

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

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all docs

60
docs citations

60
times ranked

1471
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Pomegranate Peel Extract as an Inhibitor of SARS-CoV-2 Spike Binding to Human ACE2 Receptor (in) Tj ETQq1 1 0.784314 rgBT /Over | 3.6 | 60 |
| 2 | Molecular organization of the cullin E3 ligase adaptor KCTD11. <i>Biochimie</i> , 2011, 93, 715-724. | 2.6 | 50 |
| 3 | Ubiquitin binds the amyloid β peptide and interferes with its clearance pathways. <i>Chemical Science</i> , 2019, 10, 2732-2742. | 7.4 | 46 |
| 4 | Cullin 3 Recognition Is Not a Universal Property among KCTD Proteins. <i>PLoS ONE</i> , 2015, 10, e0126808. | 2.5 | 43 |
| 5 | 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 |
| 6 | 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 |
| 7 | Neuroblastoma tumorigenesis is regulated through the Nm23-H1/h-Prune C-terminal interaction. <i>Scientific Reports</i> , 2013, 3, 1351. | 3.3 | 34 |
| 8 | Cullin3 - BTB Interface: A Novel Target for Stapled Peptides. <i>PLoS ONE</i> , 2015, 10, e0121149. | 2.5 | 33 |
| 9 | 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 |
| 10 | 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 |
| 11 | A biophysical characterization of the folded domains of KCTD12: insights into interaction with the GABA _{B2} receptor. <i>Journal of Molecular Recognition</i> , 2013, 26, 488-495. | 2.1 | 26 |
| 12 | A new cryptic host defense peptide identified in human 11-hydroxysteroid dehydrogenase-1 β -like: from in silico identification to experimental evidence. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2342-2353. | 2.4 | 26 |
| 13 | The <sc>BTB</sc> domains of the potassium channel tetramerization domain proteins prevalently assume pentameric states. <i>FEBS Letters</i> , 2016, 590, 1663-1671. | 2.8 | 25 |
| 14 | Exploring the binding of d(GGGT) ₄ 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 |
| 15 | C68 from the <i>Sulfolobus islandicus</i> plasmidâ€“virus pSSVx is a novel member of the AbrB-like transcription factor family. <i>Biochemical Journal</i> , 2011, 435, 157-166. | 3.7 | 24 |
| 16 | Structural and functional studies of Stf76 from the <i>Sulfolobus islandicus</i> plasmidâ€“virus pSSVx: a novel peculiar member of the winged helixâ€“turnâ€“helix transcription factor family. <i>Nucleic Acids Research</i> , 2014, 42, 5993-6011. | 14.5 | 24 |
| 17 | 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 |
| 18 | A Multi-Targeting Approach to Fight SARS-CoV-2 Attachment. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 186. | 3.5 | 24 |

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|----|---|-----|-----------|
| 19 | 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 |
| 20 | Insights into PPAR γ Phosphorylation and Its Inhibition Mechanism. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 4811-4823. | 6.4 | 21 |
| 21 | 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 |
| 22 | Heterotypic Sam-Sam Association between Odi-Sam1 and Arap3-Sam: Binding Affinity and Structural Insights. <i>ChemBioChem</i> , 2013, 14, 100-106. | 2.6 | 19 |
| 23 | Folding mechanisms steer the amyloid fibril formation propensity of highly homologous proteins. <i>Chemical Science</i> , 2018, 9, 3290-3298. | 7.4 | 18 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Investigating the properties of TBA variants with twin thrombin binding domains. <i>Scientific Reports</i> , 2019, 9, 9184. | 3.3 | 17 |
| 29 | Design, synthesis and characterization of a peptide able to bind proteins of the KCTD family: implications for KCTD ϵ cullin 3 recognition. <i>Journal of Peptide Science</i> , 2011, 17, 373-376. | 1.4 | 15 |
| 30 | Regulating levels of the neuromodulator α -serine in human brain: structural insight into pLG72 and α -amino acid oxidase interaction. <i>FEBS Journal</i> , 2016, 283, 3353-3370. | 4.7 | 15 |
| 31 | MucR binds multiple target sites in the promoter of its own gene and is a heat-stable protein: Is MucR a H α -NS-like protein?. <i>FEBS Open Bio</i> , 2018, 8, 711-718. | 2.3 | 15 |
| 32 | The TBC1D31/praja2 complex controls primary ciliogenesis through PKA-directed OFD1 ubiquitylation. <i>EMBO Journal</i> , 2021, 40, e106503. | 7.8 | 15 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | 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 |

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|----|---|-----|-----------|
| 37 | Sulfolobus solfataricus thiol redox puzzle: characterization of an atypical protein disulfide oxidoreductase. <i>Extremophiles</i> , 2014, 18, 219-228. | 2.3 | 13 |
| 38 | Peptide Fragments of OdiA-Sam1: Conformational Analysis and Interaction Studies with EphA2-Sam. <i>ChemBioChem</i> , 2015, 16, 1629-1636. | 2.6 | 13 |
| 39 | Ml proteins from Mesorhizobium loti and MucR from Brucella abortus: an AT-rich core DNA-target site and oligomerization ability. <i>Scientific Reports</i> , 2017, 7, 15805. | 3.3 | 13 |
| 40 | 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 |
| 41 | KCTD1: A novel modulator of adipogenesis through the interaction with the transcription factor AP2 β . <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 158514. | 2.4 | 12 |
| 42 | Design and analysis of EphA2-SAM peptide ligands: A multi-disciplinary screening approach. <i>Bioorganic Chemistry</i> , 2019, 84, 434-443. | 4.1 | 11 |
| 43 | 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 |
| 44 | NMR backbone dynamics studies of human PED/PEA15 outline protein functional sites. <i>FEBS Journal</i> , 2010, 277, 4229-4240. | 4.7 | 10 |
| 45 | 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 |
| 46 | 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 |
| 47 | Molecular insights into the role of the polyalanine region in mediating PHOX2B aggregation. <i>FEBS Journal</i> , 2019, 286, 2505-2521. | 4.7 | 9 |
| 48 | 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 |
| 49 | Elucidating the role of the pLG72 R30K substitution in schizophrenia susceptibility. <i>FEBS Letters</i> , 2017, 591, 646-655. | 2.8 | 8 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |
| 54 | 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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| 55 | Functional and structural characterization of protein disulfide oxidoreductase from <i>Thermus thermophilus</i> HB27. <i>Extremophiles</i> , 2014, 18, 723-731. | 2.3 | 4 |
| 56 | 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 |
| 57 | Targeting Ship2-Sam with peptide ligands: Novel insights from a multidisciplinary approach. <i>Bioorganic Chemistry</i> , 2022, 122, 105680. | 4.1 | 3 |
| 58 | 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 |
| 59 | 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 |