Neri Niccolai

List of Publications by Year
in descending order

36	741	516710 16	552781 26
papers	citations	h-index	g-index

38	38	38	984
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The role of oxidative stress in Friedreich's ataxia. FEBS Letters, 2018, 592, 718-727.	2.8	76
2	Probing the surface of a sweet protein: NMR study of MNEI with a paramagnetic probe. Protein Science, 2001, 10, 1498-1507.	7.6	55
3	Probing protein surface accessibility with solvent and paramagnetic molecules. Progress in Nuclear Magnetic Resonance Spectroscopy, 2009, 54, 278-289.	7.5	54
4	Guanidinoneomycin B Recognition of an HIVâ€1 RNA Helix. ChemBioChem, 2008, 9, 93-102.	2.6	46
5	Three-dimensional computation of atom depth in complex molecular structures. Bioinformatics, 2005, 21, 2856-2860.	4.1	45
6	NMR Studies of Protein Surface Accessibility. Journal of Biological Chemistry, 2001, 276, 42455-42461.	3.4	40
7	NMR Studies of Protein Hydration and TEMPOL Accessibility. Journal of Molecular Biology, 2003, 332, 437-447.	4.2	38
8	Cold Denaturation Unveiled: Molecular Mechanism of the Asymmetric Unfolding of Yeast Frataxin. ChemPhysChem, 2015, 16, 3599-3602.	2.1	32
9	NMR Studies of Lysozyme Surface Accessibility by Using Different Paramagnetic Relaxation Probes. Journal of the American Chemical Society, 2006, 128, 9290-9291.	13.7	31
10	A Computational Approach From Gene to Structure Analysis of the Human ABCA4 Transporter Involved in Genetic Retinal Diseases. , 2017, 58, 5320.		29
11	Measuring the dynamic surface accessibility of RNA with the small paramagnetic molecule TEMPOL. Nucleic Acids Research, 2008, 36, e20-e20.	14.5	25
12	NMR Structure of Î±-Bungarotoxin Free and Bound to a Mimotope of the Nicotinic Acetylcholine Receptor. Biochemistry, 2002, 41, 1457-1463.	2.5	24
13	NMR studies on the surface accessibility of the archaeal protein Sso7d by using TEMPOL and Gd(III)(DTPA-BMA) as paramagnetic probes. Biophysical Chemistry, 2008, 137, 71-75.	2.8	21
14	Investigations into the killing activity of an antimicrobial peptide active against extensively antibiotic-resistant K. pneumon iae and P. aeruginosa. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 1796-1804.	2.6	21
15	A possible strategy to fight COVID-19: Interfering with spike glycoprotein trimerization. Biochemical and Biophysical Research Communications, 2020, 528, 35-38.	2.1	21
16	On Natureâ€™s Strategy for Assigning Genetic Code Multiplicity. PLoS ONE, 2016, 11, e0148174.	2.5	18
17	Searching for protein binding sites from Molecular Dynamics simulations and paramagnetic fragment-based NMR studies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 561-566.	2.3	17
18	Toward a generalized computational workflow for exploiting transient pockets as new targets for small molecule stabilizers: Application to the homogentisate 1,2-dioxygenase mutants at the base of rare disease Alkaptonuria. Computational Biology and Chemistry, 2017, 70, 133-141.	2.3	16

#	Article	IF	Citations
19	NMR studies of BPTI aggregation by using paramagnetic relaxation reagents. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 856-862.	2.3	14
20	MD and NMR studies of Î±-bungarotoxin surface accessibility. Biochemical and Biophysical Research Communications, 2007, 356, 114-117.	2.1	14
21	NMR Studies on Structure and Dynamics of the Monomeric Derivative of BS-RNase: New Insights for 3D Domain Swapping. PLoS ONE, 2012, 7, e29076.	2.5	13
22	Peptides and small molecules blocking the CXCR4/CXCL12 axis overcome bone marrowâ€‘induced chemoresistance in acute leukemias. Oncology Reports, 2018, 41, 312-324.	2.6	12
23	The use of a ditopic Gd(III) paramagnetic probe for investigating Î±-bungarotoxin surface accessibility. Journal of Inorganic Biochemistry, 2012, 112, 25-31.	3.5	11
24	Hydration studies on the archaeal protein Sso7d using NMR measurements and MD simulations. BMC Structural Biology, 2011, 11, 44.	2.3	10
25	Atom depth analysis delineates mechanisms of protein intermolecular interactions. Biochemical and Biophysical Research Communications, 2013, 436, 725-729.	2.1	8
26	ProCoCoA: A quantitative approach for analyzing protein core composition. Computational Biology and Chemistry, 2013, 43, 29-34.	2.3	8
27	A structural bioinformatics investigation on proteinâ€“DNA complexes delineates their modes of interaction. Molecular BioSystems, 2017, 13, 1010-1017.	2.9	8
28	Glycine-induced formation and druggability score prediction of protein surface pockets. Journal of Bioinformatics and Computational Biology, 2019, 17, 1950026.	0.8	8
29	Probing the protein space for extending the detection of weak homology folds. Journal of Theoretical Biology, 2013, 320, 152-158.	1.7	7
30	NMR and MD Studies on the Interaction Between Ligand Peptides and Î±-Bungarotoxin. Journal of Molecular Biology, 2004, 339, 1169-1177.	4.2	6
31	Hot spot mapping of protein surfaces with TEMPOL: Bovine pancreatic RNase A as a model system. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 201-207.	2.3	6
32	Structural investigation of Rett-inducing MeCP2 mutations. Genes and Diseases, 2019, 6, 31-34.	3.4	5
33	SHELTERING FROM AVALANCHES OF BIOLOGICAL DATA: A NEW RESEARCH DIMENSION IN THE POST-GENOMICS ERA. Journal of the Siena Academy of Sciences, 2013, 5, 102.	0.0	0
34	Structural Bioinformatics to Unveil Weaknesses of Coronavirus Spike Glycoprotein Stability. Methods in Pharmacology and Toxicology, 2021, , 203.	0.2	0
35	Structural bioinformatics survey on disease-inducing missense mutations. Journal of Bioinformatics and Computational Biology, 2021, 19, 2150008.	0.8	0
36	Structurally Driven Selection of Human Hepatitis C Virus Mimotopes. Antiviral Therapy, 2006, 11, 917-922.	1.0	0