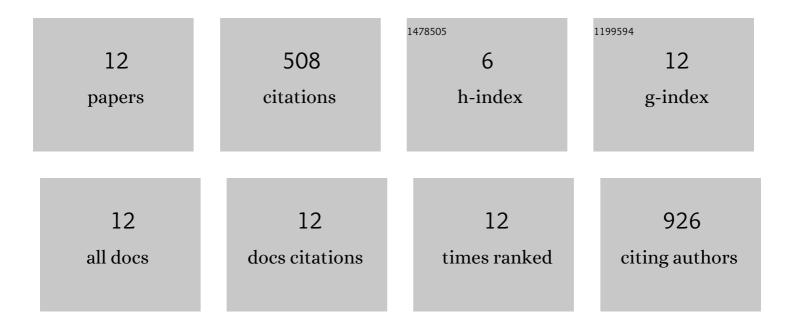
Filippo Pullara

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	Aggregation kinetics of bovine serum albumin studied by FTIR spectroscopy and light scattering. Biophysical Chemistry, 2004, 107, 175-187.	2.8	266
2	Crystal Structure of a Transcribing RNA Polymerase II Complex Reveals a Complete Transcription Bubble. Molecular Cell, 2015, 59, 258-269.	9.7	98
3	Explainable AI (xAI) for Anatomic Pathology. Advances in Anatomic Pathology, 2020, 27, 241-250.	4.3	46
4	WNT5A Inhibits Hepatocyte Proliferation and Concludes β-Catenin Signaling in Liver Regeneration. American Journal of Pathology, 2015, 185, 2194-2205.	3.8	29
5	Spatial domain analysis predicts risk of colorectal cancer recurrence and infers associated tumor microenvironment networks. Nature Communications, 2020, 11, 3515.	12.8	24
6	A general path for large-scale solubilization of cellular proteins: From membrane receptors to multiprotein complexes. Protein Expression and Purification, 2013, 87, 111-119.	1.3	17
7	Why protein conformers in molecular dynamics simulations differ from theircrystal structures: a thermodynamic insight. Turkish Journal of Chemistry, 2019, 43, 394-403.	1.2	9
8	Early stages of β2â€microglobulin aggregation and the inhibiting action of αBâ€crystallin. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1037-1046.	2.6	5
9	Mechanisms of Activation and Subunit Release in Ca ²⁺ /Calmodulin-Dependent Protein Kinase II. Journal of Physical Chemistry B, 2017, 121, 10344-10352.	2.6	5
10	Network Proteomics: From Protein Structure to Protein-Protein Interaction. BioMed Research International, 2017, 2017, 1-1.	1.9	4
11	In situ functional cell phenotyping reveals microdomain networks in colorectal cancer recurrence. Cell Reports Methods, 2021, 1, 100072.	2.9	3
12	Population reversal driven by unrestrained interactions in molecular dynamics simulations: A dialanine model. AIP Advances, 2015, 5, .	1.3	2