Francesco Musiani

List of Publications by Year
in descending order

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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	Relevance of ARID1A Mutations in Endometrial Carcinomas. Diagnostics, 2022, 12, 592.	2.6	6
2	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
3	Cloning the barley nec3 disease lesion mimic mutant using complementation by sequencing. Plant Genome, 2022, , e20187.	2.8	0
4	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
5	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
6	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
7	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
8	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
9	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
10	Nickel as a virulence factor in the Class I bacterial carcinogen, Helicobacter pylori. Seminars in Cancer Biology, 2021, 76, 143-155.	9.6	14
11	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
12	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
13	Facilitating Nitrification Inhibition through Green, Mechanochemical Synthesis of a Novel Nitrapyrin Complex. Crystal Growth and Design, 2021, 21, 5792-5799.	3.0	10
14	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
15	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
16	Structure, dynamics, and function of SrnR, a transcription factor for nickel-dependent gene expression. Metallomics, 2021, 13, .	2.4	4
17	Nickel import and export in the human pathogenHelicobacter pylori, perspectives from molecular modelling. Metallomics, 2021, 13, .	2.4	6
18	Targeting the Protein Tunnels of the Urease Accessory Complex: A Theoretical Investigation. Molecules, 2020, 25, 2911.	3.8	13

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19	Nickel and GTP Modulate Helicobacter pylori UreG Structural Flexibility. Biomolecules, 2020, 10, 1062.	4.0	9
20	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
21	The model structure of the copper-dependent ammonia monooxygenase. Journal of Biological Inorganic Chemistry, 2020, 25, 995-1007.	2.6	27
22	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
23	DNMT1 mutations leading to neurodegeneration paradoxically reflect on mitochondrial metabolism. Human Molecular Genetics, 2020, 29, 1864-1881.	2.9	19
24	Intrinsic disorder in the nickel-dependent urease network. Progress in Molecular Biology and Translational Science, 2020, 174, 307-330.	1.7	6
25	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
26	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
27	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
28	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
29	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
30	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
31	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
32	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
33	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
34	Insights into Urease Inhibition by N-(n-Butyl) Phosphoric Triamide through an Integrated Structural and Kinetic Approach. Journal of Agricultural and Food Chemistry, 2019, 67, 2127-2138.	5.2	33
35	Bioinorganic Chemistry of Nickel. Inorganics, 2019, 7, 131.	2.7	5
36	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

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37	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
38	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
39	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
40	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
41	An Evaluation of Maleicâ€Itaconic Copolymers as Urease Inhibitors. Soil Science Society of America Journal, 2018, 82, 994-1003.	2.2	9
42	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
43	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
44	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
45	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
46	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
47	Polymer-Mediated Delivery of siRNAs to Hepatocellular Carcinoma: Variables Affecting Specificity and Effectiveness. Molecules, 2018, 23, 777.	3.8	18
48	Smart urea ionic co-crystals with enhanced urease inhibition activity for improved nitrogen cycle management. Chemical Communications, 2018, 54, 7637-7640.	4.1	41
49	Protein Aggregation and Molecular Crowding. International Review of Cell and Molecular Biology, 2017, 329, 49-77.	3.2	22
50	Strategies to optimize siRNA delivery to hepatocellular carcinoma cells. Expert Opinion on Drug Delivery, 2017, 14, 797-810.	5.0	25
51	Protein Tunnels: The Case of Urease Accessory Proteins. Journal of Chemical Theory and Computation, 2017, 13, 2322-2331.	5.3	25
52	Glutamate Ligation in the Ni(II)- and Co(II)-Responsive Escherichia coli Transcriptional Regulator, RcnR. Inorganic Chemistry, 2017, 56, 6459-6476.	4.0	16
53	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
54	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

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55	Urease Inhibition in the Presence of N-(n-Butyl)thiophosphoric Triamide, a Suicide Substrate: Structure and Kinetics. Biochemistry, 2017, 56, 5391-5404.	2.5	53
56	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
57	The relationship between folding and activity in UreG, an intrinsically disordered enzyme. Scientific Reports, 2017, 7, 5977.	3.3	34
58	Inactivation of urease by catechol: Kinetics and structure. Journal of Inorganic Biochemistry, 2017, 166, 182-189.	3.5	57
59	Mathematical Modeling of Drug Release from Natural Polysaccharides Based Matrices. Natural Product Communications, 2017, 12, 1934578X1701200.	0.5	4
60	Characterization and 1.57â€…Ã… resolution structure of the key fire blight phosphatase AmsI fromErwinia amylovora. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 903-910.	0.8	8
61	Isothermal Titration Calorimetry to Characterize Enzymatic Reactions. Methods in Enzymology, 2016, 567, 215-236.	1.0	20
62	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
63	Nickel impact on human health: An intrinsic disorder perspective. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1714-1731.	2.3	151
64	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
65	Inactivation of urease by 1,4-benzoquinone: chemistry at the protein surface. Dalton Transactions, 2016, 45, 5455-5459.	3.3	61
66	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
67	Conformational ensemble of human Î±-synuclein physiological form predicted by molecular simulations. Physical Chemistry Chemical Physics, 2016, 18, 5702-5706.	2.8	32
68	Transient Interactions of a Cytosolic Protein with Macromolecular and Vesicular Cosolutes: Unspecific and Specific Effects. ChemBioChem, 2015, 16, 2633-2645.	2.6	10
69	Evolution of Macromolecular Docking Techniques: The Case Study of Nickel and Iron Metabolism in Pathogenic Bacteria. Molecules, 2015, 20, 14265-14292.	3.8	3
70	Polysaccharides for the Delivery of Antitumor Drugs. Materials, 2015, 8, 2569-2615.	2.9	110
71	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
72	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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73	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
74	Nickel-responsive transcriptional regulators. Metallomics, 2015, 7, 1305-1318.	2.4	40
75	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
76	Novel Lipid and Polymeric Materials as Delivery Systems for Nucleic Acid Based Drugs. Current Drug Metabolism, 2015, 16, 427-452.	1.2	26
77	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
78	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
79	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
80	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
81	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
82	Fluoride inhibition of Sporosarcina pasteurii urease: structure and thermodynamics. Journal of Biological Inorganic Chemistry, 2014, 19, 1243-1261.	2.6	58
83	Topological characterization of a bacterial celluloseâ€"acrylic acid polymeric matrix. European Journal of Pharmaceutical Sciences, 2014, 62, 326-333.	4.0	15
84	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
85	Nonredox Nickel Enzymes. Chemical Reviews, 2014, 114, 4206-4228.	47.7	235
86	Hot Biological Catalysis: Isothermal Titration Calorimetry to Characterize Enzymatic Reactions. Journal of Visualized Experiments, 2014, , .	0.3	7
87	Chemosensorial G-proteins-Coupled Receptors: A Perspective from Computational Methods. Advances in Experimental Medicine and Biology, 2014, 805, 441-457.	1.6	4
88	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
89	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
90	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

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91	Conformational Fluctuations of UreG, an Intrinsically Disordered Enzyme. Biochemistry, 2013, 52, 2949-2954.	2.5	33
92	Nickel and Human Health. Metal Ions in Life Sciences, 2013, 13, 321-357.	2.8	71
93	Urease. , 2013, , 2287-2292.		1
94	GOMoDo: A GPCRs Online Modeling and Docking Webserver. PLoS ONE, 2013, 8, e74092.	2.5	84
95	Structure/Function Relationships of Phospholipases C Beta. Current Protein and Peptide Science, 2013, 14, 650-657.	1.4	11
96	Crystallographic and X-ray absorption spectroscopic characterization of Helicobacter pylori 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
97	Denaturant-Induced Conformational Transitions in Intrinsically Disordered Proteins. , 2012, 896, 197-213.		4
98	Insights in the (un)structural organization of Bacillus pasteurii UreG, an intrinsically disordered GTPase enzyme. Molecular BioSystems, 2012, 8, 220-228.	2.9	44
99	Engineered biosealant strains producing inorganic and organic biopolymers. Journal of Biotechnology, 2012, 161, 181-189.	3.8	19
100	Metal Ion-Mediated DNA-Protein Interactions. Metal Ions in Life Sciences, 2012, 10, 135-170.	2.8	21
101	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
102	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
103	Holo-Ni2+Helicobacter pylori NikR contains four square-planar nickel-binding sites at physiological pH. Dalton Transactions, 2011, 40, 7831.	3.3	28
104	Zinc Inhibition of Bacterial Cytochrome bc₁ Reveals the Role of Cytochrome b E295 in Proton Release at the Q_o Site. Biochemistry, 2011, 50, 4263-4272.	2.5	30
105	Chemistry of Ni²⁺ in Urease: Sensing, Trafficking, and Catalysis. Accounts of Chemical Research, 2011, 44, 520-530.	15.6	224
106	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
107	Interaction of Selenoprotein W with 14-3-3 Proteins: A Computational Approach. Journal of Proteome Research, 2011, 10, 968-976.	3.7	29
108	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

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109	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
110	Helicobacter pylori 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
111	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
112	Zn²⁺â€linked dimerization of UreG from Helicobacter pylori, a chaperone involved in nickel trafficking and urease activation. Proteins: Structure, Function and Bioinformatics, 2009, 74, 222-239.	2.6	73
113	Conformational Equilibria in Monomeric Î±-Synuclein at the Single-Molecule Level. PLoS Biology, 2008, 6, e6.	5.6	181
114	Structural Characterization of Binding of Cu(II) to Tau Protein. Biochemistry, 2008, 47, 10841-10851.	2.5	85
115	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
116	The Ni2+ binding properties of Helicobacter pylori NikR. Chemical Communications, 2007, , 3649.	4.1	47
117	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
118	Urease: Recent Insights on the Role of Nickel. , 2007, , 241-277.		11
119	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
120	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
121	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
122	An Italian contribution to structural genomics: Understanding metalloproteins. Coordination Chemistry Reviews, 2006, 250, 1419-1450.	18.8	14
123	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
124	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
125	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
126	Structure of the Intermolecular Complex between Plastocyanin and Cytochrome f from Spinach*. Journal of Biological Chemistry, 2005, 280, 18833-18841.	3.4	20

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127	Nickel trafficking: insights into the fold and function of UreE, a urease metallochaperone. Journal of Inorganic Biochemistry, 2004, 98, 803-813.	3.5	43
128	The Asn 38â˜Cys 84 H-Bond in Plastocyanin. Journal of Physical Chemistry B, 2004, 108, 7495-7499.	2.6	7
129	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
130	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
131	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
132	NMR Solution Structure, Backbone Mobility, and Homology Modeling ofc-Type Cytochromes from Gram-Positive Bacteria. ChemBioChem, 2002, 3, 299-310.	2.6	23
133	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
134	Structure-based computational study of the catalytic and inhibition mechanisms of urease. Journal of Biological Inorganic Chemistry, 2001, 6, 300-314.	2.6	110
135	Backbone Dynamics of Plastocyanin in Both Oxidation States. Journal of Biological Chemistry, 2001, 276, 47217-47226.	3.4	50
136	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
137	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
138	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
139	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
140	Immobilization of jack bean urease on hydroxyapatite: urease immobilization in alkaline soils. Soil Biology and Biochemistry, 1998, 30, 1485-1490.	8.8	63
141	Title is missing!. Photosynthesis Research, 1997, 53, 13-21.	2.9	17
142	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
143	Bacillus pasteurii urease: A heteropolymeric enzyme with a binuclear nickel active site. Soil Biology and Biochemistry, 1996, 28, 819-821.	8.8	55
144	X-ray Absorption Spectroscopy Study of Native and Phenylphosphorodiamidate-Inhibited Bacillus pasteurii Urease. FEBS Journal, 1996, 239, 61-66.	0.2	31

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145	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
146	The high potential iron-sulfur protein (HiPIP) fromRhodoferax fermentansis competent in photosynthetic electron transfer. FEBS Letters, 1995, 357, 70-74.	2.8	62
147	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
148	Thiocarbamoyl Disulfides as Inhibitors of Urease and Ammonia Monooxygenase: Crystal Engineering for Novel Materials. Crystal Growth and Design, 0, , .	3.0	1