

Birgit Eisenhaber

List of Publications by Year in descending order

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45
papers

1,987
citations

430874

18
h-index

243625

44
g-index

47
all docs

47
docs citations

47
times ranked

3025
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of Potential GPI-modification Sites in Proprotein Sequences. <i>Journal of Molecular Biology</i> , 1999, 292, 741-758.	4.2	417
2	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.	4.2	262
3	Glycosylphosphatidylinositol Lipid Anchoring of Plant Proteins. Sensitive Prediction from Sequence- and Genome-Wide Studies for <i>Arabidopsis</i> and Rice. <i>Plant Physiology</i> , 2003, 133, 1691-1701.	4.8	185
4	Enzymes and auxiliary factors for GPI lipid anchor biosynthesis and post-translational transfer to proteins. <i>BioEssays</i> , 2003, 25, 367-385.	2.5	156
5	On filtering false positive transmembrane protein predictions. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 745-752.	2.1	128
6	TM or not TM: transmembrane protein prediction with low false positive rate using DAS-TMfilter. <i>Bioinformatics</i> , 2004, 20, 136-137.	4.1	113
7	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.	14.5	78
8	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.	3.8	64
9	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.	1.4	48
10	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
11	Prediction of sequence signals for lipid post-translational modifications: Insights from case studies. <i>Proteomics</i> , 2004, 4, 1614-1625.	2.2	42
12	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.	2.6	41
13	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.	5.2	32
14	The 160K Natural Organism Library, a unique resource for natural products research. <i>Nature Biotechnology</i> , 2018, 36, 570-573.	17.5	27
15	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.	2.2	26
16	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.	2.2	23
17	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.	2.5	22
18	Key roles of the <i>Escherichia coli</i> 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.	1.0	21

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19	Transition steps in peroxide reduction and a molecular switch for peroxide robustness of prokaryotic peroxiredoxins. <i>Scientific Reports</i> , 2016, 6, 37610.	3.3	20
20	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.	4.6	18
21	Discovery of a genetic module essential for assigning left-right asymmetry in humans and ancestral vertebrates. <i>Nature Genetics</i> , 2022, 54, 62-72.	21.4	16
22	The Recipe for Protein Sequence-Based Function Prediction and Its Implementation in the ANNOTATOR Software Environment. <i>Methods in Molecular Biology</i> , 2016, 1415, 477-506.	0.9	15
23	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. <i>Cell Cycle</i> , 2018, 17, 874-880.	2.6	14
24	Isolation and Identification of an Anthracimycin Analogue from <i>Nocardioopsis kunsanensis</i> , a Halophile from a Saltern, by Genomic Mining Strategy. <i>Journal of Genomics</i> , 2018, 6, 63-73.	0.9	13
25	Integrated Tools for Biomolecular Sequence-Based Function Prediction as Exemplified by the ANNOTATOR Software Environment. <i>Methods in Molecular Biology</i> , 2010, 609, 257-267.	0.9	13
26	Structural insight into the glycosylphosphatidylinositol transamidase subunits PIG-K and PIG-S from yeast. <i>Journal of Structural Biology</i> , 2011, 173, 271-281.	2.8	12
27	BEWARE OF MOVING TARGETS: REFERENCE PROTEOME CONTENT FLUCTUATES SUBSTANTIALLY OVER THE YEARS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1250020.	0.8	12
28	Crystallographic and solution studies of NAD ⁺ - and NADH-bound alkylhydroperoxide reductase subunit F (AhpF) from <i>Escherichia coli</i> provide insight into sequential enzymatic steps. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2015, 1847, 1139-1152.	1.0	12
29	Molecular mechanism of the <i>Escherichia coli</i> AhpC in the function of a chaperone under heat-shock conditions. <i>Scientific Reports</i> , 2018, 8, 14151.	3.3	11
30	On the necessity of dissecting sequence similarity scores into segment-specific contributions for inferring protein homology, function prediction and annotation. <i>BMC Bioinformatics</i> , 2014, 15, 166.	2.6	10
31	Low resolution solution structure of an enzymatic active AhpC 10 :AhpF 2 ensemble of the <i>Escherichia coli</i> Alkyl hydroperoxide Reductase. <i>Journal of Structural Biology</i> , 2016, 193, 13-22.	2.8	10
32	¹ H-NMR studies reveal a novel grab and release mechanism for efficient catalysis of the bacterial 2-Cys peroxiredoxin machinery. <i>FEBS Journal</i> , 2015, 282, 4620-4638.	4.7	9
33	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.	2.8	9
34	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.	4.6	9
35	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.	2.9	7
36	Low-resolution structure of the soluble domain GPAA1 (yGPAA170-247) of the glycosylphosphatidylinositol transamidase subunit GPAA1 from <i>Saccharomyces cerevisiae</i> . <i>Bioscience Reports</i> , 2013, 33, e00033.	2.4	6

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37	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.	1.3	6
38	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.	4.6	6
39	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.	3.4	5
40	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.	4.1	5
41	xHMMER3x2: Utilizing HMMER3's speed and HMMER2's sensitivity and specificity in the glocal alignment mode for improved large-scale protein domain annotation. <i>Biology Direct</i> , 2016, 11, 63.	4.6	4
42	Purification and crystallization of yeast glycosylphosphatidylinositol transamidase subunit PIG-S (PIG-S71-467). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 896-899.	0.7	3
43	HPMV: Human protein mutation viewer relating sequence mutations to protein sequence architecture and function changes. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550028.	0.8	2
44	Optimizing the Parametrization of Homologue Classification in the Pan-Genome Computation for a Bacterial Species: Case Study <i>Streptococcus pyogenes</i> . <i>Methods in Molecular Biology</i> , 2022, 2449, 299-324.	0.9	1
45	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