

# Vassiliki A Iconomidou

## List of Publications by Year in descending order

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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	A Consensus Method for the Prediction of $\alpha$ -Aggregation-Prone <sup>TM</sup> Peptides in Globular Proteins. PLoS ONE, 2013, 8, e54175.	2.5	255
2	Amyloids protect the silkmooth oocyte and embryo. FEBS Letters, 2000, 479, 141-145.	2.8	180
3	Drosophila cuticular proteins with the R&R Consensus: Annotation and classification with a new tool for discriminating RR-1 and RR-2 sequences. Insect Biochemistry and Molecular Biology, 2007, 37, 754-760.	2.7	135
4	Amyloidogenic determinants are usually not buried. BMC Structural Biology, 2009, 9, 44.	2.3	131
5	Unique features of the structural model of $\alpha$ -hard <sup>TM</sup> cuticle proteins: implications for chitin $\alpha$ -protein interactions and cross-linking in cuticle. Insect Biochemistry and Molecular Biology, 2005, 35, 553-560.	2.7	85
6	A structural model of the chitin-binding domain of cuticle proteins. Insect Biochemistry and Molecular Biology, 2002, 32, 1577-1583.	2.7	81
7	Natural Protective Amyloids. Current Protein and Peptide Science, 2008, 9, 291-309.	1.4	78
8	Consensus prediction of amyloidogenic determinants in amyloid fibril-forming proteins. International Journal of Biological Macromolecules, 2007, 41, 295-300.	7.5	70
9	Linear B-Cell Epitope Prediction for In Silico Vaccine Design: A Performance Review of Methods Available via Command-Line Interface. International Journal of Molecular Sciences, 2021, 22, 3210.	4.1	60
10	Is $\beta$ -pleated sheet the molecular conformation which dictates formation of helicoidal cuticle?. Insect Biochemistry and Molecular Biology, 1999, 29, 285-292.	2.7	48
11	$\alpha$ -Soft <sup>TM</sup> -cuticle protein secondary structure as revealed by FT-Raman, ATR FT-IR and CD spectroscopy. Insect Biochemistry and Molecular Biology, 2001, 31, 877-885.	2.7	48
12	Revisiting Histone Deacetylases in Human Tumorigenesis: The Paradigm of Urothelial Bladder Cancer. International Journal of Molecular Sciences, 2019, 20, 1291.	4.1	47
13	Amyloid fibril formation propensity is inherent into the hexapeptide tandemly repeating sequence of the central domain of silkmooth chorion proteins of the A-family. Journal of Structural Biology, 2006, 156, 480-488.	2.8	39
14	Prothymosin $\beta$ ± immunoreactive carboxyl-terminal peptide TKKQKTDEDD stimulates lymphocyte reactions, induces dendritic cell maturation and adopts a $\beta$ -sheet conformation in a sequence-specific manner. Molecular Immunology, 2009, 46, 784-792.	2.2	34
15	Structural Analysis of Peptide-Analogues of Human Zona Pellucida ZP1 Protein with Amyloidogenic Properties: Insights into Mammalian Zona Pellucida Formation. PLoS ONE, 2013, 8, e73258.	2.5	33
16	Amyloid-like fibrils from an 18-residue peptide analogue of a part of the central domain of the B-family of silkmooth chorion proteins. FEBS Letters, 2001, 499, 268-273.	2.8	30
17	A common $\alpha$ -aggregation <sup>TM</sup> interface possibly participates in the self $\alpha$ -assembly of human zona pellucida proteins. FEBS Letters, 2016, 590, 619-630.	2.8	30
18	Chameleon $\alpha$ -aggregation-prone <sup>TM</sup> 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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19	Exploring the "aggregation-prone"™ core of human Cystatin C: A structural study. <i>Journal of Structural Biology</i> , 2015, 191, 272-280.	2.8	26
20	An N-terminal pro-atrial natriuretic peptide (NT-proANP) "aggregation-prone"™ segment involved in isolated atrial amyloidosis. <i>FEBS Letters</i> , 2014, 588, 52-57.	2.8	25
21	The amyloid interactome: Exploring protein aggregation. <i>PLoS ONE</i> , 2017, 12, e0173163.	2.5	25
22	Structural studies and cytotoxicity assays of "aggregation-prone" APP <sup>S8A<sub>16</sub></sup> 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
23	Identification of a novel "aggregation-prone"/"amyloidogenic determinant"™ peptide in the sequence of the highly amyloidogenic human calcitonin. <i>FEBS Letters</i> , 2013, 587, 569-574.	2.8	18
24	Intrinsic aggregation propensity of the CsgB nucleator protein is crucial for curli fiber formation. <i>Journal of Structural Biology</i> , 2016, 195, 179-189.	2.8	18
25	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
26	A $\beta$ -solenoid model of the Pmel17 repeat domain: insights to the formation of functional amyloid fibrils. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 153-164.	2.9	17
27	The gram-negative outer membrane modeler: Automated building of lipopolysaccharide-rich bacterial outer membranes in four force fields. <i>Journal of Computational Chemistry</i> , 2019, 40, 1727-1734.	3.3	17
28	Structural studies of "aggregation-prone" peptide analogues of teleostean egg chorion ZPB proteins. <i>Biopolymers</i> , 2014, 102, 427-436.	2.4	16
29	The pentapeptide LQVVR plays a pivotal role in human cystatin C fibrillization. <i>FEBS Letters</i> , 2015, 589, 159-164.	2.8	15
30	PerMemDB: A database for eukaryotic peripheral membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183076.	2.6	14
31	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
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	13
33	FT-Raman spectroscopy as diagnostic tool of Congo red binding to amyloids. <i>Biopolymers</i> , 2003, 72, 185-192.	2.4	12
34	The silkworm eggshell as a natural amyloid shield for the safe development of insect oocyte and embryo: Insights from studies of silkworm chorion protein peptide analogues of the B famil.	2.4	12
35	AmyCo: the amyloidoses collection. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2019, 26, 112-117.	3.0	12
36	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

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37	Mining databases for protein aggregation: a review. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2017, 24, 143-152.	3.0	11
38	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
39	An amyloidogenic determinant in n-terminally pro-brain natriuretic peptide (nt-proBNP): Implications for cardiac amyloidosis. <i>Biopolymers</i> , 2012, 98, 67-75.	2.4	10
40	Hexapeptide Tandem Repeats Dictate the Formation of Silkworm Chorion, a Natural Protective Amyloid. <i>Journal of Molecular Biology</i> , 2018, 430, 3774-3783.	4.2	10
41	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
42	Third dose of the BNT162b2 vaccine results in very high levels of neutralizing antibodies against SARS-CoV-2: Results of a prospective study in 150 health professionals in Greece. <i>American Journal of Hematology</i> , 2022, 97, .	4.1	10
43	Tracking the amyloidogenic core of IAPP amyloid fibrils: Insights from micro-Raman spectroscopy. <i>Journal of Structural Biology</i> , 2017, 199, 140-152.	2.8	9
44	Hidden Aggregation Hot-Spots on Human Apolipoprotein E: A Structural Study. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2274.	4.1	9
45	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
46	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
47	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
48	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
49	Gene-Specific Intron Retention Serves as Molecular Signature that Distinguishes Melanoma from Non-Melanoma Cancer Cells in Greek Patients. <i>International Journal of Molecular Sciences</i> , 2019, 20, 937.	4.1	8
50	Delving into the amyloidogenic core of human leukocyte chemotactic factor 2. <i>Journal of Structural Biology</i> , 2019, 207, 260-269.	2.8	7
51	Î±CGRP, another amyloidogenic member of the CGRP family. <i>Journal of Structural Biology</i> , 2018, 203, 27-36.	2.8	6
52	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
53	Approaches in Gene Coexpression Analysis in Eukaryotes. <i>Biology</i> , 2022, 11, 1019.	2.8	4
54	Unraveling the aggregation propensity of human insulin C-peptide. <i>Biopolymers</i> , 2017, 108, e22882.	2.4	3

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55	Exploring Amyloidogenicity of Clusterin: A Structural and Bioinformatics Analysis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 989, 93-107.	1.6	3
56	Analysis of Single-Nucleotide Polymorphisms in Human Voltage-Gated Ion Channels. <i>Journal of Proteome Research</i> , 2019, 18, 2310-2320.	3.7	3
57	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
58	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
59	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
60	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
61	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
62	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