Dusan Turk

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7279039/publications.pdf

Version: 2024-02-01

60	4,430	117625	138484
papers	citations	34 h-index	58 g-index

62	62	62	6405
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cocaprins, Î²-Trefoil Fold Inhibitors of Cysteine and Aspartic Proteases from Coprinopsis cinerea. International Journal of Molecular Sciences, 2022, 23, 4916.	4.1	3
2	Mechanisms Applied by Protein Inhibitors to Inhibit Cysteine Proteases. International Journal of Molecular Sciences, 2021, 22, 997.	4.1	12
3	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. Science, 2021, 372, 642-646.	12.6	240
4	The Structure of Clostridioides difficile SecA2 ATPase Exposes Regions Responsible for Differential Target Recognition of the SecA1 and SecA2-Dependent Systems. International Journal of Molecular Sciences, 2020, 21, 6153.	4.1	0
5	Insights into the Maturation of Pernisine, a Subtilisin-Like Protease from the Hyperthermophilic Archaeon Aeropyrum pernix. Applied and Environmental Microbiology, 2020, 86, .	3.1	3
6	Domain sliding of two Staphylococcus aureus N-acetylglucosaminidases enables their substrate-binding prior to its catalysis. Communications Biology, 2020, 3, 178.	4.4	7
7	The structure of human thyroglobulin. Nature, 2020, 578, 627-630.	27.8	81
8	Fluorescent probes towards selective cathepsin B detection and visualization in cancer cells and patient samples. Chemical Science, 2019, 10, 8461-8477.	7.4	47
9	The Alkyne Moiety as a Latent Electrophile in Irreversible Covalent Small Molecule Inhibitors of Cathepsin K. Journal of the American Chemical Society, 2019, 141, 3507-3514.	13.7	72
10	In Silico Design of Bacterial N-acetylglucosaminidase Inhibitors with Potential Antibacterial Activity. Proceedings (mdpi), 2019, 22, 105.	0.2	0
11	A Water-Assisted Catalytic Mechanism in Glycoside Hydrolases Demonstrated on the Staphylococcus aureus Autolysin E. ACS Catalysis, 2018, 8, 4334-4345.	11.2	13
12	Selective imaging of cathepsinÂL in breast cancer by fluorescent activity-based probes. Chemical Science, 2018, 9, 2113-2129.	7.4	64
13	Discovery of (phenylureido)piperidinyl benzamides as prospective inhibitors of bacterial autolysin E from Staphylococcus aureus. Journal of Enzyme Inhibition and Medicinal Chemistry, 2018, 33, 1239-1247.	5.2	4
14	The CWB2 Cell Wall-Anchoring Module Is Revealed by the Crystal Structures of the Clostridium difficile Cell Wall Proteins Cwp8 and Cwp6. Structure, 2017, 25, 514-521.	3.3	29
15	Highly sensitive and adaptable fluorescence-quenched pair discloses the substrate specificity profiles in diverse protease families. Scientific Reports, 2017, 7, 43135.	3.3	51
16	The mechanism behind the selection of two different cleavage sites in NAG-NAM polymers. IUCrJ, 2017, 4, 185-198.	2.2	12
17	Boxes of Model Building and Visualization. Methods in Molecular Biology, 2017, 1607, 491-548.	0.9	1
18	Protease cleavage site fingerprinting by labelâ€free inâ€gel degradomics reveals <scp>pH</scp> â€dependent specificity switch of legumain. EMBO Journal, 2017, 36, 2455-2465.	7.8	58

#	Article	IF	Citations
19	The Future of Cysteine Cathepsins in Disease Management. Trends in Pharmacological Sciences, 2017, 38, 873-898.	8.7	146
20	Proline Residues as Switches in Conformational Changes Leading to Amyloid Fibril Formation. International Journal of Molecular Sciences, 2017, 18, 549.	4.1	20
21	Non-invasive in vivo imaging of tumour-associated cathepsin B by a highly selective inhibitory DARPin. Theranostics, 2017, 7, 2806-2821.	10.0	40
22	Counter Selection Substrate Library Strategy for Developing Specific Protease Substrates and Probes. Cell Chemical Biology, 2016, 23, 1023-1035.	5.2	45
23	The CC domain structure from the wheat stem rust resistance protein Sr33 challenges paradigms for dimerization in plant NLR proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12856-12861.	7.1	105
24	FEM: feature-enhanced map. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 646-666.	2.5	157
25	Development of N-(Functionalized benzoyl)-homocycloleucyl-glycinonitriles as Potent Cathepsin K Inhibitors. Journal of Medicinal Chemistry, 2015, 58, 6928-6937.	6.4	24
26	Codon Optimisation Is Key for Pernisine Expression in Escherichia coli. PLoS ONE, 2015, 10, e0123288.	2.5	9
27	Free kick instead of cross-validation in maximum-likelihood refinement of macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3124-3134.	2.5	10
28	Fungal Î²-trefoil trypsin inhibitors cnispin and cospin demonstrate the plasticity of the Î²-trefoil fold. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1749-1756.	2.3	12
29	A novel Î²â€trefoil lectin from the parasol mushroom (MacrolepiotaÂprocera) is nematotoxic. FEBS Journal, 2014, 281, 3489-3506.	4.7	33
30	Partial rotational lattice orderâ€“disorder in stefin B crystals. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1015-1025.	2.5	11
31	MAINsoftware for density averaging, model building, structure refinement and validation. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1342-1357.	2.5	81
32	Î²-Trefoil inhibitors â€“ from the work of Kunitz onward. Biological Chemistry, 2012, 393, 1043-1054.	2.5	34
33	Structural Basis of Trypsin Inhibition and Entomotoxicity of Cospin, Serine Protease Inhibitor Involved in Defense of Coprinopsis cinerea Fruiting Bodies. Journal of Biological Chemistry, 2012, 287, 3898-3907.	3.4	46
34	Cysteine cathepsins: From structure, function and regulation to new frontiers. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 68-88.	2.3	990
35	Bivalent Carbohydrate Binding Is Required for Biological Activity of Clitocybe nebularis Lectin (CNL), the N,Nâ€²-Diacetyllactosediamine (GalNAcÎ²1â€“4GlcNAc, LacdiNAc)-specific Lectin from Basidiomycete C. nebularis. Journal of Biological Chemistry, 2012, 287, 10602-10612.	3.4	51
36	Expression, purification and assembly of soluble multimeric MHC class IIâ€“invariant chain complexes. FEBS Letters, 2012, 586, 1318-1324.	2.8	8

#	Article	IF	Citations
37	Mechanisms of amyloid fibril formation â€“ focus on domainâ€swapping. FEBS Journal, 2011, 278, 2263-2282.	4.7	55
38	Stefin A displaces the occluding loop of cathepsin B only by as much as required to bind to the active site cleft. FEBS Journal, 2010, 277, 4338-4345.	4.7	48
39	Versatile Loops in Mycocypins Inhibit Three Protease Families. Journal of Biological Chemistry, 2010, 285, 308-316.	3.4	55
40	Amyloid fibril formation by human stefins: Structure, mechanism & putative functions. Biochimie, 2010, 92, 1597-1607.	2.6	25
41	The mechanism of amyloidâ€fibril formation by stefin B: Temperature and protein concentration dependence of the rates. Proteins: Structure, Function and Bioinformatics, 2009, 74, 425-436.	2.6	43
42	PURY: a database of geometric restraints of hetero compounds for refinement in complexes with macromolecular structures. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1093-1109.	2.5	21
43	Cystatins: Biochemical and structural properties, and medical relevance. Frontiers in Bioscience - Landmark, 2008, Volume, 5406.	3.0	298
44	Size and morphology of toxic oligomers of amyloidogenic proteins: a case study of human stefin B. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2008, 15, 147-159.	3.0	34
45	Inhibitory Fragment from the p41 Form of Invariant Chain Can Regulate Activity of Cysteine Cathepsins in Antigen Presentation. Journal of Biological Chemistry, 2008, 283, 14453-14460.	3.4	80
46	Two decades of thyroglobulin type-1 domain research. Biological Chemistry, 2007, 388, 1123-1130.	2.5	45
47	Essential Role of Proline Isomerization in Stefin B Tetramer Formation. Journal of Molecular Biology, 2007, 366, 1569-1579.	4.2	93
48	Mouse stefins A1 and A2 (Stfa1andStfa2) differentiate between papain-like endo- and exopeptidases. FEBS Letters, 2006, 580, 4195-4199.	2.8	23
49	Regulating Cysteine Protease Activity: Essential Role of Protease Inhibitors as Guardians and Regulators. Medicinal Chemistry Reviews Online, 2005, 2, 283-297.	0.1	7
50	Different propensity to form amyloid fibrils by two homologous proteins-Human stefins A and B: Searching for an explanation. Proteins: Structure, Function and Bioinformatics, 2004, 55, 417-425.	2.6	41
51	Lysosomal cysteine proteases (cathepsins): promising drug targets. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 203-213.	2.5	109
52	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. Journal of Molecular Biology, 2003, 326, 875-885.	4.2	102
53	Papain-like lysosomal cysteine proteases and their inhibitors: drug discovery targets?. Biochemical Society Symposia, 2003, 70, 15-30.	2.7	37
54	Regulating Cysteine Protease Activity: Essential Role of Protease Inhibitors As Guardians and Regulators. Current Pharmaceutical Design, 2002, 8, 1623-1637.	1.9	221

#	Article	IF	Citations
55	Biochemical characterization of human cathepsin X revealed that the enzyme is an exopeptidase, acting as carboxymonopeptidase or carboxydipeptidase. FEBS Journal, 2000, 267, 5404-5412.	0.2	70
56	Crystal structure of the apoptotic suppressor CrmA in its cleaved form. Structure, 2000, 8, 789-797.	3.3	55
57	The p41 Fragment Story. IUBMB Life, 1999, 48, 7-12.	3.4	10
58	Crystal structure of MHC class II-associated p41 Ii fragment bound to cathepsin L reveals the structural basis for differentiation between cathepsins L and S. EMBO Journal, 1999, 18, 793-803.	7.8	188
59	Crystal structure of the wild-type human procathepsin B at 2.5 Ã... resolution reveals the native active site of a papain-like cysteine protease zymogen. Journal of Molecular Biology, 1997, 271, 774-788.	4.2	111
60	Crystal structures of human procathepsin B at 3.2 and 3.3 Ã... resolution reveal an interaction motif between a papain-like cysteine protease and its propeptide. FEBS Letters, 1996, 384, 211-214.	2.8	131