Francesco Musiani

List of Publications by Year
in descending order

148 papers	6,040 citations	61984 43 h-index	88630 70 g-index
155 all docs	155 docs citations	155 times ranked	5763 citing authors

#	Article	IF	Citations
1	A new proposal for urease mechanism based on the crystal structures of the native and inhibited enzyme from Bacillus pasteurii: why urea hydrolysis costs two nickels. Structure, 1999, 7, 205-216.	3.3	462
2	Nonredox Nickel Enzymes. Chemical Reviews, 2014, 114, 4206-4228.	47.7	235
3	Chemistry of Ni²⁺ in Urease: Sensing, Trafficking, and Catalysis. Accounts of Chemical Research, 2011, 44, 520-530.	15.6	224
4	Conformational Equilibria in Monomeric Î±-Synuclein at the Single-Molecule Level. PLoS Biology, 2008, 6, e6.	5.6	181
5	Nickel impact on human health: An intrinsic disorder perspective. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1714-1731.	2.3	151
6	Structural properties of the nickel ions in urease: novel insights into the catalytic and inhibition mechanisms. Coordination Chemistry Reviews, 1999, 190-192, 331-355.	18.8	147
7	Molecular Details of Urease Inhibition by Boric Acid:Â Insights into the Catalytic Mechanism. Journal of the American Chemical Society, 2004, 126, 3714-3715.	13.7	142
8	Structure-based computational study of the catalytic and inhibition mechanisms of urease. Journal of Biological Inorganic Chemistry, 2001, 6, 300-314.	2.6	110
9	Bifidobacterial enolase, a cell surface receptor for human plasminogen involved in the interaction with the host. Microbiology (United Kingdom), 2009, 155, 3294-3303.	1.8	110
10	Polysaccharides for the Delivery of Antitumor Drugs. Materials, 2015, 8, 2569-2615.	2.9	110
11	High-Field NMR Studies of Oxidized Blue Copper Proteins:Â The Case of Spinach Plastocyanin. Journal of the American Chemical Society, 1999, 121, 2037-2046.	13.7	105
12	Identification of Inhibitors of SARS-CoV-2 3CL-Pro Enzymatic Activity Using a Small Molecule in Vitro Repurposing Screen. ACS Pharmacology and Translational Science, 2021, 4, 1096-1110.	4.9	101
13	Identification of the iron ions of high potential iron protein from Chromatium vinosum within the protein frame through two-dimensional NMR experiments. Journal of the American Chemical Society, 1992, 114, 3332-3340.	13.7	97
14	The structure-based reaction mechanism of urease, a nickel dependent enzyme: tale of a long debate. Journal of Biological Inorganic Chemistry, 2020, 25, 829-845.	2.6	92
15	UreG, a Chaperone in the Urease Assembly Process, Is an Intrinsically Unstructured GTPase That Specifically Binds Zn2+. Journal of Biological Chemistry, 2005, 280, 4684-4695.	3.4	91
16	Structural Characterization of Binding of Cu(II) to Tau Protein. Biochemistry, 2008, 47, 10841-10851.	2.5	85
17	GOMoDo: A GPCRs Online Modeling and Docking Webserver. PLoS ONE, 2013, 8, e74092.	2.5	84
18	<i>Helicobacter pylori</i> UreE, a urease accessory protein: specific Ni2+- and Zn2+-binding properties and interaction with its cognate UreG. Biochemical Journal, 2009, 422, 91-100.	3.7	83

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19	Structural Basis for Ni2+Transport and Assembly of the Urease Active Site by the Metallochaperone UreE from Bacillus pasteurii. Journal of Biological Chemistry, 2001, 276, 49365-49370.	3.4	74
20	Jack bean (Canavalia ensiformis) urease. Probing acidâ€“base groups of the active site by pH variation. Plant Physiology and Biochemistry, 2005, 43, 651-658.	5.8	74
21	Zn²⁺â€linked dimerization of UreG from <i>Helicobacter pylori</i>, a chaperone involved in nickel trafficking and urease activation. Proteins: Structure, Function and Bioinformatics, 2009, 74, 222-239.	2.6	73
22	Nickel and Human Health. Metal Ions in Life Sciences, 2013, 13, 321-357.	2.8	71
23	Evidence for a Transient Additional Ligand Binding Site in the TAS2R46 Bitter Taste Receptor. Journal of Chemical Theory and Computation, 2015, 11, 4439-4449.	5.3	70
24	The RNA Hydrolysis and the Cytokinin Binding Activities of PR-10 Proteins Are Differently Performed by Two Isoforms of the Pru p 1 Peach Major Allergen and Are Possibly Functionally Related. Plant Physiology, 2009, 150, 1235-1247.	4.8	66
25	The Structure of the Elusive Ureaseâ€“Urea Complex Unveils the Mechanism of a Paradigmatic Nickelâ€Dependent Enzyme. Angewandte Chemie - International Edition, 2019, 58, 7415-7419.	13.8	66
26	The First Solution Structure of a Paramagnetic Copper(II) Protein:Â The Case of Oxidized Plastocyanin from the CyanobacteriumSynechocystisPCC6803. Journal of the American Chemical Society, 2001, 123, 2405-2413.	13.7	65
27	Immobilization of jack bean urease on hydroxyapatite: urease immobilization in alkaline soils. Soil Biology and Biochemistry, 1998, 30, 1485-1490.	8.8	63
28	High-Affinity Ni2+ Binding Selectively Promotes Binding of Helicobacter pylori NikR to Its Target Urease Promoter. Journal of Molecular Biology, 2008, 383, 1129-1143.	4.2	63
29	The high potential iron-sulfur protein (HiPIP) fromRhodoferax fermentansis competent in photosynthetic electron transfer. FEBS Letters, 1995, 357, 70-74.	2.8	62
30	Inactivation of urease by 1,4-benzoquinone: chemistry at the protein surface. Dalton Transactions, 2016, 45, 5455-5459.	3.3	61
31	Fluoride inhibition of Sporosarcina pasteurii urease: structure and thermodynamics. Journal of Biological Inorganic Chemistry, 2014, 19, 1243-1261.	2.6	58
32	Inactivation of urease by catechol: Kinetics and structure. Journal of Inorganic Biochemistry, 2017, 166, 182-189.	3.5	57
33	Biochemical Studies onMycobacterium tuberculosisUreG and Comparative Modeling Reveal Structural and Functional Conservation among the Bacterial UreG Familyâ€. Biochemistry, 2007, 46, 3171-3182.	2.5	56
34	Bacillus pasteurii urease: A heteropolymeric enzyme with a binuclear nickel active site. Soil Biology and Biochemistry, 1996, 28, 819-821.	8.8	55
35	The structure of urease inactivated by Ag(<scp>i</scp>): a new paradigm for enzyme inhibition by heavy metals. Dalton Transactions, 2018, 47, 8240-8247.	3.3	54
36	Urease Inhibition in the Presence of <i>N</i>-(<i>n</i>-Butyl)thiophosphoric Triamide, a Suicide Substrate: Structure and Kinetics. Biochemistry, 2017, 56, 5391-5404.	2.5	53

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37	Crystallographic and X-ray absorption spectroscopic characterization of <i>Helicobacter pylori</i> UreE bound to Ni2+ and Zn2+ reveals a role for the disordered C-terminal arm in metal trafficking. Biochemical Journal, 2012, 441, 1017-1035.	3.7	52
38	Backbone Dynamics of Plastocyanin in Both Oxidation States. Journal of Biological Chemistry, 2001, 276, 47217-47226.	3.4	50
39	The Nickel Site of Bacillus pasteurii UreE, a Urease Metallo-Chaperone, As Revealed by Metal-Binding Studies and X-ray Absorption Spectroscopy. Biochemistry, 2006, 45, 6495-6509.	2.5	49
40	The crystal structure of Sporosarcina pasteurii urease in a complex with citrate provides new hints for inhibitor design. Journal of Biological Inorganic Chemistry, 2013, 18, 391-399.	2.6	49
41	Intrinsically Disordered Structure of Bacillus pasteurii UreG As Revealed by Steady-State and Time-Resolved Fluorescence Spectroscopy. Biochemistry, 2006, 45, 8918-8930.	2.5	47
42	The Ni2+ binding properties of Helicobacter pylori NikR. Chemical Communications, 2007, , 3649.	4.1	47
43	Insights in the (un)structural organization of Bacillus pasteurii UreG, an intrinsically disordered GTPase enzyme. Molecular BioSystems, 2012, 8, 220-228.	2.9	44
44	Molecular landscape of the interaction between the urease accessory proteins UreE and UreG. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1662-1674.	2.3	44
45	A Blueprint for High Affinity SARS-CoV-2 Mpro Inhibitors from Activity-Based Compound Library Screening Guided by Analysis of Protein Dynamics. ACS Pharmacology and Translational Science, 2021, 4, 1079-1095.	4.9	44
46	Nickel trafficking: insights into the fold and function of UreE, a urease metallochaperone. Journal of Inorganic Biochemistry, 2004, 98, 803-813.	3.5	43
47	Kinetic and structural studies reveal a unique binding mode of sulfite to the nickel center in urease. Journal of Inorganic Biochemistry, 2016, 154, 42-49.	3.5	42
48	Novel Dual-Action Plant Fertilizer and Urease Inhibitor: UreaÂ·Catechol Cocrystal. Characterization and Environmental Reactivity. ACS Sustainable Chemistry and Engineering, 2019, 7, 2852-2859.	6.7	42
49	Smart urea ionic co-crystals with enhanced urease inhibition activity for improved nitrogen cycle management. Chemical Communications, 2018, 54, 7637-7640.	4.1	41
50	Nickel binding properties of Helicobacter pylori UreF, an accessory protein in the nickel-based activation of urease. Journal of Biological Inorganic Chemistry, 2014, 19, 319-334.	2.6	40
51	Nickel-responsive transcriptional regulators. Metallomics, 2015, 7, 1305-1318.	2.4	40
52	Molecular characterization of Bacillus pasteurii UreE, a metal-binding chaperone for the assembly of the urease active site. Journal of Biological Inorganic Chemistry, 2002, 7, 623-631.	2.6	39
53	FeON-FeOFF: the Helicobacter pylori Fur regulator commutates iron-responsive transcription by discriminative readout of opposed DNA grooves. Nucleic Acids Research, 2014, 42, 3138-3151.	14.5	38
54	A model-based proposal for the role of UreF as a GTPase-activating protein in the urease active site biosynthesis. Proteins: Structure, Function and Bioinformatics, 2007, 68, 749-761.	2.6	36

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55	Deciphering OPA1 mutations pathogenicity by combined analysis of human, mouse and yeast cell models. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 3496-3514.	3.8	36
56	Molecular Dynamics Simulations Identify Time Scale of Conformational Changes Responsible for Conformational Selection in Molecular Recognition of HIV-1 Transactivation Responsive RNA. Journal of the American Chemical Society, 2014, 136, 15631-15637.	13.7	35
57	The relationship between folding and activity in UreG, an intrinsically disordered enzyme. Scientific Reports, 2017, 7, 5977.	3.3	34
58	Conformational Fluctuations of UreG, an Intrinsically Disordered Enzyme. Biochemistry, 2013, 52, 2949-2954.	2.5	33
59	Insights into Urease Inhibition by <i>N</i>-(<i>n</i>-Butyl) Phosphoric Triamide through an Integrated Structural and Kinetic Approach. Journal of Agricultural and Food Chemistry, 2019, 67, 2127-2138.	5.2	33
60	Computational Study of the DNA-Binding Protein Helicobacter pylori NikR: The Role of Ni2+ 2 Francesco Musiani and Branimir BertoÅ¡a contributed equally to the simulations presented here.. Journal of Chemical Theory and Computation, 2010, 6, 3503-3515.	5.3	32
61	Biochemical and structural studies on native and recombinant Glycine max UreG: a detailed characterization of a plant urease accessory protein. Plant Molecular Biology, 2012, 78, 461-475.	3.9	32
62	Unraveling the Helicobacter pylori UreG zinc binding site using X-ray absorption spectroscopy (XAS) and structural modeling. Journal of Biological Inorganic Chemistry, 2012, 17, 353-361.	2.6	32
63	Conformational ensemble of human Î±-synuclein physiological form predicted by molecular simulations. Physical Chemistry Chemical Physics, 2016, 18, 5702-5706.	2.8	32
64	Predicting ligand binding poses for low-resolution membrane protein models: Perspectives from multiscale simulations. Biochemical and Biophysical Research Communications, 2018, 498, 366-374.	2.1	32
65	Multifunctional Urea Cocrystal with Combined Ureolysis and Nitrification Inhibiting Capabilities for Enhanced Nitrogen Management. ACS Sustainable Chemistry and Engineering, 2019, 7, 13369-13378.	6.7	32
66	X-ray Absorption Spectroscopy Study of Native and Phenylphosphorodiamidate-Inhibited Bacillus pasteurii Urease. FEBS Journal, 1996, 239, 61-66.	0.2	31
67	Zinc Inhibition of Bacterial Cytochrome <i>bc</i>₁ Reveals the Role of Cytochrome <i>b</i> E295 in Proton Release at the Q_o Site. Biochemistry, 2011, 50, 4263-4272.	2.5	30
68	Pliable natural biocide: Jaburetox is an intrinsically disordered insecticidal and fungicidal polypeptide derived from jack bean urease. FEBS Journal, 2015, 282, 1043-1064.	4.7	30
69	Inhibition Mechanism of Urease by Au(III) Compounds Unveiled by X-ray Diffraction Analysis. ACS Medicinal Chemistry Letters, 2019, 10, 564-570.	2.8	30
70	Interaction of Selenoprotein W with 14-3-3 Proteins: A Computational Approach. Journal of Proteome Research, 2011, 10, 968-976.	3.7	29
71	Holo-Ni2+Helicobacter pylori NikR contains four square-planar nickel-binding sites at physiological pH. Dalton Transactions, 2011, 40, 7831.	3.3	28
72	Targeting Helicobacter pylori urease activity and maturation: In-cell high-throughput approach for drug discovery. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2245-2253.	2.4	28

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73	The model structure of the copper-dependent ammonia monooxygenase. Journal of Biological Inorganic Chemistry, 2020, 25, 995-1007.	2.6	27
74	Novel Lipid and Polymeric Materials as Delivery Systems for Nucleic Acid Based Drugs. Current Drug Metabolism, 2015, 16, 427-452.	1.2	26
75	Strategies to optimize siRNA delivery to hepatocellular carcinoma cells. Expert Opinion on Drug Delivery, 2017, 14, 797-810.	5.0	25
76	Protein Tunnels: The Case of Urease Accessory Proteins. Journal of Chemical Theory and Computation, 2017, 13, 2322-2331.	5.3	25
77	Rationalization of the reduction potentials within the series of the high potential iron-sulfur proteins. Inorganica Chimica Acta, 1995, 240, 251-256.	2.4	23
78	NMR Solution Structure, Backbone Mobility, and Homology Modeling ofc-Type Cytochromes from Gram-Positive Bacteria. ChemBioChem, 2002, 3, 299-310.	2.6	23
79	High potential ironâ€"sulfur proteins and their role as soluble electron carriers in bacterial photosynthesis: tale of a discovery. Photosynthesis Research, 2005, 85, 115-131.	2.9	23
80	Urease Inhibitory Potential and Soil Ecotoxicity of Novel â€œPolyphenolsâ€"Deep Eutectic Solventsâ€• Formulations. ACS Sustainable Chemistry and Engineering, 2019, 7, 15558-15567.	6.7	23
81	The conformational response to Zn(II) and Ni(II) binding of Sporosarcina pasteurii UreG, an intrinsically disordered GTPase. Journal of Biological Inorganic Chemistry, 2014, 19, 1341-1354.	2.6	22
82	Protein Aggregation and Molecular Crowding. International Review of Cell and Molecular Biology, 2017, 329, 49-77.	3.2	22
83	Metal Ion-Mediated DNA-Protein Interactions. Metal Ions in Life Sciences, 2012, 10, 135-170.	2.8	21
84	Selectivity of Ni(II) and Zn(II) binding to Sporosarcina pasteurii UreE, a metallochaperone in the urease assembly: a calorimetric and crystallographic study. Journal of Biological Inorganic Chemistry, 2013, 18, 1005-1017.	2.6	21
85	The Impact of pH on Catalytically Critical Protein Conformational Changes: The Case of the Urease, a Nickel Enzyme. Chemistry - A European Journal, 2019, 25, 12145-12158.	3.3	21
86	Structure of the Intermolecular Complex between Plastocyanin and Cytochrome f from Spinach*. Journal of Biological Chemistry, 2005, 280, 18833-18841.	3.4	20
87	Isothermal Titration Calorimetry to Characterize Enzymatic Reactions. Methods in Enzymology, 2016, 567, 215-236.	1.0	20
88	Structure and dynamics of Helicobacter pylori nickel-chaperone HypA: an integrated approach using NMR spectroscopy, functional assays and computational tools. Journal of Biological Inorganic Chemistry, 2018, 23, 1309-1330.	2.6	20
89	Engineered biosealant strains producing inorganic and organic biopolymers. Journal of Biotechnology, 2012, 161, 181-189.	3.8	19
90	Intrinsic disorder and metal binding in UreG proteins from Archae hyperthermophiles: GTPase enzymes involved in the activation of Ni(II) dependent urease. Journal of Biological Inorganic Chemistry, 2015, 20, 739-755.	2.6	19

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91	DNMT1 mutations leading to neurodegeneration paradoxically reflect on mitochondrial metabolism. Human Molecular Genetics, 2020, 29, 1864-1881.	2.9	19
92	On the interaction of Helicobacter pylori NikR, aÂNi(II)-responsive transcription factor, with the urease operator: in solution and in silico studies. Journal of Biological Inorganic Chemistry, 2015, 20, 1021-1037.	2.6	18
93	Polymer-Mediated Delivery of siRNAs to Hepatocellular Carcinoma: Variables Affecting Specificity and Effectiveness. Molecules, 2018, 23, 777.	3.8	18
94	Title is missing!. Photosynthesis Research, 1997, 53, 13-21.	2.9	17
95	Structure of the UreDâ€"UreFâ€"UreGâ€"UreE complex in Helicobacter pylori: a model study. Journal of Biological Inorganic Chemistry, 2013, 18, 571-577.	2.6	17
96	Glutamate Ligation in the Ni(II)- and Co(II)-Responsive <i>Escherichia coli</i> Transcriptional Regulator, RcnR. Inorganic Chemistry, 2017, 56, 6459-6476.	4.0	16
97	The carbon monoxide dehydrogenase accessory protein CooJ is a histidine-rich multidomain dimer containing an unexpected Ni(II)-binding site. Journal of Biological Chemistry, 2019, 294, 7601-7614.	3.4	16
98	Topological characterization of a bacterial celluloseâ€"acrylic acid polymeric matrix. European Journal of Pharmaceutical Sciences, 2014, 62, 326-333.	4.0	15
99	An Italian contribution to structural genomics: Understanding metalloproteins. Coordination Chemistry Reviews, 2006, 250, 1419-1450.	18.8	14
100	Model Structures of Helicobacter pylori UreD(H) Domains: A Putative Molecular Recognition Platform. Journal of Chemical Information and Modeling, 2011, 51, 1513-1520.	5.4	14
101	Surface plasmon resonance and isothermal titration calorimetry to monitor the Ni(II)-dependent binding of Helicobacter pylori NikR to DNA. Analytical and Bioanalytical Chemistry, 2016, 408, 7971-7980.	3.7	14
102	Combining Different Docking Engines and Consensus Strategies to Design and Validate Optimized Virtual Screening Protocols for the SARS-CoV-2 3CL Protease. Molecules, 2021, 26, 797.	3.8	14
103	Nickel as a virulence factor in the Class I bacterial carcinogen, Helicobacter pylori. Seminars in Cancer Biology, 2021, 76, 143-155.	9.6	14
104	Glucose-1-phosphate uridylyltransferase from Erwinia amylovora : Activity, structure and substrate specificity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1348-1357.	2.3	13
105	Targeting the Protein Tunnels of the Urease Accessory Complex: A Theoretical Investigation. Molecules, 2020, 25, 2911.	3.8	13
106	Application of Molecular Dynamics to the Investigation of Metalloproteins Involved in Metal Homeostasis. European Journal of Inorganic Chemistry, 2018, 2018, 4661-4677.	2.0	12
107	Inhibition of Urease, a Niâ€Enzyme: The Reactivity of a Key Thiol With Monoâ€• and Diâ€Substituted Catechols Elucidated by Kinetic, Structural, and Theoretical Studies. Angewandte Chemie - International Edition, 2021, 60, 6029-6035.	13.8	12
108	Urease: Recent Insights on the Role of Nickel. , 2007, , 241-277.		11

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109	Development of a multisite model for Ni(II) ion in solution from thermodynamic and kinetic data. Journal of Computational Chemistry, 2017, 38, 1834-1843.	3.3	11
110	Structure/Function Relationships of Phospholipases C Beta. Current Protein and Peptide Science, 2013, 14, 650-657.	1.4	11
111	Electron Transfer from HiPIP to the Photooxidized Tetraheme Cytochrome Subunit of Allochromatium vinosum Reaction Center:â€‰ New Insights from Site-Directed Mutagenesis and Computational Studies. Biochemistry, 2004, 43, 437-445.	2.5	10
112	Transient Interactions of a Cytosolic Protein with Macromolecular and Vesicular Cosolutes: Unspecific and Specific Effects. ChemBioChem, 2015, 16, 2633-2645.	2.6	10
113	On the role of a specific insert in acetate permeases (ActP) for tellurite uptake in bacteria: Functional and structural studies. Journal of Inorganic Biochemistry, 2016, 163, 103-109.	3.5	10
114	Structural analysis of the interaction between Jaburetox, an intrinsically disordered protein, and membrane models. Colloids and Surfaces B: Biointerfaces, 2017, 159, 849-860.	5.0	10
115	Kinetic and structural analysis of the inactivation of urease by mixed-ligand phosphine halide Ag(I) complexes. Journal of Inorganic Biochemistry, 2021, 218, 111375.	3.5	10
116	Facilitating Nitrification Inhibition through Green, Mechanochemical Synthesis of a Novel Nitrapyrin Complex. Crystal Growth and Design, 2021, 21, 5792-5799.	3.0	10
117	Medicinal Au(<scp>i</scp>) compounds targeting urease as prospective antimicrobial agents: unveiling the structural basis for enzyme inhibition. Dalton Transactions, 2021, 50, 14444-14452.	3.3	10
118	An Evaluation of Maleicâ€Itaconic Copolymers as Urease Inhibitors. Soil Science Society of America Journal, 2018, 82, 994-1003.	2.2	9
119	A Solventâ€Exposed Cysteine Forms a Peculiar Ni II â€Binding Site in the Metallochaperone CooT from Rhodospirillum rubrum. Chemistry - A European Journal, 2019, 25, 15351-15360.	3.3	9
120	Nickel and GTP Modulate Helicobacter pylori UreG Structural Flexibility. Biomolecules, 2020, 10, 1062.	4.0	9
121	Characterization and 1.57â€…Ã… resolution structure of the key fire blight phosphatase AmsI from<i>Erwinia amylovora</i>. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 903-910.	0.8	8
122	Soyuretox, an Intrinsically Disordered Polypeptide Derived from Soybean (Glycine Max) Ubiquitous Urease with Potential Use as a Biopesticide. International Journal of Molecular Sciences, 2019, 20, 5401.	4.1	8
123	Definition of the Binding Architecture to a Target Promoter of HP1043, the Essential Master Regulator of Helicobacter pylori. International Journal of Molecular Sciences, 2021, 22, 7848.	4.1	8
124	The Asn 38âˆ’Cys 84 H-Bond in Plastocyanin. Journal of Physical Chemistry B, 2004, 108, 7495-7499.	2.6	7
125	Hot Biological Catalysis: Isothermal Titration Calorimetry to Characterize Enzymatic Reactions. Journal of Visualized Experiments, 2014, , .	0.3	7
126	Molecular Modelling of the Ni(II)-Responsive Synechocystis PCC 6803 Transcriptional Regulator InrS in the Metal Bound Form. Inorganics, 2019, 7, 76.	2.7	7

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127	The Structure of the Elusive Ureaseâ€“Urea Complex Unveils the Mechanism of a Paradigmatic Nickelâ€Dependent Enzyme. Angewandte Chemie, 2019, 131, 7493-7497.	2.0	7
128	Dynamic characterization and substrate binding of cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenaseâ€”an enzyme used in bioremediation. Journal of Molecular Modeling, 2014, 20, 2531.	1.8	6
129	The structural and functional characterization of Malus domestica double bond reductase MdDBR provides insights towards the identification of its substrates. International Journal of Biological Macromolecules, 2021, 171, 89-99.	7.5	6
130	Probing the transport of Ni(II) ions through the internal tunnels of the Helicobacter pylori UreDFG multimeric protein complex. Journal of Inorganic Biochemistry, 2021, 223, 111554.	3.5	6
131	Intrinsic disorder in the nickel-dependent urease network. Progress in Molecular Biology and Translational Science, 2020, 174, 307-330.	1.7	6
132	Nickel import and export in the human pathogen<i>Helicobacter pylori</i>, perspectives from molecular modelling. Metallomics, 2021, 13, .	2.4	6
133	Relevance of ARID1A Mutations in Endometrial Carcinomas. Diagnostics, 2022, 12, 592.	2.6	6
134	Cyclic voltammetry and spectroelectrochemistry of cytochrome c8 from Rubrivivax gelatinosus. Implications in photosynthetic electron transfer. Inorganica Chimica Acta, 1997, 263, 379-384.	2.4	5
135	Bioinorganic Chemistry of Nickel. Inorganics, 2019, 7, 131.	2.7	5
136	Partitioning the structural features that underlie expansin-like and elicitor activities of cerato-platanin. International Journal of Biological Macromolecules, 2020, 165, 2845-2854.	7.5	5
137	Denaturant-Induced Conformational Transitions in Intrinsically Disordered Proteins. , 2012, 896, 197-213.		4
138	Mathematical Modeling of Drug Release from Natural Polysaccharides Based Matrices. Natural Product Communications, 2017, 12, 1934578X1701200.	0.5	4
139	Pseudomonas pseudoalcaligenes KF 707 grown with biphenyl expresses a cytochrome caa 3 oxidase that uses cytochrome c 4 as electron donor. FEBS Letters, 2018, 592, 901-915.	2.8	4
140	The cytochrome b lysine 329 residue is critical for ubihydroquinone oxidation and proton release at the Qo site of bacterial cytochrome bc1. Biochimica Et Biophysica Acta - Bioenergetics, 2019, 1860, 167-179.	1.0	4
141	Chemosensorial G-proteins-Coupled Receptors: A Perspective from Computational Methods. Advances in Experimental Medicine and Biology, 2014, 805, 441-457.	1.6	4
142	Structure, dynamics, and function of SrnR, a transcription factor for nickel-dependent gene expression. Metallomics, 2021, 13, .	2.4	4
143	Evolution of Macromolecular Docking Techniques: The Case Study of Nickel and Iron Metabolism in Pathogenic Bacteria. Molecules, 2015, 20, 14265-14292.	3.8	3
144	Inhibition of Urease, a Niâ€Enzyme: The Reactivity of a Key Thiol With Monoâ€•and Diâ€Substituted Catechols Elucidated by Kinetic, Structural, and Theoretical Studies. Angewandte Chemie, 2021, 133, 6094-6100.	2.0	3

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145	New Insights on Rotenone Resistance of Complex I Induced by the m.11778G>A/MT-ND4 Mutation Associated with Leberâ€™s Hereditary Optic Neuropathy. Molecules, 2022, 27, 1341.	3.8	3
146	Urease. , 2013, , 2287-2292.		1
147	Thiocarbamoyl Disulfides as Inhibitors of Urease and Ammonia Monooxygenase: Crystal Engineering for Novel Materials. Crystal Growth and Design, 0, , .	3.0	1
148	Cloning the barley <i>nec3</i> disease lesion mimic mutant using complementation by sequencing. Plant Genome, 2022, , e20187.	2.8	0