

Stefano Ricagno

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

2,364
citations

218381

26
h-index

223531

46
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75
all docs

75
docs citations

75
times ranked

2991
citing authors

#	ARTICLE	IF	CITATIONS
1	Protease-sensitive regions in amyloid light chains: what a common pattern of fragmentation across organs suggests about aggregation. <i>FEBS Journal</i> , 2022, 289, 494-506.	2.2	25
2	Cu(II) Binding Increases the Soluble Toxicity of Amyloidogenic Light Chains. <i>International Journal of Molecular Sciences</i> , 2022, 23, 950.	1.8	1
3	<sc>l</sc>- to <sc>d</sc>-Amino Acid Substitution in the Immunodominant LCMV-Derived Epitope gp33 Highlights the Sensitivity of the TCR Recognition Mechanism for the MHC/Peptide Structure and Dynamics. <i>ACS Omega</i> , 2022, 7, 9622-9635.	1.6	1
4	An N-glycosylation hotspot in immunoglobulin λ light chains is associated with AL amyloidosis. <i>Leukemia</i> , 2022, 36, 2076-2085.	3.3	10
5	Multi- <i>e</i> GO: An in silico lens to look into protein aggregation kinetics at atomic resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	7
6	Neuroserpin: structure, function, physiology and pathology. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 6409-6430.	2.4	16
7	β 2-microglobulin triggers NLRP3 inflammasome activation in tumor-associated macrophages to promote multiple myeloma progression. <i>Immunity</i> , 2021, 54, 1772-1787.e9.	6.6	49
8	Biochemical and biophysical comparison of human and mouse β 2 microglobulin reveals the molecular determinants of low amyloid propensity. <i>FEBS Journal</i> , 2020, 287, 546-560.	2.2	11
9	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. <i>Journal of Molecular Biology</i> , 2020, 432, 845-860.	2.0	26
10	Embelin as Lead Compound for New Neuroserpin Polymerization Inhibitors. <i>Life</i> , 2020, 10, 111.	1.1	10
11	Two novel fish paralogs provide insights into the Rid family of imine deaminases active in pre-empting enamine/imine metabolic damage. <i>Scientific Reports</i> , 2020, 10, 10135.	1.6	4
12	Conformational Stability and Dynamics in Crystals Recapitulate Protein Behavior in Solution. <i>Biophysical Journal</i> , 2020, 119, 978-988.	0.2	3
13	Mass spectrometry characterization of light chain fragmentation sites in cardiac AL amyloidosis: insights into the timing of proteolysis. <i>Journal of Biological Chemistry</i> , 2020, 295, 16572-16584.	1.6	32
14	Glycosylation Tunes Neuroserpin Physiological and Pathological Properties. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3235.	1.8	11
15	Modulating the cardiotoxic behaviour of immunoglobulin light chain dimers through point mutations. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2019, 26, 105-106.	1.4	4
16	The concurrency of several biophysical traits links immunoglobulin light chains with toxicity in AL amyloidosis. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2019, 26, 107-108.	1.4	2
17	Investigating the Molecular Basis of the Aggregation Propensity of the Pathological D76N Mutant of Beta-2 Microglobulin: Role of the Denatured State. <i>International Journal of Molecular Sciences</i> , 2019, 20, 396.	1.8	5
18	Cryo-EM structure of cardiac amyloid fibrils from an immunoglobulin light chain AL amyloidosis patient. <i>Nature Communications</i> , 2019, 10, 1269.	5.8	113

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19	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. <i>Nature Communications</i> , 2018, 9, 1658.	5.8	53
20	An Asp to Asn mutation is a toxic trigger in beta-2 microglobulin: structure and biophysics. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2017, 24, 15-16.	1.4	2
21	Concurrent structural and biophysical traits link with immunoglobulin light chains amyloid propensity. <i>Scientific Reports</i> , 2017, 7, 16809.	1.6	50
22	FRET studies of various conformational states adopted by transthyretin. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3577-3598.	2.4	7
23	Embelin binds to human neuroserpin and impairs its polymerisation. <i>Scientific Reports</i> , 2016, 6, 18769.	1.6	13
24	Rational design of mutations that change the aggregation rate of a protein while maintaining its native structure and stability. <i>Scientific Reports</i> , 2016, 6, 25559.	1.6	47
25	Tools for the rational design of bivalent microtubule-targeting drugs. <i>Biochemical and Biophysical Research Communications</i> , 2016, 479, 48-53.	1.0	10
26	Molecular basis of a novel renal amyloidosis due to N184K gelsolin variant. <i>Scientific Reports</i> , 2016, 6, 33463.	1.6	12
27	A covalent homodimer probing early oligomers along amyloid aggregation. <i>Scientific Reports</i> , 2015, 5, 14651.	1.6	13
28	Wild Type Beta-2 Microglobulin and DE Loop Mutants Display a Common Fibrillar Architecture. <i>PLoS ONE</i> , 2015, 10, e0122449.	1.1	14
29	Decoding the Structural Bases of D76N β 2-Microglobulin High Amyloidogenicity through Crystallography and Asn-Scan Mutagenesis. <i>PLoS ONE</i> , 2015, 10, e0144061.	1.1	22
30	Functional and dysfunctional conformers of human neuroserpin characterized by optical spectroscopies and Molecular Dynamics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 110-117.	1.1	13
31	Class I Major Histocompatibility Complex, the Trojan Horse for Secretion of Amyloidogenic β 2-Microglobulin. <i>Journal of Biological Chemistry</i> , 2014, 289, 3318-3327.	1.6	22
32	Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. <i>Journal of the American Chemical Society</i> , 2014, 136, 12489-12497.	6.6	254
33	Edge strand engineering prevents native-like aggregation in <i>Sulfolobus solfataricus</i> acylphosphatase. <i>FEBS Journal</i> , 2014, 281, 4072-4084.	2.2	13
34	Hereditary Systemic Amyloidosis Due to Asp76Asn Variant β 2-Microglobulin. <i>New England Journal of Medicine</i> , 2012, 366, 2276-2283.	13.9	172
35	Structure, Stability, and Aggregation of β 2-Microglobulin Mutants: Insights from a Fourier Transform Infrared Study in Solution and in the Crystalline State. <i>Biophysical Journal</i> , 2012, 102, 1676-1684.	0.2	31
36	On the molecular structure of human neuroserpin polymers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 8-13.	1.5	21

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37	A recurrent Dâ€strand association interface is observed in Î²â€ microglobulin oligomers. FEBS Journal, 2012, 279, 1131-1143.	2.2	18
38	The Tempered Polymerization of Human Neuroserpin. PLoS ONE, 2012, 7, e32444.	1.1	28
39	Dâ€strand perturbation and amyloid propensity in betaâ€ microglobulin. FEBS Journal, 2011, 278, 2349-2358.	2.2	13
40	The two tryptophans of Î²2-microglobulin have distinct roles in function and folding and might represent two independent responses to evolutionary pressure. BMC Evolutionary Biology, 2011, 11, 159.	3.2	16
41	Characterization of Î²2â€microglobulin conformational intermediates associated to different fibrillation conditions. Journal of Mass Spectrometry, 2011, 46, 734-741.	0.7	13
42	The effects of an ideal Î²-turn on Î²-2 microglobulin fold stability. Journal of Biochemistry, 2011, 150, 39-47.	0.9	9
43	DEâ€loop mutations affect Î²2 microglobulin stability, oligomerization, and the lowâ€pH unfolded form. Protein Science, 2010, 19, 1386-1394.	3.1	43
44	Molecular bases of neuroserpin function and pathology. Biomolecular Concepts, 2010, 1, 117-130.	1.0	9
45	Two Latent and Two Hyperstable Polymeric Forms of Human Neuroserpin. Biophysical Journal, 2010, 99, 3402-3411.	0.2	20
46	Fibrillar vs Crystalline Full-Length Î²-2-Microglobulin Studied by High-Resolution Solid-State NMR Spectroscopy. Journal of the American Chemical Society, 2010, 132, 5556-5557.	6.6	32
47	Human beta-2 microglobulin W60V mutant structure: Implications for stability and amyloid aggregation. Biochemical and Biophysical Research Communications, 2009, 380, 543-547.	1.0	29
48	Recognition of RNA Cap in the Wesselsbron Virus NS5 Methyltransferase Domain: Implications for RNA-Capping Mechanisms in Flavivirus. Journal of Molecular Biology, 2009, 385, 140-152.	2.0	78
49	Human Neuroserpin: Structure and Time-Dependent Inhibition. Journal of Molecular Biology, 2009, 388, 109-121.	2.0	41
50	CtBP1/BARS Gly172 â†' Glu mutant structure: Impairing NAD(H)-binding and dimerization. Biochemical and Biophysical Research Communications, 2009, 381, 70-74.	1.0	21
51	The Controlling Roles of Trp60 and Trp95 in Î²2-Microglobulin Function, Folding and Amyloid Aggregation Properties. Journal of Molecular Biology, 2008, 378, 887-897.	2.0	82
52	DE loop mutations affect Î²2-microglobulin stability and amyloid aggregation. Biochemical and Biophysical Research Communications, 2008, 377, 146-150.	1.0	36
53	De Novo Initiation of RNA Synthesis by the Arterivirus RNA-Dependent RNA Polymerase. Journal of Virology, 2007, 81, 8384-8395.	1.5	60
54	The crystal structure of FdxA, a 7Fe ferredoxin from Mycobacterium smegmatis. Biochemical and Biophysical Research Communications, 2007, 360, 97-102.	1.0	16

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55	Crystallization and preliminary X-ray diffraction analysis of Nsp15 from SARS coronavirus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 409-411.	0.7	10
56	Detection and characterization of merohedral twinning in crystals of oxalyl-coenzyme A decarboxylase from <i>Oxalobacter formigenes</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 122-128.	1.1	3
57	Crystal Structure of the Receptor-Binding Protein Head Domain from <i>Lactococcus lactis</i> Phage bIL170. <i>Journal of Virology</i> , 2006, 80, 9331-9335.	1.5	62
58	Crystal structure and mechanistic determinants of SARS coronavirus nonstructural protein 15 define an endoribonuclease family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11892-11897.	3.3	161
59	The enzymes of oxalate metabolism: unexpected structures and mechanisms. <i>Archives of Biochemistry and Biophysics</i> , 2005, 433, 176-192.	1.4	141
60	Kinetic and Mechanistic Characterization of the Formyl-CoA Transferase from <i>Oxalobacter formigenes</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 36003-36012.	1.6	51
61	Crystal structure of 1-deoxy-d-xylulose-5-phosphate reductoisomerase from <i>Zymomonas mobilis</i> at 1.9-Å... resolution. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1698, 37-44.	1.1	34
62	Formyl-CoA transferase encloses the CoA binding site at the interface of an interlocked dimer. <i>EMBO Journal</i> , 2003, 22, 3210-3219.	3.5	45
63	Crystal structure of thiamindiphosphate-dependent indolepyruvate decarboxylase from <i>Enterobacter cloacae</i> , an enzyme involved in the biosynthesis of the plant hormone indole-3-acetic acid. <i>FEBS Journal</i> , 2003, 270, 2312-2321.	0.2	65
64	Crystallization and preliminary crystallographic analysis of formyl-CoA transferase from <i>Oxalobacter formigenes</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1276-1277.	2.5	4
65	Crystal Structure of the Productive Ternary Complex of Dihydropyrimidine Dehydrogenase with NADPH and 5-Iodouracil. <i>Journal of Biological Chemistry</i> , 2002, 277, 13155-13166.	1.6	51
66	DcE2F, a Functional Plant E2F-like Transcriptional Activator from <i>Daucus carota</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 19258-19267.	1.6	58