MUMMALS: multiple sequence alignment improved by using hidden Markov models with local structural information. <i>Nucleic Acids Research</i> , 2006 , 34, 4364-74	20.1	97
45	LocNES: a computational tool for locating classical NESs in CRM1 cargo proteins. <i>Bioinformatics</i> , 2015 , 31, 1357-65	7.2	80
44	Remote homology between Munc13 MUN domain and vesicle tethering complexes. <i>Journal of Molecular Biology</i> , 2009 , 391, 509-17	6.5	59
43	Multiple protein sequence alignment. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 382-6	8.1	54
42	PROMALS web server for accurate multiple protein sequence alignments. <i>Nucleic Acids Research</i> , 2007 , 35, W649-52	20.1	54
41	CREST--a large and diverse superfamily of putative transmembrane hydrolases. <i>Biology Direct</i> , 2011 , 6, 37	7.2	51
40	Computed structures of core eukaryotic protein complexes. <i>Science</i> , 2021 , 374, eabm4805	33.3	51
39	Expansion of type II CAAX proteases reveals evolutionary origin of secretase subunit APH-1. <i>Journal of Molecular Biology</i> , 2011 , 410, 18-26	6.5	50

38	Prediction of functional specificity determinants from protein sequences using log-likelihood ratios. <i>Bioinformatics</i> , 2006 , 22, 164-71	7.2	49
37	Targeting the Conserved Fusion Loop of HAP2 Inhibits the Transmission of Plasmodium berghei and falciparum. <i>Cell Reports</i> , 2017 , 21, 2868-2878	10.6	43
36	Unexpected diversity in Shisa-like proteins suggests the importance of their roles as transmembrane adaptors. <i>Cellular Signalling</i> , 2012 , 24, 758-69	4.9	40
35	Flatworm-specific transcriptional regulators promote the specification of tegumental progenitors in. <i>ELife</i> , 2018 , 7,	8.9	36
34	Requirement of the fusogenic micropeptide myomixer for muscle formation in zebrafish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 11950-11955	11.5	35
33	Peptidase family U34 belongs to the superfamily of N-terminal nucleophile hydrolases. <i>Protein Science</i> , 2003 , 12, 1131-5	6.3	29
32	The Rho GTPase inactivation domain in Vibrio cholerae MARTX toxin has a circularly permuted papain-like thiol protease fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77, 413-9	4.2	28
31	A new family of predicted Krüppel-like factor genes and pseudogenes in placental mammals. <i>PLoS ONE</i> , 2013 , 8, e81109	3.7	28
30	Cysteine-rich domains related to Frizzled receptors and Hedgehog-interacting proteins. <i>Protein Science</i> , 2012 , 21, 1172-84	6.3	27
29	The cytoplasmic domain of the gamete membrane fusion protein HAP2 targets the protein to the fusion site in Chlamydomonas and regulates the fusion reaction. <i>Development (Cambridge)</i> , 2015 , 142, 962-71	6.6	24
28	Using protein design for homology detection and active site searches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 11361-6	11.5	24
27	COG3926 and COG5526: a tale of two new lysozyme-like protein families. <i>Protein Science</i> , 2005 , 14, 2574-81	4.8	22
26	Combining evolutionary and structural information for local protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 782-94	4.2	21
25	Functional Assessment of Lipoyltransferase-1 Deficiency in Cells, Mice, and Humans. <i>Cell Reports</i> , 2019 , 27, 1376-1386.e6	10.6	19
24	Absence of TLR11 in Mice Does Not Confer Susceptibility to Salmonella Typhi. <i>Cell</i> , 2016 , 164, 827-8	56.2	15
23	C2H2 zinc finger proteins of the SP/KLF, Wilms tumor, EGR, Hucbein, and Klumpfuss families in metazoans and beyond. <i>Gene</i> , 2015 , 573, 91-9	3.8	14
22	Topology evaluation of models for difficult targets in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1673-1686	4.2	14
21	Expansion of divergent SEA domains in cell surface proteins and nucleoporin 54. <i>Protein Science</i> , 2017 , 26, 617-630	6.3	13

20	Breaking the singleton of germination protease. <i>Protein Science</i> , 2002 , 11, 691-7	6.3	10
19	The P5 protein from bacteriophage phi-6 is a distant homolog of lytic transglycosylases. <i>Protein Science</i> , 2005 , 14, 1370-4	6.3	10
18	ECOD: identification of distant homology among multidomain and transmembrane domain proteins. <i>BMC Molecular and Cell Biology</i> , 2019 , 20, 18	2.7	9
17	Structural prerequisites for CRM1-dependent nuclear export signaling peptides: accessibility, adapting conformation, and the stability at the binding site. <i>Scientific Reports</i> , 2019 , 9, 6627	4.9	8
16	An ancient autoproteolytic domain found in GAIN, ZU5 and Nucleoporin98. <i>Journal of Molecular Biology</i> , 2014 , 426, 3935-3945	6.5	8
15	Crystal Structure of the CLOCK Transactivation Domain Exon19 in Complex with a Repressor. <i>Structure</i> , 2017 , 25, 1187-1194.e3	5.2	6
14	Using homology relations within a database markedly boosts protein sequence similarity search. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 7003-8	11.5	6
13	TMEM120A is a coenzyme A-binding membrane protein with structural similarities to ELOVL fatty acid elongase. <i>ELife</i> , 2021 , 10,	8.9	6
12	Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. <i>PLoS Computational Biology</i> , 2020 , 16, e1007775	5	5
11	CPDadh: a new peptidase family homologous to the cysteine protease domain in bacterial MARTX toxins. <i>Protein Science</i> , 2009 , 18, 856-62	6.3	5
10	A sequence family database built on ECOD structural domains. <i>Bioinformatics</i> , 2018 , 34, 2997-3003	7.2	4
9	Conserved evolutionary units in the heme-copper oxidase superfamily revealed by novel homologous protein families. <i>Protein Science</i> , 2014 , 23, 1220-34	6.3	4
8	The DBSAV Database: Predicting Deleteriousness of Single Amino Acid Variations in the Human Proteome. <i>Journal of Molecular Biology</i> , 2021 , 433, 166915	6.5	4
7	FlyXCDB-A Resource for Drosophila Cell Surface and Secreted Proteins and Their Extracellular Domains. <i>Journal of Molecular Biology</i> , 2018 , 430, 3353-3411	6.5	3
6	SFESA: a web server for pairwise alignment refinement by secondary structure shifts. <i>BMC Bioinformatics</i> , 2015 , 16, 282	3.6	2
5	pCRM1exportome: database of predicted CRM1-dependent Nuclear Export Signal (NES) motifs in cancer-related genes. <i>Bioinformatics</i> , 2020 , 36, 961-963	7.2	2
4	A pathogenic UFSP2 variant in an autosomal recessive form of pediatric neurodevelopmental anomalies and epilepsy. <i>Genetics in Medicine</i> , 2021 , 23, 900-908	8.1	2
3	A Fifth of the Protein World: Rossmann-like Proteins as an Evolutionarily Successful Structural unit. <i>Journal of Molecular Biology</i> , 2021 , 433, 166788	6.5	2

2 Completeness and Consistency in Structural Domain Classifications. *ACS Omega*, **2021**, 6, 15698-15707 3.9 o

1 Evolutionary origin and sequence signatures of the heterodimeric ABCG5/ABCG8 transporter..
Protein Science, **2022**, 31, e4297 6.3