

# Luciano Lp Pirone

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

1,091  
citations

361413  
20  
h-index

501196  
28  
g-index

60  
all docs

60  
docs citations

60  
times ranked

1471  
citing authors

#	ARTICLE	IF	CITATIONS
1	Selective Photo-Assisted Eradication of Triple-Negative Breast Cancer Cells through Aptamer Decoration of Doped Conjugated Polymer Nanoparticles. <i>Pharmaceutics</i> , 2022, 14, 626.	4.5	24
2	Targeting Ship2-Sam with peptide ligands: Novel insights from a multidisciplinary approach. <i>Bioorganic Chemistry</i> , 2022, 122, 105680.	4.1	3
3	Design, Synthesis, and Anticancer Activity of a Selenium-Containing Galectin-3 and Galectin-9N Inhibitor. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2581.	4.1	7
4	Pomegranate Peel Extract as an Inhibitor of SARS-CoV-2 Spike Binding to Human ACE2 Receptor (in) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.6	60
5	The TBC1D31/praja2 complex controls primary ciliogenesis through PKA-directed OFD1 ubiquitylation. <i>EMBO Journal</i> , 2021, 40, e106503.	7.8	15
6	More Is Always Better Than One: The N-Terminal Domain of the Spike Protein as Another Emerging Target for Hampering the SARS-CoV-2 Attachment to Host Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6462.	4.1	14
7	Screening a Molecular Fragment Library to Modulate the PED/PEA15-Phospholipase D1 Interaction in Cellular Lysate Environments. <i>ACS Chemical Biology</i> , 2021, 16, 2798-2807.	3.4	2
8	Exploring the Ability of Cyclic Peptides to Target SAM Domains: A Computational and Experimental Study. <i>ChemBioChem</i> , 2020, 21, 702-711.	2.6	9
9	A Multi-Targeting Approach to Fight SARS-CoV-2 Attachment. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 186.	3.5	24
10	Structural Insight of the Full-Length Ros Protein: A Prototype of the Prokaryotic Zinc-Finger Family. <i>Scientific Reports</i> , 2020, 10, 9283.	3.3	11
11	Insights into PPAR $\beta$ Phosphorylation and Its Inhibition Mechanism. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 4811-4823.	6.4	21
12	Synthesis of diglycosylated (di)sulfides and comparative evaluation of their antiproliferative effect against tumor cell lines: A focus on the nature of sugar-recognizing mediators involved. <i>Carbohydrate Research</i> , 2019, 482, 107740.	2.3	10
13	Molecular basis of the scalp-ear-nipple syndrome unraveled by the characterization of disease-causing KCTD1 mutants. <i>Scientific Reports</i> , 2019, 9, 10519.	3.3	18
14	Investigating the properties of TBA variants with twin thrombin binding domains. <i>Scientific Reports</i> , 2019, 9, 9184.	3.3	17
15	KCTD1: A novel modulator of adipogenesis through the interaction with the transcription factor AP2 $\beta$ . <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 158514.	2.4	12
16	A physicochemical investigation on the metal binding properties of TtSmtB, a thermophilic member of the ArsR/SmtB transcription factor family. <i>International Journal of Biological Macromolecules</i> , 2019, 138, 1056-1063.	7.5	7
17	Ubiquitin binds the amyloid $\beta$ peptide and interferes with its clearance pathways. <i>Chemical Science</i> , 2019, 10, 2732-2742.	7.4	46
18	Molecular insights into the role of the polyalanine region in mediating <sc>PHOX</sc>2B aggregation. <i>FEBS Journal</i> , 2019, 286, 2505-2521.	4.7	9

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19	Focusing on the functional characterization of the anserinase from <i>Oreochromis niloticus</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 130, 158-165.	7.5	2
20	Design and analysis of EphA2-SAM peptide ligands: A multi-disciplinary screening approach. <i>Bioorganic Chemistry</i> , 2019, 84, 434-443.	4.1	11
21	A selective $\alpha_5\beta_1$ integrin antagonist hidden into the anophelin family protein cE5 from the malaria vector <i>Anopheles gambiae</i> . <i>Peptide Science</i> , 2018, 110, e24054.	1.8	7
22	Folding mechanisms steer the amyloid fibril formation propensity of highly homologous proteins. <i>Chemical Science</i> , 2018, 9, 3290-3298.	7.4	18
23	The essential player in adipogenesis GRP78 is a novel KCTD15 interactor. <i>International Journal of Biological Macromolecules</i> , 2018, 115, 469-475.	7.5	17
24	MucR binds multiple target sites in the promoter of its own gene and is a heat-stable protein: Is MucR a Hsp-like protein?. <i>FEBS Open Bio</i> , 2018, 8, 711-718.	2.3	15
25	Identifying the region responsible for <i>Brucella abortus</i> MucR higher-order oligomer formation and examining its role in gene regulation. <i>Scientific Reports</i> , 2018, 8, 17238.	3.3	14
26	Sam domain-based stapled peptides: Structural analysis and interaction studies with the Sam domains from the EphA2 receptor and the lipid phosphatase Ship2. <i>Bioorganic Chemistry</i> , 2018, 80, 602-610.	4.1	17
27	Elucidating the role of the pLG72 R30K substitution in schizophrenia susceptibility. <i>FEBS Letters</i> , 2017, 591, 646-655.	2.8	8
28	A new cryptic host defense peptide identified in human 11-hydroxysteroid dehydrogenase-1 $\beta$ -like: from in silico identification to experimental evidence. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2342-2353.	2.4	26
29	Insights into the anticancer properties of the first antimicrobial peptide from Archaea. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2155-2164.	2.4	29
30	Structural investigation of a C-terminal EphA2 receptor mutant: Does mutation affect the structure and interaction properties of the Sam domain?. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1095-1104.	2.3	3
31	Functional analyses yield detailed insight into the mechanism of thrombin inhibition by the antihemostatic salivary protein cE5 from <i>Anopheles gambiae</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 12632-12642.	3.4	20
32	The Sam-Sam interaction between Ship2 and the EphA2 receptor: design and analysis of peptide inhibitors. <i>Scientific Reports</i> , 2017, 7, 17474.	3.3	17
33	Ml proteins from <i>Mesorhizobium loti</i> and MucR from <i>Brucella abortus</i> : an AT-rich core DNA-target site and oligomerization ability. <i>Scientific Reports</i> , 2017, 7, 15805.	3.3	13
34	The BTB domains of the potassium channel tetramerization domain proteins prevalently assume pentameric states. <i>FEBS Letters</i> , 2016, 590, 1663-1671.	2.8	25
35	Exploring the binding of d(GGGT) <sub>4</sub> to the HIV-1 integrase: An approach to investigate G-quadruplex aptamer/target protein interactions. <i>Biochimie</i> , 2016, 127, 19-22.	2.6	25
36	Proteins involved in sleep homeostasis: Biophysical characterization of INC and its partners. <i>Biochimie</i> , 2016, 131, 106-114.	2.6	6

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37	Regulating levels of the neuromodulator L-serine in human brain: structural insight into pLG72 and L-amino acid oxidase interaction. <i>FEBS Journal</i> , 2016, 283, 3353-3370.	4.7	15
38	Targeting EphA2-Sam and Its Interactome: Design and Evaluation of Helical Peptides Enriched in Charged Residues. <i>ChemBioChem</i> , 2016, 17, 2179-2188.	2.6	14
39	The identification of a novel <i>Sulfolobus islandicus</i> CAMP-like peptide points to archaeal microorganisms as cell factories for the production of antimicrobial molecules. <i>Microbial Cell Factories</i> , 2015, 14, 126.	4.0	24
40	Peptide Fragments of Odin-Sam1: Conformational Analysis and Interaction Studies with EphA2-Sam. <i>ChemBioChem</i> , 2015, 16, 1629-1636.	2.6	13
41	Cullin3 - BTB Interface: A Novel Target for Stapled Peptides. <i>PLoS ONE</i> , 2015, 10, e0121149.	2.5	33
42	Cullin 3 Recognition Is Not a Universal Property among KCTD Proteins. <i>PLoS ONE</i> , 2015, 10, e0126808.	2.5	43
43	Structural and functional studies of Stf76 from the <i>Sulfolobus islandicus</i> plasmid virus pSSVx: a novel peculiar member of the winged helix-turn-helix transcription factor family. <i>Nucleic Acids Research</i> , 2014, 42, 5993-6011.	14.5	24
44	<i>Sulfolobus solfataricus</i> thiol redox puzzle: characterization of an atypical protein disulfide oxidoreductase. <i>Extremophiles</i> , 2014, 18, 219-228.	2.3	13
45	Molecular recognition of Cullin3 by KCTDs: Insights from experimental and computational investigations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1289-1298.	2.3	31
46	Functional and structural characterization of protein disulfide oxidoreductase from <i>Thermus thermophilus</i> HB27. <i>Extremophiles</i> , 2014, 18, 723-731.	2.3	4
47	A biophysical characterization of the folded domains of KCTD12: insights into interaction with the GABA <sub>B2</sub> receptor. <i>Journal of Molecular Recognition</i> , 2013, 26, 488-495.	2.1	26
48	Molecular basis of the PED/PEA15 interaction with the C-terminal fragment of phospholipase D1 revealed by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1572-1580.	2.3	10
49	Heterotypic Sam-Sam Association between Odin-Sam1 and Arap3-Sam: Binding Affinity and Structural Insights. <i>ChemBioChem</i> , 2013, 14, 100-106.	2.6	19
50	Thermal and Chemical Stability of Two Homologous POZ/BTB Domains of KCTD Proteins Characterized by a Different Oligomeric Organization. <i>BioMed Research International</i> , 2013, 2013, 1-8.	1.9	13
51	Mapping Functional Interaction Sites of Human Prune C-terminal Domain by NMR Spectroscopy in Human Cell Lysates. <i>Chemistry - A European Journal</i> , 2013, 19, 12217-12220.	3.3	12
52	Neuroblastoma tumorigenesis is regulated through the Nm23-H1/h-Prune C-terminal interaction. <i>Scientific Reports</i> , 2013, 3, 1351.	3.3	34
53	Solution Structure of the First Sam Domain of Odin and Binding Studies with the EphA2 Receptor. <i>Biochemistry</i> , 2012, 51, 2136-2145.	2.5	34
54	Molecular organization of the cullin E3 ligase adaptor KCTD11. <i>Biochimie</i> , 2011, 93, 715-724.	2.6	50

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55	C68 from the <i>Sulfolobus islandicus</i> plasmid- $\phi$ virus pSSVx is a novel member of the AbrB-like transcription factor family. <i>Biochemical Journal</i> , 2011, 435, 157-166.	3.7	24
56	Expression, purification, crystallization and preliminary X-ray crystallographic analysis of a major fragment of the resuscitation-promoting factor RpfB from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 164-168.	0.7	7
57	Design, synthesis and characterization of a peptide able to bind proteins of the KCTD family: implications for KCTD $\epsilon$ -cullin 3 recognition. <i>Journal of Peptide Science</i> , 2011, 17, 373-376.	1.4	15
58	NMR backbone dynamics studies of human PED/PEA $\epsilon$ 15 outline protein functional sites. <i>FEBS Journal</i> , 2010, 277, 4229-4240.	4.7	10
59	Identification and characterization of 1-Cys peroxiredoxin from <i>Sulfolobus solfataricus</i> and its involvement in the response to oxidative stress. <i>FEBS Journal</i> , 2006, 273, 721-731.	4.7	36