

Radhakrishnan Mahalakshmi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7922967/publications.pdf>

Version: 2024-02-01

74
papers

1,331
citations

430874

18
h-index

395702

33
g-index

76
all docs

76
docs citations

76
times ranked

1631
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering a Hyperstable <i>Yersinia pestis</i> Outer Membrane Protein Ail Using Thermodynamic Design. <i>Journal of the American Chemical Society</i> , 2022, 144, 1545-1555.	13.7	2
2	Mitochondrial protein translocation machinery: From TOM structural biogenesis to functional regulation. <i>Journal of Biological Chemistry</i> , 2022, 298, 101870.	3.4	11
3	Editorial: VDAC Structure and Function: An Up-to-Date View. <i>Frontiers in Physiology</i> , 2022, 13, 871586.	2.8	1
4	Interplay of protein primary sequence, lipid membrane, and chaperone in β -barrel assembly. <i>Protein Science</i> , 2021, 30, 624-637.	7.6	5
5	Molecular Assembly Pathway of Mitochondrial SAM50 in Native Membranes. <i>Biophysical Journal</i> , 2021, 120, 285a.	0.5	0
6	De novo design of metal-binding cleft in a Trp-Trp stapled thermostable β -hairpin peptide. <i>Peptide Science</i> , 2021, 113, e24240.	1.8	2
7	Cellular Interactome of Mitochondrial Voltage-Dependent Anion Channels: Oligomerization and Channel (Mis)Regulation. <i>ACS Chemical Neuroscience</i> , 2021, 12, 3497-3515.	3.5	8
8	Reversible folding energetics of <i>Yersinia</i> Ail barrel reveals a hyperfluorescent intermediate. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183097.	2.6	2
9	Single-residue physicochemical characteristics kinetically partition membrane protein self-assembly and aggregation. <i>Journal of Biological Chemistry</i> , 2020, 295, 1181-1194.	3.4	7
10	Molecular Switch between Structural Compaction and Thermodynamic Stability by the Xxx-Pro Interface in Transmembrane β -Barrels. <i>Biochemistry</i> , 2020, 59, 303-314.	2.5	0
11	Evolutionary selection of a 19-stranded mitochondrial β -barrel scaffold bears structural and functional significance. <i>Journal of Biological Chemistry</i> , 2020, 295, 14653-14665.	3.4	12
12	Linking Folding Landscape with Function in the Human Mitochondrial VDAC2. <i>Biophysical Journal</i> , 2020, 118, 367a.	0.5	0
13	Oxidative Thiol Modifications as Molecular Redox Sensors in Human Mitochondria. <i>Biophysical Journal</i> , 2020, 118, 449a.	0.5	0
14	Dynamic Plasticity of Mitochondrial VDAC2 Revealed by Single-Molecule Electrophysiology. <i>Biophysical Journal</i> , 2020, 118, 273a.	0.5	0
15	Single-residue physicochemical characteristics kinetically partition membrane protein self-assembly and aggregation. <i>Journal of Biological Chemistry</i> , 2020, 295, 1181-1194.	3.4	6
16	Do folding elements trade-off with function in the human mitochondrial metabolite transporter?. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	0
17	Helix-strand interaction regulates stability and aggregation of the human mitochondrial membrane protein channel VDAC3. <i>Journal of General Physiology</i> , 2019, 151, 489-504.	1.9	10
18	Hydrophobic Characteristic Is Energetically Preferred for Cysteine in a Model Membrane Protein. <i>Biophysical Journal</i> , 2019, 117, 25-35.	0.5	15

#	ARTICLE	IF	CITATIONS
19	Aromatic interactions in β -hairpin scaffold stability: A historical perspective. Archives of Biochemistry and Biophysics, 2019, 661, 39-49.	3.0	10
20	Human Mitochondrial VDAC Functionality Governs Scaffold Stability. Biophysical Journal, 2018, 114, 243a.	0.5	0
21	Folding Determinants of Transmembrane β -Barrels Using Engineered OMP Chimeras. Biochemistry, 2018, 57, 1987-1996.	2.5	11
22	Position-Specific contribution of interface tryptophans on membrane protein energetics. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 451-457.	2.6	10
23	Hydrophobic Mismatch Modulates Stability and Plasticity of Human Mitochondrial VDAC2. Biophysical Journal, 2018, 115, 2386-2394.	0.5	16
24	Salvaging the Thermodynamic Destabilization of Interface Histidine in Transmembrane β -Barrels. Biochemistry, 2018, 57, 6669-6678.	2.5	9
25	Direct Structural Annotation of Membrane Protein Aggregation Loci using Peptide-Based Reverse Mapping. Journal of Physical Chemistry Letters, 2018, 9, 2967-2971.	4.6	4
26	Solvation driven conformational transitions in the second transmembrane domain of mycobacteriophage holin. Biopolymers, 2017, 108, .	2.4	3
27	Metamorphic Proteins: Emergence of Dual Protein Folds from One Primary Sequence. Biochemistry, 2017, 56, 2971-2984.	2.5	52
28	Transmembrane β -barrels: Evolution, folding and energetics. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 2467-2482.	2.6	49
29	Energetics of side-chain partitioning of β -signal residues in unassisted folding of a transmembrane β -barrel protein. Journal of Biological Chemistry, 2017, 292, 12351-12365.	3.4	13
30	Structural plasticity of T4 transcription co-activator gp33 revealed by a protease-resistant unfolded state. Biochemical and Biophysical Research Communications, 2017, 492, 61-66.	2.1	0
31	Mitochondrial VDAC2 and cell homeostasis: highlighting hidden structural features and unique functionalities. Biological Reviews, 2017, 92, 1843-1858.	10.4	19
32	Stereopositional Outcome in the Packing of Dissimilar Aromatics in Designed β -Hairpins. Chemistry - A European Journal, 2016, 22, 4147-4156.	3.3	4
33	Unexpected Modifications of Cysteines in VDAC3: Indication that VDAC3 may Signal the Mitochondrial Intermembrane Redox State. Biophysical Journal, 2016, 110, 19a.	0.5	0
34	Control of human VDAC-2 scaffold dynamics by interfacial tryptophans is position specific. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 2993-3004.	2.6	7
35	Approaches for Preparation and Biophysical Characterization of Transmembrane β -Barrels. Springer Protocols, 2016, , 49-116.	0.3	1
36	Distinct Structural Elements Govern the Folding, Stability, and Catalysis in the Outer Membrane Enzyme PagP. Biochemistry, 2016, 55, 4960-4970.	2.5	7

#	ARTICLE	IF	CITATIONS
37	Engineering a Transmembrane Nanopore Ion Channel from a Membrane Breaker Peptide. <i>Journal of Physical Chemistry Letters</i> , 2016, 7, 2298-2303.	4.6	15
38	Capping Î²-Hairpin with N-Terminal <sc>d</sc>-Amino acid stabilizes peptide scaffold. <i>Biopolymers</i> , 2016, 106, 260-266.	2.4	8
39	<sc>VDAC</sc>: Mitochondrial outer membrane regulator masquerading as a channel?. <i>FEBS Journal</i> , 2016, 283, 1831-1836.	4.7	24
40	Role of cysteines in mammalian VDAC isoforms' function. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1219-1227.	1.0	64
41	Molecular Mechanism of Holin Transmembrane Domain I in Pore Formation and Bacterial Cell Death. <i>ACS Chemical Biology</i> , 2016, 11, 910-920.	3.4	23
42	VDAC3 as a sensor of oxidative state of the intermembrane space of mitochondria: the putative role of cysteine residue modifications. <i>Oncotarget</i> , 2016, 7, 2249-2268.	1.8	78
43	Implications of aromatic-aromatic interactions: From protein structures to peptide models. <i>Protein Science</i> , 2015, 24, 1920-1933.	7.6	132
44	N-helix and Cysteines Inter-regulate Human Mitochondrial VDAC-2 Function and Biochemistry. <i>Journal of Biological Chemistry</i> , 2015, 290, 30240-30252.	3.4	24
45	NMR Analysis of Tuning Cross-Strand Phe/Tyr/Trp-Trp Interactions in Designed Î²-Hairpin Peptides: Terminal Switch from <sc>l</sc> to <sc>d</sc> Amino Acid as a Strategy for Î²-Hairpin Capping. <i>Journal of Physical Chemistry B</i> , 2015, 119, 5376-5385.	2.6	15
46	Trp-Trp Cross-Linking: A Structure-Reactivity Relationship in the Formation and Design of Hyperstable Peptide Î²-Hairpin and Î±-Helix Scaffolds. <i>Organic Letters</i> , 2015, 17, 2498-2501.	4.6	18
47	Nature of aryl-tyrosine interactions contribute to Î²-hairpin scaffold stability: NMR evidence for alternate ring geometry. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 4220-4230.	2.8	4
48	Residue-Dependent Thermodynamic Cost and Barrel Plasticity Balances Activity in the PhoPQ-Activated Enzyme PagP of <i>Salmonella typhimurium</i> . <i>Biochemistry</i> , 2015, 54, 5712-5722.	2.5	17
49	Thermodynamic, structural and functional properties of membrane protein inclusion bodies are analogous to purified counterparts: case study from bacteria and humans. <i>RSC Advances</i> , 2015, 5, 1227-1234.	3.6	15
50	Structure Stabilizing Role of Aromatic Interactions is Decided by Spatial Arrangement of Aromatic Pairs: A Case Study with Designed Peptide Î²-Hairpins. , 2015, , .		0
51	Folding and Stability of Transmembrane b-Barrels of Bacterial and Human Origin: Probing Underlying Similarities and Principal Differences Using In vitro Systems. <i>Proceedings of the Indian National Science Academy</i> , 2015, 81, .	1.4	0
52	Juxtamembrane tryptophans have distinct roles in defining the OmpX barrel-micelle boundary and facilitating protein-micelle association. <i>FEBS Letters</i> , 2014, 588, 4464-4471.	2.8	14
53	Unusual post-translational protein modifications: the benefits of sophistication. <i>RSC Advances</i> , 2014, 4, 33958-33974.	3.6	15
54	Comparative analysis of cross strand aromatic-Phe interactions in designed peptide Î²-hairpins. <i>Organic and Biomolecular Chemistry</i> , 2014, 12, 2053-2061.	2.8	14

#	ARTICLE	IF	CITATIONS
55	Asymmetric Contribution of Aromatic Interactions Stems from Spatial Positioning of the Interacting Aryl Pairs in β -Hairpins. <i>ChemBioChem</i> , 2014, 15, 2357-2360.	2.6	17
56	Differential Contribution of Tryptophans to the Folding and Stability of the Attachment Invasion Locus Transmembrane β -Barrel from <i>Yersinia pestis</i> . <i>Scientific Reports</i> , 2014, 4, 6508.	3.3	18
57	Influence of Protein α Helix Micelle Ratios and Cysteine Residues on the Kinetic Stability and Unfolding Rates of Human Mitochondrial VDAC-2. <i>PLoS ONE</i> , 2014, 9, e87701.	2.5	17
58	Cysteine Residues Impact the Stability and Micelle Interaction Dynamics of the Human Mitochondrial β -Barrel Anion Channel hVDAC-2. <i>PLoS ONE</i> , 2014, 9, e92183.	2.5	13
59	Stabilizing effect of electrostatic vs. aromatic interactions in diproline nucleated peptide β -hairpins. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 15321.	2.8	8
60	Pro-Gly mediated conformational switch of mycobacteriophage D29 holin transmembrane domain I is lipid concentration driven. <i>Chemical Communications</i> , 2013, 49, 9594.	4.1	12
61	Modulation of Human Mitochondrial Voltage-dependent Anion Channel 2 (hVDAC-2) Structural Stability by Cysteine-assisted Barrel-lipid Interactions. <i>Journal of Biological Chemistry</i> , 2013, 288, 25584-25592.	3.4	39
62	Methionine Mutations of Outer Membrane Protein X Influence Structural Stability and Beta-Barrel Unfolding. <i>PLoS ONE</i> , 2013, 8, e79351.	2.5	27
63	Modulating lipid dynamics and membrane fluidity to drive rapid folding of a transmembrane barrel. <i>Scientific Reports</i> , 2013, 3, 1989.	3.3	51
64	Expression, refolding, and initial structural characterization of the <i>Y. pestis</i> Ail outer membrane protein in lipids. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 482-489.	2.6	21
65	Characterization of folded conformations in a tetrapeptide containing two tryptophan residues by vibrational circular dichroism. <i>Chirality</i> , 2009, 21, E76-85.	2.6	7
66	Aromatic interactions in tryptophan-containing peptides: crystal structures of model tryptophan peptides and phenylalanine analogs*. <i>Chemical Biology and Drug Design</i> , 2008, 65, 113-129.	1.1	23
67	Orientation of the <i>Escherichia coli</i> Outer Membrane Protein OmpX in Phospholipid Bilayer Membranes Determined by Solid-State NMR. <i>Biochemistry</i> , 2008, 47, 6531-6538.	2.5	59
68	NMR structural studies of the bacterial outer membrane protein OmpX in oriented lipid bilayer membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 3216-3224.	2.6	29
69	Tryptophan rich peptides: Influence of indole rings on backbone conformation. <i>Biopolymers</i> , 2007, 88, 36-54.	2.4	14
70	NMR Analysis of Aromatic Interactions in Designed Peptide β -Hairpins. <i>Journal of the American Chemical Society</i> , 2006, 128, 1125-1138.	13.7	93
71	Non-Protein Amino Acids in the Design of Secondary Structure Scaffolds. , 2006, 340, 71-94.		30
72	Tryptophan-containing peptide helices: interactions involving the indole side chain*. <i>Chemical Biology and Drug Design</i> , 2005, 66, 277-296.	1.1	22

#	ARTICLE	IF	CITATIONS
73	Circular Dichroism of Designed Peptide Helices and β^2 -Hairpins: Analysis of Trp- and Tyr-Rich Peptides. ChemBioChem, 2005, 6, 2152-2158.	2.6	48
74	Functional characterization of the pentapeptide QYNAD on rNa v 1.2 channels and its NMR structure. Pflugers Archiv European Journal of Physiology, 2004, 447, 895-907.	2.8	7