

Gregor GünÄar

List of Publications by Year in descending order

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32
papers

1,973
citations

394421

19
h-index

477307

29
g-index

32
all docs

32
docs citations

32
times ranked

2726
citing authors

#	ARTICLE	IF	CITATIONS
1	Revised Definition of Substrate Binding Sites of Papain-Like Cysteine Proteases. <i>Biological Chemistry</i> , 1998, 379, 137-148.	2.5	218
2	Crystal structure of MHC class II-associated p41 li fragment bound to cathepsin L reveals the structural basis for differentiation between cathepsins L and S. <i>EMBO Journal</i> , 1999, 18, 793-803.	7.8	188
3	Crystal structure of porcine cathepsin H determined at 2.1 Å resolution: location of the mini-chain C-terminal carboxyl group defines cathepsin H aminopeptidase function. <i>Structure</i> , 1998, 6, 51-61.	3.3	161
4	Lysosomal cathepsins: structure, role in antigen processing and presentation, and cancer. <i>Advances in Enzyme Regulation</i> , 2002, 42, 285-303.	2.6	160
5	Crystal Structures of Flax Rust Avirulence Proteins AvrL567-A and -D Reveal Details of the Structural Basis for Flax Disease Resistance Specificity. <i>Plant Cell</i> , 2007, 19, 2898-2912.	6.6	143
6	Lysosomal cysteine proteases (cathepsins): promising drug targets. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 203-213.	2.5	109
7	Crystal Structure of Stefin A in Complex with Cathepsin H: N-terminal Residues of Inhibitors can Adapt to the Active Sites of Endo- and Exopeptidases. <i>Journal of Molecular Biology</i> , 2003, 326, 875-885.	4.2	102
8	Essential Role of Proline Isomerization in Stefin B Tetramer Formation. <i>Journal of Molecular Biology</i> , 2007, 366, 1569-1579.	4.2	93
9	Crystal structure and its bearing towards an understanding of key biological functions of EpCAM. <i>Nature Communications</i> , 2014, 5, 4764.	12.8	86
10	Inhibitory Fragment from the p41 Form of Invariant Chain Can Regulate Activity of Cysteine Cathepsins in Antigen Presentation. <i>Journal of Biological Chemistry</i> , 2008, 283, 14453-14460.	3.4	80
11	Crystal structure of cathepsin X: a flip-flop of the ring of His23 allows carboxy-monopeptidase and carboxy-dipeptidase activity of the protease. <i>Structure</i> , 2000, 8, 305-313.	3.3	79
12	Structural basis for recruitment of tandem hotdog domains in acyl-CoA thioesterase 7 and its role in inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10382-10387.	7.1	71
13	Biochemical characterization of human cathepsin X revealed that the enzyme is an exopeptidase, acting as carboxymonopeptidase or carboxydipeptidase. <i>FEBS Journal</i> , 2000, 267, 5404-5412.	0.2	70
14	Molecular basis of Colorado potato beetle adaptation to potato plant defence at the level of digestive cysteine proteinases. <i>Insect Biochemistry and Molecular Biology</i> , 2004, 34, 365-375.	2.7	62
15	Crystallography and protein-protein interactions: biological interfaces and crystal contacts. <i>Biochemical Society Transactions</i> , 2008, 36, 1438-1441.	3.4	61
16	Averaged kick maps: less noise, more signal and probably less bias. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 921-931.	2.5	59
17	Mechanisms of amyloid fibril formation – focus on domain-swapping. <i>FEBS Journal</i> , 2011, 278, 2263-2282.	4.7	55
18	Different propensity to form amyloid fibrils by two homologous proteins-Human stefins A and B: Searching for an explanation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 417-425.	2.6	41

#	ARTICLE	IF	CITATIONS
19	Phosphorylation of C-terminal tyrosine 526 in FUS impairs its nuclear import. <i>Journal of Cell Science</i> , 2015, 128, 4151-9.	2.0	27
20	Analysis of the N-terminal region of human MLKL, as well as two distinct MLKL isoforms, reveals new insights into necroptotic cell death. <i>Bioscience Reports</i> , 2016, 36, e00291.	2.4	21
21	Folding and amyloid-fibril formation for a series of human stefins' chimeras: Any correlation?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 918-927.	2.6	19
22	Focusing in on structural genomics: The University of Queensland structural biology pipeline. <i>New Biotechnology</i> , 2006, 23, 281-289.	2.7	14
23	The use of Co ²⁺ for crystallization and structure determination, using a conventional monochromatic X-ray source, of flax rust avirulence protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 209-213.	0.7	14
24	The p41 Fragment Story. <i>IUBMB Life</i> , 1999, 48, 7-12.	3.4	10
25	The p41 Fragment Story. <i>IUBMB Life</i> , 1999, 48, 7-12.	3.4	9
26	Modulation of Contact Order Effects in the Two-State Folding of Stefins A and B. <i>Biophysical Journal</i> , 2011, 100, 2268-2274.	0.5	8
27	Proper evaluation of chemical cross-linking-based spatial restraints improves the precision of modeling homo-oligomeric protein complexes. <i>BMC Bioinformatics</i> , 2019, 20, 464.	2.6	7
28	Application of lectin immobilized on polyHIPE monoliths for bioprocess monitoring of glycosylated proteins. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2021, 1174, 122731.	2.3	4
29	Overview of the Pipeline for Structural and Functional Characterization of Macrophage Proteins at the University of Queensland. <i>Methods in Molecular Biology</i> , 2008, 426, 577-587.	0.9	1
30	Lysosomal cysteine proteinases: Structure and regulation. , 1999, , 211-224.		1
31	Lysosomal Cysteine Proteases and Their Protein Inhibitor. , 2002, , 227-240.		0
32	Thyroxine hormones visualized by the cryo-EM structure of bovine thyroglobulin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1346-1347.	2.3	0