Nicola Salvi

List of Publications by Year
in descending order

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46	1,577	279487 23	315357 38
papers	citations	h-index	g-index

55	55	55	1921
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Measles virus nucleo- and phosphoproteins form liquid-like phase-separated compartments that promote nucleocapsid assembly. Science Advances, 2020, 6, eaaz7095.	4.7	148
2	On the Dewarâ€“Chattâ€“Duncanson Model for Catalytic Gold(I) Complexes. Chemistry - A European Journal, 2010, 16, 7231-7240.	1.7	91
3	Identification of Dynamic Modes in an Intrinsically Disordered Protein Using Temperature-Dependent NMR Relaxation. Journal of the American Chemical Society, 2016, 138, 6240-6251.	6.6	90
4	Multi-Timescale Dynamics in Intrinsically Disordered Proteins from NMR Relaxation and Molecular Simulation. Journal of Physical Chemistry Letters, 2016, 7, 2483-2489.	2.1	88
5	Distribution of Pico- and Nanosecond Motions in Disordered Proteins from Nuclear Spin Relaxation. Biophysical Journal, 2015, 109, 988-999.	0.2	77
6	Boosting the Sensitivity of Ligandâ€“Protein Screening by NMR of Long-Lived States. Journal of the American Chemical Society, 2012, 134, 11076-11079.	6.6	75
7	Structure of the eukaryotic translation initiation factor eIF4E in complex with 4EGI-1 reveals an allosteric mechanism for dissociating eIF4G. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3187-95.	3.3	72
8	Characterization of intrinsically disordered proteins and their dynamic complexes: From in vitro to cell-like environments. Progress in Nuclear Magnetic Resonance Spectroscopy, 2018, 109, 79-100.	3.9	67
9	Deciphering the Dynamic Interaction Profile of an Intrinsically Disordered Protein by NMR Exchange Spectroscopy. Journal of the American Chemical Society, 2018, 140, 1148-1158.	6.6	64
10	Drug Screening Boosted by Hyperpolarized Longâ€Lived States in NMR. ChemMedChem, 2014, 9, 2509-2515.	1.6	63
11	A Unified Description of Intrinsically Disordered Protein Dynamics under Physiological Conditions Using NMR Spectroscopy. Journal of the American Chemical Society, 2019, 141, 17817-17829.	6.6	55
12	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. Nature Communications, 2018, 9, 1658.	5.8	53
13	NMR Provides Unique Insight into the Functional Dynamics and Interactions of Intrinsically Disordered Proteins. Chemical Reviews, 2022, 122, 9331-9356.	23.0	51
14	Analytical Description of NMR Relaxation Highlights Correlated Dynamics in Intrinsically Disordered Proteins. Angewandte Chemie - International Edition, 2017, 56, 14020-14024.	7.2	50
15	Solvent-dependent segmental dynamics in intrinsically disordered proteins. Science Advances, 2019, 5, eaax2348.	4.7	50
16	The intrinsically disordered SARS-CoV-2 nucleoprotein in dynamic complex with its viral partner nsp3a. Science Advances, 2022, 8, eabm4034.	4.7	50
17	Large-Scale Conformational Dynamics Control H5N1 Influenza Polymerase PB2 Binding to Importin Î±. Journal of the American Chemical Society, 2015, 137, 15122-15134.	6.6	49
18	Atomic resolution conformational dynamics of intrinsically disordered proteins from NMR spin relaxation. Progress in Nuclear Magnetic Resonance Spectroscopy, 2017, 102-103, 43-60.	3.9	43

#	Article	IF	Citations
19	Molecular basis of host-adaptation interactions between influenza virus polymerase PB2 subunit and ANP32A. Nature Communications, 2020, 11, 3656.	5.8	43
20	Ion pairing in NHC gold(I) olefin complexes: A combined experimental/theoretical study. Journal of Organometallic Chemistry, 2010, 695, 2679-2686.	0.8	42
21	Time Scales of Slow Motions in Ubiquitin Explored by Heteronuclear Double Resonance. Journal of the American Chemical Society, 2012, 134, 2481-2484.	6.6	30
22	Challenges in preparing, preserving and detecting para-water in bulk: overcoming proton exchange and other hurdles. Physical Chemistry Chemical Physics, 2015, 17, 26819-26827.	1.3	29
23	Large-Scale Recombinant Production of the SARS-CoV-2 Proteome for High-Throughput and Structural Biology Applications. Frontiers in Molecular Biosciences, 2021, 8, 653148.	1.6	29
24	Intrinsically Disordered Tardigrade Proteins Selfâ€Assemble into Fibrous Gels in Response to Environmental Stress. Angewandte Chemie - International Edition, 2022, 61, .	7.2	28
25	Visualizing protein breathing motions associated with aromatic ring flipping. Nature, 2022, 602, 695-700.	13.7	26
26	1H, 13C and 15N Backbone chemical shift assignments of the n-terminal and central intrinsically disordered domains of SARS-CoV-2 nucleoprotein. Biomolecular NMR Assignments, 2021, 15, 255-260.	0.4	17
27	Probing Protein Dynamics Using Multifield Variable Temperature NMR Relaxation and Molecular Dynamics Simulation. Journal of Physical Chemistry B, 2018, 122, 9697-9702.	1.2	15
28	The membrane anchor of the transcriptional activator SREBP is characterized by intrinsic conformational flexibility. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12390-12395.	3.3	14
29	The Role of Dynamics and Allostery in the Inhibition of the eIF4E/eIF4G Translation Initiation Factor Complex. Angewandte Chemie - International Edition, 2016, 55, 7176-7179.	7.2	14
30	Dynamic Descriptions of Highly Flexible Molecules from NMR Dipolar Couplings: Physical Basis and Limitations. Journal of the American Chemical Society, 2017, 139, 5011-5014.	6.6	13
31	Control of Cross Relaxation of Multipleâ€Quantum Coherences Induced by Fast Chemical Exchange under Heteronuclear Doubleâ€Resonance Irradiation. ChemPhysChem, 2011, 12, 333-341.	1.0	8
32	Cross-correlated relaxation measurements under adiabatic sweeps: determination of local order in proteins. Journal of Biomolecular NMR, 2015, 63, 353-365.	1.6	6
33	1H, 13C and 15N backbone chemical shift assignments of SARS-CoV-2 nsp3a. Biomolecular NMR Assignments, 2021, 15, 173-176.	0.4	5
34	Solid-state carbon-13 NMR and computational characterization of the N719 ruthenium sensitizer adsorbed on TiO2 nanoparticles. Dalton Transactions, 2014, 43, 6389.	1.6	4
35	Analytical Description of NMR Relaxation Highlights Correlated Dynamics in Intrinsically Disordered Proteins. Angewandte Chemie, 2017, 129, 14208-14212.	1.6	4
36	Dynamic Nuclear Polarization and Other Magnetic Ideas at EPFL. Chimia, 2012, 66, 734.	0.3	3

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37	Applications of Hyperpolarisation and NMR Long-Lived States in Drug Screening. Annual Reports on NMR Spectroscopy, 2019, 96, 1-33.	0.7	3
38	Theoretical tools for the design of NMR relaxation dispersion pulse sequences. Progress in Nuclear Magnetic Resonance Spectroscopy, 2015, 88-89, 105-115.	3.9	2
39	Intrinsically Disordered Tardigrade Proteins Selfâ€Assemble into Fibrous Gels in Response to Environmental Stress. Angewandte Chemie, 2022, 134, e202109961.	1.6	2
40	The Role of Dynamics and Allostery in the Inhibition of the eIF4E/eIF4G Translation Initiation Factor Complex. Angewandte Chemie, 2016, 128, 7292-7295.	1.6	1
41	Ensemble descriptions of IDPs and IDRs: Integrating simulation and experiment. , 2019, , 37-64.		1
42	Extending Timescales and Narrowing Linewidths in NMR. Chimia, 2011, 65, 652.	0.3	0
43	InnenrÃ¼cktitelbild: Analytical Description of NMR Relaxation Highlights Correlated Dynamics in Intrinsically Disordered Proteins (Angew. Chem. 45/2017). Angewandte Chemie, 2017, 129, 14507-14507.	1.6	0
44	Experimental Results. Springer Theses, 2014, , 65-89.	0.0	0
45	Analytical Models for Relaxation Dispersion Experiments. Springer Theses, 2014, , 33-53.	0.0	0
46	Theoretical Principles. Springer Theses, 2014, , 9-31.	0.0	0