Birgit Eisenhaber

List of Publications by Year
in descending order

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	Discovery of a genetic module essential for assigning left–right asymmetry in humans and ancestral vertebrates. Nature Genetics, 2022, 54, 62-72.	21.4	16
2	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.	0.9	1
3	Functional Classification of Super-Large Families of Enzymes Based on Substrate Binding Pocket Residues for Biocatalysis and Enzyme Engineering Applications. Frontiers in Bioengineering and Biotechnology, 2021, 9, 701120.	4.1	5
4	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. Biology Direct, 2021, 16, 4.	4.6	9
5	Structural modelling of the lumenal domain of human GPAA1, the metallo-peptide synthetase subunit of the transamidase complex, reveals zinc-binding mode and two flaps surrounding the active site. Biology Direct, 2020, 15, 14.	4.6	6
6	Hypocrisy Around Medical Patient Data: Issues of Access for Biomedical Research, Data Quality, Usefulness for the Purpose and Omics Data as Game Changer. Asian Bioethics Review, 2019, 11, 189-207.	1.3	6
7	Genomics-driven discovery of a biosynthetic gene cluster required for the synthesis of BII-Rafflesfungin from the fungus Phoma sp. F3723. BMC Genomics, 2019, 20, 374.	2.8	9
8	Active site CP-loop dynamics modulate substrate binding, catalysis, oligomerization, stability, over-oxidation and recycling of 2-Cys Peroxiredoxins. Free Radical Biology and Medicine, 2018, 118, 59-70.	2.9	7
9	Molecular mechanism of the Escherichia coli AhpC in the function of a chaperone under heat-shock conditions. Scientific Reports, 2018, 8, 14151.	3.3	11
10	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. Proteomics, 2018, 18, e1800093.	2.2	26
11	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.	2.6	14
12	The 160K Natural Organism Library, a unique resource for natural products research. Nature Biotechnology, 2018, 36, 570-573.	17.5	27
13	Isolation and Identification of an Anthracimycin Analogue from <i>Nocardiopsis kunsanensis</i>, a Halophile from a Saltern, by Genomic Mining Strategy. Journal of Genomics, 2018, 6, 63-73.	0.9	13
14	Essential role of the flexible linker on the conformational equilibrium of bacterial peroxiredoxin reductase for effective regeneration of peroxiredoxin. Journal of Biological Chemistry, 2017, 292, 6667-6679.	3.4	5
15	Prenylation of viral proteins by enzymes of the host: Virus–driven rationale for therapy with statins and FT/GGT1 inhibitors. BioEssays, 2017, 39, 1700014.	2.5	22
16	Charged residues next to transmembrane regions revisited: "Positive-inside rule" is complemented by the "negative inside depletion/outside enrichment rule". BMC Biology, 2017, 15, 66.	3.8	64
17	xHMMER3x2: Utilizing HMMER3's speed and HMMER2's sensitivity and specificity in the glocal alignment mode for improved large-scale protein domain annotation. Biology Direct, 2016, 11, 63.	4.6	4
18	Transition steps in peroxide reduction and a molecular switch for peroxide robustness of prokaryotic peroxiredoxins. Scientific Reports, 2016, 6, 37610.	3.3	20

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19	The Recipe for Protein Sequence-Based Function Prediction and Its Implementation in the ANNOTATOR Software Environment. Methods in Molecular Biology, 2016, 1415, 477-506.	0.9	15
20	Low resolution solution structure of an enzymatic active AhpC 10 :AhpF 2 ensemble of the Escherichia coli Alkyl hydroperoxide Reductase. Journal of Structural Biology, 2016, 193, 13-22.	2.8	10
21	Single‐residue posttranslational modification sites at the N‐terminus, C‐terminus or in‐between: To be or not to be exposed for enzyme access. Proteomics, 2015, 15, 2525-2546.	2.2	23
22	dissectHMMER: a HMMER-based score dissection framework that statistically evaluates fold-critical sequence segments for domain fold similarity. Biology Direct, 2015, 10, 39.	4.6	18
23	<scp>NMR</scp> studies reveal a novel grab and release mechanism for efficient catalysis of the bacterial 2‐Cys peroxiredoxin machinery. FEBS Journal, 2015, 282, 4620-4638.	4.7	9
24	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.	1.0	12
25	HPMV: Human protein mutation viewer â€" relating sequence mutations to protein sequence architecture and function changes. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550028.	0.8	2
26	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. Cell Cycle, 2014, 13, 1912-1917.	2.6	41
27	Structure, mechanism and ensemble formation of the alkylhydroperoxide reductase subunits AhpC and AhpF from<i>Escherichia coli</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2848-2862.	2.5	47
28	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.	2.6	10
29	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. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 1932-1943.	1.0	21
30	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
31	How bioinformatics influences health informatics: usage of biomolecular sequences, expression profiles and automated microscopic image analyses for clinical needs and public health. Health Information Science and Systems, 2013, 1, 2.	5.2	32
32	Low-resolution structure of the soluble domain GPAA1 (yGPAA170â€"247) of the glycosylphosphatidylinositol transamidase subunit GPAA1 from Saccharomyces cerevisiae. Bioscience Reports, 2013, 33, e00033.	2.4	6
33	BEWARE OF MOVING TARGETS: REFERENCE PROTEOME CONTENT FLUCTUATES SUBSTANTIALLY OVER THE YEARS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250020.	0.8	12
34	Structural insight into the glycosylphosphatidylinositol transamidase subunits PIG-K and PIG-S from yeast. Journal of Structural Biology, 2011, 173, 271-281.	2.8	12
35	Purification and crystallization of yeast glycosylphosphatidylinositol transamidase subunit PIG-S (PIG-S71â€"467). Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 896-899.	0.7	3
36	Integrated Tools for Biomolecular Sequence-Based Function Prediction as Exemplified by the ANNOTATOR Software Environment. Methods in Molecular Biology, 2010, 609, 257-267.	0.9	13

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37	Posttranslational Modifications and Subcellular Localization Signals: Indicators of Sequence Regions without Inherent 3D Structure?. Current Protein and Peptide Science, 2007, 8, 197-203.	1.4	48
38	TM or not TM: transmembrane protein prediction with low false positive rate using DAS-TMfilter. Bioinformatics, 2004, 20, 136-137.	4.1	113
39	Prediction of sequence signals for lipid post-translational modifications: Insights from case studies. Proteomics, 2004, 4, 1614-1625.	2.2	42
40	A Sensitive Predictor for Potential GPI Lipid Modification Sites in Fungal Protein Sequences and its Application to Genome-wide Studies for Aspergillus nidulans, Candida albicans Neurospora crassa, Saccharomyces cerevisiae and Schizosaccharomyces pombe. Journal of Molecular Biology, 2004, 337, 243-253.	4.2	262
41	Enzymes and auxiliary factors for GPI lipid anchor biosynthesis and post‐translational transfer to proteins. BioEssays, 2003, 25, 367-385.	2.5	156
42	Glycosylphosphatidylinositol Lipid Anchoring of Plant Proteins. Sensitive Prediction from Sequence- and Genome-Wide Studies for Arabidopsis and Rice. Plant Physiology, 2003, 133, 1691-1701.	4.8	185
43	Prediction of lipid posttranslational modifications and localization signals from protein sequences: big-Â, NMT and PTS1. Nucleic Acids Research, 2003, 31, 3631-3634.	14.5	78
44	On filtering false positive transmembrane protein predictions. Protein Engineering, Design and Selection, 2002, 15, 745-752.	2.1	128
45	Prediction of Potential GPI-modification Sites in Proprotein Sequences. Journal of Molecular Biology, 1999, 292, 741-758.	4.2	417