

Vassiliki A Iconomidou

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

1,887
citations

331670

21
h-index

276875

41
g-index

67
all docs

67
docs citations

67
times ranked

2428
citing authors

#	ARTICLE	IF	CITATIONS
1	Third dose of the <scp>BNT162b2</scp> vaccine results in very high levels of neutralizing antibodies against <scp>SARS-CoV-2</scp>: Results of a prospective study in 150 health professionals in Greece. <i>American Journal of Hematology</i> , 2022, 97, .	4.1	10
2	Clusterin in Alzheimer's disease: An amyloidogenic inhibitor of amyloid formation?. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2022, 1868, 166384.	3.8	11
3	Arabidopsis thaliana Plant Natriuretic Peptide Active Domain Forms Amyloid-like Fibrils in a pH-Dependent Manner. <i>Plants</i> , 2022, 11, 9.	3.5	2
4	LiGloNs: A computational method for the detection and classification of ligand-gated ion channels. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022, 1864, 183956.	2.6	1
5	SARS-CoV-2 Neutralizing Antibodies Kinetics Postvaccination in Cancer Patients under Treatment with Immune Checkpoint Inhibition. <i>Cancers</i> , 2022, 14, 2796.	3.7	9
6	SARS-CoV-2 Amino Acid Mutations Detection in Greek Patients Infected in the First Wave of the Pandemic. <i>Microorganisms</i> , 2022, 10, 1430.	3.6	0
7	Approaches in Gene Coexpression Analysis in Eukaryotes. <i>Biology</i> , 2022, 11, 1019.	2.8	4
8	Exploring the conservation of Alzheimer-related pathways between <i>H. sapiens</i> and <i>C. elegans</i> : a network alignment approach. <i>Scientific Reports</i> , 2021, 11, 4572.	3.3	10
9	Linear B-Cell Epitope Prediction for In Silico Vaccine Design: A Performance Review of Methods Available via Command-Line Interface. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3210.	4.1	60
10	From Proteomic Mapping to Invasion-Metastasis-Cascade Systemic Biomarkering and Targeted Drugging of Mutant BRAF-Dependent Human Cutaneous Melanomagenesis. <i>Cancers</i> , 2021, 13, 2024.	3.7	5
11	PerMemDB: A database for eukaryotic peripheral membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183076.	2.6	14
12	Extended Human G-Protein Coupled Receptor Network: Cell-Type-Specific Analysis of G-Protein Coupled Receptor Signaling Pathways. <i>Journal of Proteome Research</i> , 2020, 19, 511-524.	3.7	12
13	Investigation of the interaction of DAD1-LIKE LIPASE 3 (DALL3) with Selenium Binding Protein 1 (SBP1) in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2020, 291, 110357.	3.6	9
14	Visualization and analysis of the interaction network of proteins associated with blood-cell targeting autoimmune diseases. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165714.	3.8	3
15	ANTISOMA: A Computational Pipeline for the Reduction of the Aggregation Propensity of Monoclonal Antibodies. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1194, 359-371.	1.6	0
16	The amyloid interactome 2: mapping protein aggregation. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2019, 26, 142-143.	3.0	1
17	Novel interactions of Selenium Binding Protein family with the PICOT containing proteins AtGRXS14 and AtGRXS16 in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2019, 281, 102-112.	3.6	8
18	Delving into the amyloidogenic core of human leukocyte chemotactic factor 2. <i>Journal of Structural Biology</i> , 2019, 207, 260-269.	2.8	7

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19	AmyCo: the amyloidoses collection. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2019, 26, 112-117.	3.0	12
20	Hidden Aggregation Hot-Spots on Human Apolipoprotein E: A Structural Study. International Journal of Molecular Sciences, 2019, 20, 2274.	4.1	9
21	The gram-negative outer membrane modeler: Automated building of lipopolysaccharide-rich bacterial outer membranes in four force fields. Journal of Computational Chemistry, 2019, 40, 1727-1734.	3.3	17
22	Gene-Specific Intron Retention Serves as Molecular Signature that Distinguishes Melanoma from Non-Melanoma Cancer Cells in Greek Patients. International Journal of Molecular Sciences, 2019, 20, 937.	4.1	8
23	Analysis of Single-Nucleotide Polymorphisms in Human Voltage-Gated Ion Channels. Journal of Proteome Research, 2019, 18, 2310-2320.	3.7	3
24	Revisiting Histone Deacetylases in Human Tumorigenesis: The Paradigm of Urothelial Bladder Cancer. International Journal of Molecular Sciences, 2019, 20, 1291.	4.1	47
25	Î±CGRP, another amyloidogenic member of the CGRP family. Journal of Structural Biology, 2018, 203, 27-36.	2.8	6
26	Hexapeptide Tandem Repeats Dictate the Formation of Silkmoth Chorion, a Natural Protective Amyloid. Journal of Molecular Biology, 2018, 430, 3774-3783.	4.2	10
27	Unraveling the aggregation propensity of human insulin C-peptide. Biopolymers, 2017, 108, e22882.	2.4	3
28	Tracking the amyloidogenic core of IAPP amyloid fibrils: Insights from micro-Raman spectroscopy. Journal of Structural Biology, 2017, 199, 140-152.	2.8	9
29	Exploring Amyloidogenicity of Clusterin: A Structural and Bioinformatics Analysis. Advances in Experimental Medicine and Biology, 2017, 989, 93-107.	1.6	3
30	Mining databases for protein aggregation: a review. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2017, 24, 143-152.	3.0	11
31	The amyloid interactome: Exploring protein aggregation. PLoS ONE, 2017, 12, e0173163.	2.5	25
32	Identification of an amyloid fibril forming segment of human Pmel17 repeat domain (<sc>RPT</sc>) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.4	18
33	Intrinsic aggregation propensity of the CsgB nucleator protein is crucial for curli fiber formation. Journal of Structural Biology, 2016, 195, 179-189.	2.8	18
34	A common "aggregation-prone" interface possibly participates in the self-assembly of human zona pellucida proteins. FEBS Letters, 2016, 590, 619-630.	2.8	30
35	A Î²-solenoid model of the Pmel17 repeat domain: insights to the formation of functional amyloid fibrils. Journal of Computer-Aided Molecular Design, 2016, 30, 153-164.	2.9	17
36	Chameleon "aggregation-prone" segments of apoA-I: A model of amyloid fibrils formed in apoA-I amyloidosis. International Journal of Biological Macromolecules, 2015, 79, 711-718.	7.5	29

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37	Exploring the β -aggregation-prone™ core of human Cystatin C: A structural study. <i>Journal of Structural Biology</i> , 2015, 191, 272-280.	2.8	26
38	Structural studies and cytotoxicity assays of β -aggregation-prone β -APP ⁸¹⁶ and its non-amyloidogenic variants suggest its important role in fibrillogenesis and cytotoxicity of human amylin. <i>Biopolymers</i> , 2015, 104, 196-205.	2.4	19
39	The pentapeptide LQVVR plays a pivotal role in human cystatin C fibrillization. <i>FEBS Letters</i> , 2015, 589, 159-164.	2.8	15
40	Structural studies of β -aggregation-prone β -peptide analogues of teleostean egg chorion ZPB proteins. <i>Biopolymers</i> , 2014, 102, 427-436.	2.4	16
41	An N-terminal pro-atrial natriuretic peptide (NT-proANP) β -aggregation-prone™ segment involved in isolated atrial amyloidosis. <i>FEBS Letters</i> , 2014, 588, 52-57.	2.8	25
42	Identification of a novel β -aggregation-prone™/ β -amyloidogenic determinant™ peptide in the sequence of the highly amyloidogenic human calcitonin. <i>FEBS Letters</i> , 2013, 587, 569-574.	2.8	18
43	LepChorionDB, a database of Lepidopteran chorion proteins and a set of tools useful for the identification of chorion proteins in Lepidopteran proteomes. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 189-196.	2.7	8
44	A Consensus Method for the Prediction of β -Aggregation-Prone™ Peptides in Globular Proteins. <i>PLoS ONE</i> , 2013, 8, e54175.	2.5	255
45	Structural Analysis of Peptide-Analogues of Human Zona Pellucida ZP1 Protein with Amyloidogenic Properties: Insights into Mammalian Zona Pellucida Formation. <i>PLoS ONE</i> , 2013, 8, e73258.	2.5	33
46	An amyloidogenic determinant in N-terminal pro-brain natriuretic peptide (nt-probnp): Implications for cardiac amyloidoses. <i>Biopolymers</i> , 2012, 98, 67-75.	2.4	10
47	The silkmoth eggshell as a natural amyloid shield for the safe development of insect oocyte and embryo: Insights from studies of silkmoth chorion protein peptide analogues of the B famil. <i>Biopolymers</i> , 2011, 96, 723-733.	2.4	12
48	A possible structural model of members of the CPF family of cuticular proteins implicating binding to components other than chitin. <i>Journal of Insect Physiology</i> , 2010, 56, 1420-1426.	2.0	17
49	Amyloidogenic determinants are usually not buried. <i>BMC Structural Biology</i> , 2009, 9, 44.	2.3	131
50	Prothymosin β immunoreactive carboxyl-terminal peptide TKKQKTDEDD stimulates lymphocyte reactions, induces dendritic cell maturation and adopts a β -sheet conformation in a sequence-specific manner. <i>Molecular Immunology</i> , 2009, 46, 784-792.	2.2	34
51	Natural Protective Amyloids. <i>Current Protein and Peptide Science</i> , 2008, 9, 291-309.	1.4	78
52	Drosophila cuticular proteins with the R&R Consensus: Annotation and classification with a new tool for discriminating RR-1 and RR-2 sequences. <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 754-760.	2.7	135
53	Dogfish egg case structural studies by ATR FT-IR and FT-Raman spectroscopy. <i>International Journal of Biological Macromolecules</i> , 2007, 41, 102-108.	7.5	13
54	Consensus prediction of amyloidogenic determinants in amyloid fibril-forming proteins. <i>International Journal of Biological Macromolecules</i> , 2007, 41, 295-300.	7.5	70

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55	Amyloid fibril formation propensity is inherent into the hexapeptide tandemly repeating sequence of the central domain of silkmoth chorion proteins of the A-family. <i>Journal of Structural Biology</i> , 2006, 156, 480-488.	2.8	39
56	Unique features of the structural model of α -hard α ™ cuticle proteins: implications for chitin α protein interactions and cross-linking in cuticle. <i>Insect Biochemistry and Molecular Biology</i> , 2005, 35, 553-560.	2.7	85
57	FT-Raman spectroscopy as diagnostic tool of Congo red binding to amyloids. <i>Biopolymers</i> , 2003, 72, 185-192.	2.4	12
58	A structural model of the chitin-binding domain of cuticle proteins. <i>Insect Biochemistry and Molecular Biology</i> , 2002, 32, 1577-1583.	2.7	81
59	α -Soft α -cuticle protein secondary structure as revealed by FT-Raman, ATR FT-IR and CD spectroscopy. <i>Insect Biochemistry and Molecular Biology</i> , 2001, 31, 877-885.	2.7	48
60	Amyloid-like fibrils from an 18-residue peptide analogue of a part of the central domain of the B-family of silkmoth chorion proteins. <i>FEBS Letters</i> , 2001, 499, 268-273.	2.8	30
61	Amyloids protect the silkmoth oocyte and embryo. <i>FEBS Letters</i> , 2000, 479, 141-145.	2.8	180
62	Is β^2 -pleated sheet the molecular conformation which dictates formation of helicoidal cuticle?. <i>Insect Biochemistry and Molecular Biology</i> , 1999, 29, 285-292.	2.7	48