Olivier Cala

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8894331/publications.pdf

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22	744	567281 15	677142 22
papers	citations	h-index	g-index

22	22	22	1141
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Critical assessment of metabolism and related growth and quality traits in trout fed spirulina-supplemented plant-based diets. Aquaculture, 2022, 553, 738033.	3.5	3
2	Pulse sequence and sample formulation optimization for dipolar order mediated ¹Hâ†'¹³C cross-polarization. Physical Chemistry Chemical Physics, 2021, 23, 9457-9465.	2.8	6
3	Direct observation of hyperpolarization breaking through the spin diffusion barrier. Science Advances, 2021, 7, .	10.3	26
4	Boosting dissolution-dynamic nuclear polarization by multiple-step dipolar order mediated 1Hâ†'13C cross-polarization. Journal of Magnetic Resonance Open, 2021, 8-9, 100018.	1.1	3
5	Porous functionalized polymers enable generating and transporting hyperpolarized mixtures of metabolites. Nature Communications, 2021, 12, 4695.	12.8	23
6	Practical dissolution dynamic nuclear polarization. Progress in Nuclear Magnetic Resonance Spectroscopy, 2021, 126-127, 59-100.	7.5	30
7	Protonation tuned dipolar order mediated 1Hâ†'13C cross-polarization for dissolution-dynamic nuclear polarization experiments. Solid State Nuclear Magnetic Resonance, 2021, 116, 101762.	2.3	2
8	Dipolar order mediated ¹Hâ€‰â†'â€‰¹³C cross-polarization for dissolution-dynamic nuclear polarization. Magnetic Resonance, 2020, 1, 89-96.	1.9	9
9	1D NMR WaterLOGSY as an efficient method for fragment-based lead discovery. Journal of Enzyme Inhibition and Medicinal Chemistry, 2019, 34, 1218-1225.	5.2	31
10	Enabling STD-NMR fragment screening using stabilized native GPCR: A case study of adenosine receptor. Scientific Reports, 2018, 8, 8142.	3.3	45
11	Fragment-based discovery of a new family of non-peptidic small-molecule cyclophilin inhibitors with potent antiviral activities. Nature Communications, 2016, 7, 12777.	12.8	67
12	Overview of Probing Proteinâ€Ligand Interactions Using NMR. Current Protocols in Protein Science, 2015, 81, 17.18.1-17.18.24.	2.8	19
13	Ligand-Orientation Based Fragment Selection in STD NMR Screening. Journal of Medicinal Chemistry, 2015, 58, 8739-8742.	6.4	47
14	Proteinâ€“ligand structure guided by backbone and side-chain proton chemical shift perturbations. Journal of Biomolecular NMR, 2014, 60, 147-156.	2.8	16
15	NMR-based analysis of proteinâ€“ligand interactions. Analytical and Bioanalytical Chemistry, 2014, 406, 943-956.	3.7	132
16	Comparing Binding Modes of Analogous Fragments Using NMR in Fragment-Based Drug Design: Application to PRDX5. PLoS ONE, 2014, 9, e102300.	2.5	19
17	Virtual and Biophysical Screening Targeting the Î³-Tubulin Complex â€“ A New Target for the Inhibition of Microtubule Nucleation. PLoS ONE, 2013, 8, e63908.	2.5	13
18	The Colloidal State of Tannins Impacts the Nature of Their Interaction with Proteins: The Case of Salivary Proline-Rich Protein/Procyanidins Binding. Langmuir, 2012, 28, 17410-17418.	3.5	71

#	Article	IF	Citations
19	Towards a Molecular Interpretation of Astringency: Synthesis, 3D Structure, Colloidal State, and Human Saliva Protein Recognition of Procyanidins. Planta Medica, 2011, 77, 1116-1122.	1.3	19
20	NMR and molecular modeling of wine tannins binding to saliva proteins: revisiting astringency from molecular and colloidal prospects. FASEB Journal, 2010, 24, 4281-4290.	0.5	98
21	NMR of human saliva protein/wine tannin complexes. Towards deciphering astringency with physico-chemical tools. Comptes Rendus Chimie, 2010, 13, 449-452.	0.5	14
22	Structure and epimerase activity of anthocyanidin reductase fromVitis vinifera. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 989-1000.	2.5	51