

Frank Eisenhaber

List of Publications by Year in descending order

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155
papers

14,970
citations

31902

53
h-index

18606

119
g-index

167
all docs

167
docs citations

167
times ranked

18981
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation of chromatin structure by site-specific histone H3 methyltransferases. <i>Nature</i> , 2000, 406, 593-599.	13.7	2,497
2	Fat Mobilization in Adipose Tissue Is Promoted by Adipose Triglyceride Lipase. <i>Science</i> , 2004, 306, 1383-1386.	6.0	1,744
3	The double cubic lattice method: Efficient approaches to numerical integration of surface area and volume and to dot surface contouring of molecular assemblies. <i>Journal of Computational Chemistry</i> , 1995, 16, 273-284.	1.5	785
4	The Tudor domain "Royal Family"™: Tudor, plant Agenet, Chromo, PWWP and MBT domains. <i>Trends in Biochemical Sciences</i> , 2003, 28, 69-74.	3.7	448
5	Predicting function: from genes to genomes and back 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 283, 707-725.	2.0	433
6	Prediction of Potential GPI-modification Sites in Proprotein Sequences. <i>Journal of Molecular Biology</i> , 1999, 292, 741-758.	2.0	417
7	A Sensitive Predictor for Potential GPI Lipid Modification Sites in Fungal Protein Sequences and its Application to Genome-wide Studies for <i>Aspergillus nidulans</i> , <i>Candida albicans</i> , <i>Neurospora crassa</i> , <i>Saccharomyces cerevisiae</i> and <i>Schizosaccharomyces pombe</i> . <i>Journal of Molecular Biology</i> , 2004, 337, 243-253.	2.0	262
8	Pds5 cooperates with cohesin in maintaining sister chromatid cohesion. <i>Current Biology</i> , 2000, 10, 1557-1564.	1.8	237
9	Rotamers: To be or not to be?. <i>Journal of Molecular Biology</i> , 1993, 230, 592-612.	2.0	230
10	Eco1 Is a Novel Acetyltransferase that Can Acetylate Proteins Involved in Cohesion. <i>Current Biology</i> , 2002, 12, 323-328.	1.8	228
11	The STIR-domain superfamily in signal transduction, development and immunity. <i>Trends in Biochemical Sciences</i> , 2003, 28, 226-229.	3.7	225
12	Human Scc4 Is Required for Cohesin Binding to Chromatin, Sister-Chromatid Cohesion, and Mitotic Progression. <i>Current Biology</i> , 2006, 16, 863-874.	1.8	223
13	N-terminal N -myristoylation of proteins: prediction of substrate proteins from amino acid sequence 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2002, 317, 541-557.	2.0	222
14	Kleisins: A Superfamily of Bacterial and Eukaryotic SMC Protein Partners. <i>Molecular Cell</i> , 2003, 11, 571-575.	4.5	209
15	Two Fission Yeast Homologs of <i>Drosophila</i> Mei-S332 Are Required for Chromosome Segregation during Meiosis I and II. <i>Current Biology</i> , 2004, 14, 287-301.	1.8	203
16	Prediction of Peroxisomal Targeting Signal 1 Containing Proteins from Amino Acid Sequence. <i>Journal of Molecular Biology</i> , 2003, 328, 581-592.	2.0	199
17	The WD40 Propeller Domain of Cdh1 Functions as a Destruction Box Receptor for APC/C Substrates. <i>Molecular Cell</i> , 2005, 18, 543-553.	4.5	198
18	Improved strategy in analytic surface calculation for molecular systems: Handling of singularities and computational efficiency. <i>Journal of Computational Chemistry</i> , 1993, 14, 1272-1280.	1.5	192

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19	Glycosylphosphatidylinositol Lipid Anchoring of Plant Proteins. Sensitive Prediction from Sequence- and Genome-Wide Studies for Arabidopsis and Rice. <i>Plant Physiology</i> , 2003, 133, 1691-1701.	2.3	185
20	TPR Subunits of the Anaphase-Promoting Complex Mediate Binding to the Activator Protein CDH1. <i>Current Biology</i> , 2003, 13, 1459-1468.	1.8	182
21	N-terminal N -myristoylation of proteins: refinement of the sequence motif and its taxon-specific differences 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2002, 317, 523-540.	2.0	181
22	Human Rif1, ortholog of a yeast telomeric protein, is regulated by ATM and 53BP1 and functions in the S-phase checkpoint. <i>Genes and Development</i> , 2004, 18, 2108-2119.	2.7	181
23	Refinement and prediction of protein prenylation motifs. <i>Genome Biology</i> , 2005, 6, R55.	13.9	173
24	Ubiquitylation in plants: a post-genomic look at a post-translational modification. <i>Trends in Plant Science</i> , 2001, 6, 463-470.	4.3	170
25	Motif Refinement of the Peroxisomal Targeting Signal 1 and Evaluation of Taxon-specific Differences. <i>Journal of Molecular Biology</i> , 2003, 328, 567-579.	2.0	161
26	Post-translational GPI lipid anchor modification of proteins in kingdoms of life: analysis of protein sequence data from complete genomes. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 17-25.	1.0	156
27	Enzymes and auxiliary factors for GPI lipid anchor biosynthesis and post-translational transfer to proteins. <i>BioEssays</i> , 2003, 25, 367-385.	1.2	156
28	Myristoylation of viral and bacterial proteins. <i>Trends in Microbiology</i> , 2004, 12, 178-185.	3.5	148
29	Phosphorylation-Induced Autoinhibition Regulates the Cytoskeletal Protein Lethal (2) giant larvae. <i>Current Biology</i> , 2005, 15, 276-282.	1.8	148
30	Towards Complete Sets of Farnesylated and Geranylgeranylated Proteins. <i>PLoS Computational Biology</i> , 2007, 3, e66.	1.5	144
31	Molecular Cloning and Characterization of Endosialin, a C-type Lectin-like Cell Surface Receptor of Tumor Endothelium. <i>Journal of Biological Chemistry</i> , 2001, 276, 7408-7414.	1.6	133
32	Protein Structure Prediction: Recognition of Primary, Secondary, and Tertiary Structural Features from Amino Acid Sequence. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 1995, 30, 1-94.	2.3	132
33	pKaPS: prediction of protein kinase A phosphorylation sites with the simplified kinase-substrate binding model. <i>Biology Direct</i> , 2007, 2, 1.	1.9	131
34	On filtering false positive transmembrane protein predictions. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 745-752.	1.0	128
35	Principles of Helix-Helix Packing in Proteins: The Helical Lattice Superposition Model. <i>Journal of Molecular Biology</i> , 1996, 255, 536-553.	2.0	113
36	TM or not TM: transmembrane protein prediction with low false positive rate using DAS-TMfilter. <i>Bioinformatics</i> , 2004, 20, 136-137.	1.8	113

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37	Homology-based fold predictions for <i>Mycoplasma genitalium</i> proteins 1 Edited by G. Von Heijne. <i>Journal of Molecular Biology</i> , 1998, 280, 323-326.	2.0	112
38	<i>S. pombe</i> meiotic linear elements contain proteins related to synaptonemal complex components. <i>Journal of Cell Science</i> , 2004, 117, 3343-3351.	1.2	108
39	Protein prenyltransferases. <i>Genome Biology</i> , 2003, 4, 212.	13.9	106
40	Automated annotation of GPI anchor sites: case study <i>C. elegans</i> . <i>Trends in Biochemical Sciences</i> , 2000, 25, 340-341.	3.7	105
41	RNAase-III enzyme Dicer maintains signaling pathways for differentiation and survival in mouse cortical neural stem cells. <i>Journal of Cell Science</i> , 2010, 123, 586-594.	1.2	97
42	Crystal structure of the p14/MP1 scaffolding complex: How a twin couple attaches mitogen-activated protein kinase signaling to late endosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10984-10989.	3.3	89
43	SPACER: server for predicting allosteric communication and effects of regulation. <i>Nucleic Acids Research</i> , 2013, 41, W266-W272.	6.5	88
44	SUMO conjugation in plants. <i>Planta</i> , 2004, 220, 1-8.	1.6	86
45	Comparison of atomic solvation parametric sets: Applicability and limitations in protein folding and binding. <i>Protein Science</i> , 1995, 4, 2499-2509.	3.1	84
46	Prediction of lipid posttranslational modifications and localization signals from protein sequences: big-Å, NMT and PTS1. <i>Nucleic Acids Research</i> , 2003, 31, 3631-3634.	6.5	78
47	MYRbase: analysis of genome-wide glycine myristoylation enlarges the functional spectrum of eukaryotic myristoylated proteins. <i>Genome Biology</i> , 2004, 5, R21.	13.9	76
48	Mapping the sequence mutations of the 2009 H1N1 influenza A virus neuraminidase relative to drug and antibody binding sites. <i>Biology Direct</i> , 2009, 4, 18.	1.9	73
49	Prediction of secondary structural content of proteins from their amino acid composition alone. I. New analytic vector decomposition methods. , 1996, 25, 157-168.		72
50	Prediction of secondary structural content of proteins from their amino acid composition alone. II. The paradox with secondary structural class. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 169-179.	1.5	70
51	A new common mutation in the hemagglutinin of the 2009 (H1N1) influenza A virus. <i>PLOS Currents</i> , 2010, 2, RRN1162.	1.4	68
52	Experimental testing of predicted myristoylation targets involved in asymmetric cell division and calcium-dependent signalling. <i>Cell Cycle</i> , 2008, 7, 3709-3719.	1.3	65
53	Charged residues next to transmembrane regions revisited: "Positive-inside rule" is complemented by the "negative inside depletion/outside enrichment rule". <i>BMC Biology</i> , 2017, 15, 66.	1.7	64
54	Prediction of Posttranslational Modification of Proteins from Their Amino Acid Sequence. <i>Methods in Molecular Biology</i> , 2010, 609, 365-384.	0.4	59

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55	More Than 1,001 Problems with Protein Domain Databases: Transmembrane Regions, Signal Peptides and the Issue of Sequence Homology. <i>PLoS Computational Biology</i> , 2010, 6, e1000867.	1.5	56
56	ANNIE: integrated de novo protein sequence annotation. <i>Nucleic Acids Research</i> , 2009, 37, W435-W440.	6.5	51
57	Hydrophobic regions on protein surfaces: definition based on hydration shell structure and a quick method for their computation. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 1121-1133.	1.0	50
58	Proteins with two SUMO-like domains in chromatin-associated complexes: the RENi (Rad60-Esc2-NIP45) family. <i>BMC Bioinformatics</i> , 2005, 6, 22.	1.2	49
59	Structural Requirements for Interaction of Peroxisomal Targeting Signal 2 and Its Receptor PEX7. <i>Journal of Biological Chemistry</i> , 2011, 286, 45048-45062.	1.6	49
60	Posttranslational Modifications and Subcellular Localization Signals: Indicators of Sequence Regions without Inherent 3D Structure?. <i>Current Protein and Peptide Science</i> , 2007, 8, 197-203.	0.7	48
61	Protein function machinery: from basic structural units to modulation of activity. <i>Current Opinion in Structural Biology</i> , 2017, 42, 67-74.	2.6	48
62	Structure, mechanism and ensemble formation of the alkylhydroperoxide reductase subunits AhpC and AhpF from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2848-2862.	2.5	47
63	SNEV is an evolutionarily conserved splicing factor whose oligomerization is necessary for spliceosome assembly. <i>Nucleic Acids Research</i> , 2005, 33, 6868-6883.	6.5	46
64	Molecular Cloning and Characterization of EndoGlyx-1, an EMILIN-like Multisubunit Glycoprotein of Vascular Endothelium. <i>Journal of Biological Chemistry</i> , 2001, 276, 48588-48595.	1.6	45
65	The Brix domain protein family – a key to the ribosomal biogenesis pathway?. <i>Trends in Biochemical Sciences</i> , 2001, 26, 345-347.	3.7	44
66	Prediction of sequence signals for lipid post-translational modifications: Insights from case studies. <i>Proteomics</i> , 2004, 4, 1614-1625.	1.3	42
67	Parameterization of disorder predictors for large-scale applications requiring high specificity by using an extended benchmark dataset. <i>BMC Genomics</i> , 2010, 11, S15.	1.2	42
68	Transamidase subunit GAA1/GPAA1 is a M28 family metallo-peptide-synthetase that catalyzes the peptide bond formation between the substrate protein's omega-site and the GPI lipid anchor's phosphoethanolamine. <i>Cell Cycle</i> , 2014, 13, 1912-1917.	1.3	41
69	Hydrophobic regions on protein surfaces. Derivation of the solvation energy from their area distribution in crystallographic protein structures. <i>Protein Science</i> , 1996, 5, 1676-1686.	3.1	40
70	Nuclear import of a lipid-modified transcription factor. <i>Cell Cycle</i> , 2011, 10, 3897-3911.	1.3	40
71	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPAR β . <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 4049-4064.	2.4	38
72	Prediction of secondary structural content of proteins from their amino acid composition alone. II. The paradox with secondary structural class. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 169-179.	1.5	37

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73	The substrate specificity profile of human granzyme A. <i>Biological Chemistry</i> , 2010, 391, 983-97.	1.2	37
74	Linking transcriptional mediators via the GACKIX domain super family. <i>Current Biology</i> , 2004, 14, R54-R55.	1.8	36
75	Cleaning of raw peptide MS/MS spectra: Improved protein identification following deconvolution of multiply charged peaks, isotope clusters, and removal of background noise. <i>Proteomics</i> , 2006, 6, 5117-5131.	1.3	35
76	A DECADE AFTER THE FIRST FULL HUMAN GENOME SEQUENCING: WHEN WILL WE UNDERSTAND OUR OWN GENOME?. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1271001.	0.3	35
77	Hidden localization motifs: naturally occurring peroxisomal targeting signals in non-peroxisomal proteins. <i>Genome Biology</i> , 2004, 5, R97.	13.9	32
78	How bioinformatics influences health informatics: usage of biomolecular sequences, expression profiles and automated microscopic image analyses for clinical needs and public health. <i>Health Information Science and Systems</i> , 2013, 1, 2.	3.4	32
79	Application of a sensitive collection heuristic for very large protein families: evolutionary relationship between adipose triglyceride lipase (ATGL) and classic mammalian lipases. <i>BMC Bioinformatics</i> , 2006, 7, 164.	1.2	29
80	Not all transmembrane helices are born equal: Towards the extension of the sequence homology concept to membrane proteins. <i>Biology Direct</i> , 2011, 6, 57.	1.9	28
81	A Reversible Association between Smc Coiled Coils Is Regulated by Lysine Acetylation and Is Required for Cohesin Association with the DNA. <i>Molecular Cell</i> , 2016, 63, 1044-1054.	4.5	27
82	The 160K Natural Organism Library, a unique resource for natural products research. <i>Nature Biotechnology</i> , 2018, 36, 570-573.	9.4	27
83	Darkness in the Human Gene and Protein Function Space: Widely Modest or Absent Illumination by the Life Science Literature and the Trend for Fewer Protein Function Discoveries Since 2000. <i>Proteomics</i> , 2018, 18, e1800093.	1.3	26
84	Post-translational Regulation of Radioactive Iodine Therapy Response in Papillary Thyroid Carcinoma. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	24
85	Single-residue posttranslational modification sites at the N-terminus, C-terminus or in-between: To be or not to be exposed for enzyme access. <i>Proteomics</i> , 2015, 15, 2525-2546.	1.3	23
86	Prenylation of viral proteins by enzymes of the host: Virus-driven rationale for therapy with statins and FT/GGT1 inhibitors. <i>BioEssays</i> , 2017, 39, 1700014.	1.2	22
87	Key roles of the Escherichia coli AhpC C-terminus in assembly and catalysis of alkylhydroperoxide reductase, an enzyme essential for the alleviation of oxidative stress. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 1932-1943.	0.5	21
88	Transmembrane helix: simple or complex. <i>Nucleic Acids Research</i> , 2012, 40, W370-W375.	6.5	20
89	Knockout of the non-essential gene SUGCT creates diet-linked, age-related microbiome disbalance with a diabetes-like metabolic syndrome phenotype. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 3423-3439.	2.4	19
90	dissectHMMER: a HMMER-based score dissection framework that statistically evaluates fold-critical sequence segments for domain fold similarity. <i>Biology Direct</i> , 2015, 10, 39.	1.9	18

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91	Prediction of Protein Function. , 2006, , 39-54.		17
92	A CH domain-containing N terminus in NuMA?. Protein Science, 2009, 11, 2281-2284.	3.1	16
93	Discovering novel SNPs that are correlated with patient outcome in a Singaporean cancer patient cohort treated with gemcitabine-based chemotherapy. BMC Cancer, 2018, 18, 555.	1.1	16
94	Discovery of a genetic module essential for assigning leftâ€“right asymmetry in humans and ancestral vertebrates. Nature Genetics, 2022, 54, 62-72.	9.4	16
95	Are knowledge-based potentials derived from protein structure sets discriminative with respect to amino acid types?. , 1998, 31, 225-246.		15
96	Can molecular mechanisms of biological processes be extracted from expression profiles? Case study: endothelial contribution to tumor-induced angiogenesis. BioEssays, 2001, 23, 1159-1175.	1.2	15
97	Arxes: retrotransposed genes required for adipogenesis. Nucleic Acids Research, 2011, 39, 3224-3239.	6.5	15
98	The Recipe for Protein Sequence-Based Function Prediction and Its Implementation in the ANNOTATOR Software Environment. Methods in Molecular Biology, 2016, 1415, 477-506.	0.4	15
99	Function of a membrane-embedded domain evolutionarily multiplied in the GPI lipid anchor pathway proteins PIG-B, PIG-M, PIG-U, PIG-W, PIG-V, and PIG-Z. Cell Cycle, 2018, 17, 874-880.	1.3	14
100	Isolation and Identification of an Anthracimycin Analogue from <i>Nocardioopsis kunsanensis</i> , a Halophile from a Saltern, by Genomic Mining Strategy. Journal of Genomics, 2018, 6, 63-73.	0.6	13
101	Integrated Tools for Biomolecular Sequence-Based Function Prediction as Exemplified by the ANNOTATOR Software Environment. Methods in Molecular Biology, 2010, 609, 257-267.	0.4	13
102	Induction of Short Interspersed Nuclear Repeat-containing Transcripts in Epithelial Cells upon Infection with a Chicken Adenovirus. Journal of Molecular Biology, 2003, 328, 779-790.	2.0	12
103	Blom71± Is a Novel Heterogeneous Nuclear Ribonucleoprotein K Homology Domain Protein Involved in Pre-mRNA Splicing That Interacts with SNEVPrp19-Pso4. Journal of Biological Chemistry, 2009, 284, 29193-29204.	1.6	12
104	Structural insight into the glycosylphosphatidylinositol transamidase subunits PIG-K and PIG-S from yeast. Journal of Structural Biology, 2011, 173, 271-281.	1.3	12
105	BEWARE OF MOVING TARGETS: REFERENCE PROTEOME CONTENT FLUCTUATES SUBSTANTIALLY OVER THE YEARS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250020.	0.3	12
106	Crystallographic and solution studies of NAD+- and NADH-bound alkylhydroperoxide reductase subunit F (AhpF) from Escherichia coli provide insight into sequential enzymatic steps. Biochimica Et Biophysica Acta - Bioenergetics, 2015, 1847, 1139-1152.	0.5	12
107	Potential Human Adaptation Mutation of Influenza A(H5N1) Virus, Canada. Emerging Infectious Diseases, 2014, 20, 1580-1582.	2.0	10
108	On the necessity of dissecting sequence similarity scores into segment-specific contributions for inferring protein homology, function prediction and annotation. BMC Bioinformatics, 2014, 15, 166.	1.2	10

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109	Low resolution solution structure of an enzymatic active AhpC 10 :AhpF 2 ensemble of the Escherichia coli Alkyl hydroperoxide Reductase. <i>Journal of Structural Biology</i> , 2016, 193, 13-22.	1.3	10
110	Iron Supplementation Delays Aging and Extends Cellular Lifespan through Potentiation of Mitochondrial Function. <i>Cells</i> , 2022, 11, 862.	1.8	10
111	To kill or to be killed: pangenome analysis of Escherichia coli strains reveals a tailocin specific for pandemic ST131. <i>BMC Biology</i> , 2022, 20, .	1.7	10
112	Hydrophobic regions on protein surfaces. <i>Journal of Computer - Aided Molecular Design</i> , 1999, 17, 27-42.	1.0	9
113	<scp>NMR</scp> studies reveal a novel grab and release mechanism for efficient catalysis of the bacterial 2â€Cys peroxiredoxin machinery. <i>FEBS Journal</i> , 2015, 282, 4620-4638.	2.2	9
114	Genomics-driven discovery of a biosynthetic gene cluster required for the synthesis of BII-Rafflesfungin from the fungus <i>Phoma</i> sp. F3723. <i>BMC Genomics</i> , 2019, 20, 374.	1.2	9
115	Conserved sequence motifs in human TMTC1, TMTC2, TMTC3, and TMTC4, new O-mannosyltransferases from the GT-C/PMT clan, are rationalized as ligand binding sites. <i>Biology Direct</i> , 2021, 16, 4.	1.9	9
116	IS LGI2 THE CANDIDATE GENE FOR PARTIAL EPILEPSY WITH PERICENTRAL SPIKES?. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 117-127.	0.3	8
117	THE JANUS-FACED E-VALUES OF HMMER2: EXTREME VALUE DISTRIBUTION OR LOGISTIC FUNCTION?. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 179-206.	0.3	8
118	Brief Overview of Bioinformatics Activities in Singapore. <i>PLoS Computational Biology</i> , 2009, 5, e1000508.	1.5	7
119	Discovery of a novel splice variant of Fcar (CD89) unravels sequence segments necessary for efficient secretion: A story of bad signal peptides and good ones that nevertheless do not make it. <i>Cell Cycle</i> , 2017, 16, 457-467.	1.3	7
120	Active site CP-loop dynamics modulate substrate binding, catalysis, oligomerization, stability, over-oxidation and recycling of 2-Cys Peroxiredoxins. <i>Free Radical Biology and Medicine</i> , 2018, 118, 59-70.	1.3	7
121	Detecting Atypical Examples of Known Domain Types by Sequence Similarity Searching: The SBASE Domain Library Approach. <i>Current Protein and Peptide Science</i> , 2010, 11, 538-549.	0.7	6
122	Investigation of causes of oseltamivir chemoprophylaxis failures during influenza A (H1N1-2009) outbreaks. <i>Journal of Clinical Virology</i> , 2011, 50, 104-108.	1.6	6
123	Low-resolution structure of the soluble domain GPAA1 (yGPAA170â€“247) of the glycosylphosphatidylinositol transamidase subunit GPAA1 from <i>Saccharomyces cerevisiae</i> . <i>Bioscience Reports</i> , 2013, 33, e00033.	1.1	6
124	Hypocrisy Around Medical Patient Data: Issues of Access for Biomedical Research, Data Quality, Usefulness for the Purpose and Omics Data as Game Changer. <i>Asian Bioethics Review</i> , 2019, 11, 189-207.	0.9	6
125	Structural modelling of the luminal domain of human GPAA1, the metallo-peptide synthetase subunit of the transamidase complex, reveals zinc-binding mode and two flaps surrounding the active site. <i>Biology Direct</i> , 2020, 15, 14.	1.9	6
126	The PICLS high-throughput screening method for agents extending cellular longevity identifies 2,5-anhydro-D-mannitol as novel anti-aging compound. <i>GeroScience</i> , 2023, 45, 141-158.	2.1	6

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127	Essential role of the flexible linker on the conformational equilibrium of bacterial peroxiredoxin reductase for effective regeneration of peroxiredoxin. <i>Journal of Biological Chemistry</i> , 2017, 292, 6667-6679.	1.6	5
128	The Geographic Variation of Surveillance and Zoonotic Spillover Potential of Influenza Viruses in Domestic Poultry and Swine. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofy318.	0.4	5
129	Functional Classification of Super-Large Families of Enzymes Based on Substrate Binding Pocket Residues for Biocatalysis and Enzyme Engineering Applications. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 701120.	2.0	5
130	Protein Sequenceâ€“Structureâ€“Functionâ€“Network Links Discovered with the ANNOTATOR Software Suite: Application to ELYS/Mel-28. , 2012, , 111-143.		5
131	xHMMER3x2: Utilizing HMMER3â€™s speed and HMMER2â€™s sensitivity and specificity in the glocal alignment mode for improved large-scale protein domain annotation. <i>Biology Direct</i> , 2016, 11, 63.	1.9	4
132	Identification and engineering of 32 membered antifungal macrolactone notonesomycins. <i>Microbial Cell Factories</i> , 2020, 19, 71.	1.9	4
133	The Janus-faced E-values of HMMER2: extreme value distribution or logistic function?. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 9, 179-206.	0.3	4
134	Sequence complexity of proteins and its significance in annotation. , 2005, , .		3
135	Purification and crystallization of yeast glycosylphosphatidylinositol transamidase subunit PIG-S (PIG-S71â€™467). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 896-899.	0.7	3
136	MOTIF DISCOVERY WITH DATA MINING IN 3D PROTEIN STRUCTURE DATABASES: DISCOVERY, VALIDATION AND PREDICTION OF THE U-SHAPE ZINC BINDING ("HUF-ZINC") MOTIF. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340008.	0.3	3
137	A SIMPLE SHORTCUT TO UNSUPERVISED ALIGNMENT-FREE PHYLOGENETIC GENOME GROUPINGS, EVEN FROM UNASSEMBLED SEQUENCING READS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1343005.	0.3	3
138	In memoriam of Narayanaswamy Srinivasan (1962â€™2021). <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 909-911.	1.5	3
139	Stops GeneJockeys being taken for a ride. <i>Trends in Cell Biology</i> , 1998, 8, 377-378.	3.6	2
140	THE 24TH INTERNATIONAL CONFERENCE ON GENOME INFORMATICS, GIW2013, IN SINGAPORE. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1302003.	0.3	2
141	10 years for the <i>Journal of Bioinformatics and Computational Biology</i> (2003â€™2013) â€™ A retrospective. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1471001.	0.3	2
142	HPMV: Human protein mutation viewer â€™ relating sequence mutations to protein sequence architecture and function changes. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550028.	0.3	2
143	Novel insights into the vancomycin-resistant <i>Enterococcus faecalis</i> (V583) alkylhydroperoxide reductase subunit F. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3201-3214.	1.1	2
144	A Perspective on Rational Designs of a Hemagglutinin Based Universal Influenza Vaccine. <i>Current Pharmaceutical Design</i> , 2016, 22, 3547-3554.	0.9	2

#	ARTICLE	IF	CITATIONS
145	Guest Editorial for the International Conference on Genome Informatics (GIW 2013). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 5-6.	1.9	1
146	Effect of the additional cysteine 503 of vancomycin-resistant Enterococcus faecalis (V583) alkylhydroperoxide reductase subunit F (AhpF) and the mechanism of AhpF and subunit C assembling. Free Radical Biology and Medicine, 2019, 138, 10-22.	1.3	1
147	In Memory of Vladimir B. Bajic (1952–2019). Genomics, Proteomics and Bioinformatics, 2019, 17, 473-474.	3.0	1
148	A Perspective on Rational Designs of a Hemagglutinin Based Universal Influenza Vaccine. Current Pharmaceutical Design, 2016, , .	0.9	1
149	Optimizing the Parametrization of Homologue Classification in the Pan-Genome Computation for a Bacterial Species: Case Study Streptococcus pyogenes. Methods in Molecular Biology, 2022, 2449, 299-324.	0.4	1
150	International Conference on Genome Informatics (GIW 2013) in Singapore: introduction to the systems biology contributions. BMC Systems Biology, 2013, 7, 11.	3.0	0
151	AUTOMATIC PHYLOGENETIC CLASSIFICATION OF BACTERIAL BETA-LACTAMASE SEQUENCES INCLUDING STRUCTURAL AND ANTIBIOTIC SUBSTRATE PREFERENCE INFORMATION. Journal of Bioinformatics and Computational Biology, 2013, 11, 1343011.	0.3	0
152	Unix interfaces, Kleisli, buccandin structure, etc. – The heroic beginning of bioinformatics in Singapore. Journal of Bioinformatics and Computational Biology, 2014, 12, 1471002.	0.3	0
153	Understanding the Functions of Peroxisomal Proteins: The Peroxisomal Proteome, Peroxisomal Import, Proteases and Other Protein Families and Their Network Organization: What Has Computational Biology Contributed?. , 2014, , 187-232.		0
154	Translational Informatics Management System (TIMS): Towards OMICS based clinical data management for long term curation of clinical studies. Journal of Open Source Software, 2019, 4, 1533.	2.0	0
155	Editorial: Innovative Strategies From Synthetic Biology and Bacterial Pathways to Master Biochemical Environmental Challenges. Frontiers in Bioengineering and Biotechnology, 2021, 9, 828632.	2.0	0