Laura Cendron

List of Publications by Year
in descending order

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84 papers	2,357 citations	196777 29 h-index	274796 44 g-index
86 all docs	86 docs citations	86 times ranked	3784 citing authors

#	Article	IF	Citations
1	Transcriptomic and genomic studies classify NKL54 as a histone deacetylase inhibitor with indirect influence on MEF2-dependent transcription. Nucleic Acids Research, 2022, 50, 2566-2586.	6.5	12
2	The Roc domain of LRRK2 as a hub for protein-protein interactions: a focus on PAK6 and its impact on RAB phosphorylation. Brain Research, 2022, 1778, 147781.	1.1	7
3	Structural Analysis of Human Serum Albumin in Complex with the Fibrate Drug Gemfibrozil. International Journal of Molecular Sciences, 2022, 23, 1769.	1.8	7
4	The Family Keeps on Growing: Four Novel Fungal OYEs Characterized. International Journal of Molecular Sciences, 2022, 23, 3050.	1.8	4
5	Copper Binding and Oligomerization Studies of the Metal Resistance Determinant CrdA from Helicobacter pylori. Molecules, 2022, 27, 3387.	1.7	0
6	Asymmetric Proton Transfer Catalysis by Stereocomplementary Old Yellow Enzymes for Câ•C Bond Isomerization Reaction. ACS Catalysis, 2022, 12, 7396-7405.	5.5	7
7	Synthesis and direct assay of large macrocycle diversities by combinatorial late-stage modification at picomole scale. Nature Communications, 2022, 13, .	5.8	14
8	Unveiling the binding mode of perfluorooctanoic acid to human serum albumin. Protein Science, 2021, 30, 830-841.	3.1	25
9	A New Thermophilic Ene-Reductase from the Filamentous Anoxygenic Phototrophic Bacterium Chloroflexus aggregans. Microorganisms, 2021, 9, 953.	1.6	7
10	Two new ene-reductases from photosynthetic extremophiles enlarge the panel of old yellow enzymes: CtOYE and GsOYE. Applied Microbiology and Biotechnology, 2020, 104, 2051-2066.	1.7	14
11	Inhibition of the transcriptional repressor LexA: Withstanding drug resistance by inhibiting the bacterial mechanisms of adaptation to antimicrobials. Life Sciences, 2020, 241, 117116.	2.0	16
12	Virtual screening identifies broad-spectrum Î²-lactamase inhibitors with activity on clinically relevant serine- and metallo-carbapenemases. Scientific Reports, 2020, 10, 12763.	1.6	25
13	Câ€•terminal tails mimicking bioactive intermediates cause different plasma degradation patterns and kinetics in neuropeptides Î³â€•MSH, Î±â€•MSH, and neurotensin. Journal of Peptide Science, 2020, 26, e3279.	0.8	2
14	Protein electrostatics: From computational and structural analysis to discovery of functional fingerprints and biotechnological design. Computational and Structural Biotechnology Journal, 2020, 18, 1774-1789.	1.9	44
15	Macrocycle synthesis strategy based on step-wise â€œadding and reactingâ€•three components enables screening of large combinatorial libraries. Chemical Science, 2020, 11, 7858-7863.	3.7	12
16	From the Amelioration of a NADP⁺â€•dependent Formate Dehydrogenase to the Discovery of a New Enzyme: Round Trip from Theory to Practice. ChemCatChem, 2020, 12, 2478-2487.	1.8	10
17	Targeting the Class A Carbapenemase GES-5 via Virtual Screening. Biomolecules, 2020, 10, 304.	1.8	1
18	Chloroplast Calcium Signaling in the Spotlight. Frontiers in Plant Science, 2020, 11, 186.	1.7	34

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19	4-Amino-1,2,4-triazole-3-thione as a Promising Scaffold for the Inhibition of Serine and Metallo-Î²-Lactamases. Pharmaceuticals, 2020, 13, 52.	1.7	13
20	Thiol-to-amine cyclization reaction enables screening of large libraries of macrocyclic compounds and the generation of sub-kilodalton ligands. Science Advances, 2019, 5, eaaw2851.	4.7	30
21	Phosphorylation of p23-1 cochaperone by protein kinase CK2 affects root development in Arabidopsis. Scientific Reports, 2019, 9, 9846.	1.6	5
22	A-to-I editing of Malacoherpesviridae RNAs supports the antiviral role of ADAR1 in mollusks. BMC Evolutionary Biology, 2019, 19, 149.	3.2	20
23	Phenylboronic Acids Probing Molecular Recognition against Class A and Class C Î²-lactamases. Antibiotics, 2019, 8, 171.	1.5	9
24	A chloroplast-localized mitochondrial calcium uniporter transduces osmotic stress in Arabidopsis. Nature Plants, 2019, 5, 581-588.	4.7	56
25	Structural Aspects of Helicobacter pylori Antibiotic Resistance. Advances in Experimental Medicine and Biology, 2019, 1149, 227-241.	0.8	15
26	X-ray Crystallography Deciphers the Activity of Broad-Spectrum Boronic Acid Î²-Lactamase Inhibitors. ACS Medicinal Chemistry Letters, 2019, 10, 650-655.	1.3	30
27	First virtual screening and experimental validation of inhibitors targeting GES-5 carbapenemase. Journal of Computer-Aided Molecular Design, 2019, 33, 295-305.	1.3	9
28	Ten Years with New Delhi Metallo-Î²-lactamase-1 (NDM-1): From Structural Insights to Inhibitor Design. ACS Infectious Diseases, 2019, 5, 9-34.	1.8	123
29	Phenylboronic Acid Derivatives as Validated Leads Active in Clinical Strains Overexpressing KPCâ€•2: A Step against Bacterial Resistance. ChemMedChem, 2018, 13, 713-724.	1.6	24
30	Structure-Based Virtual Screening for the Discovery of Novel Inhibitors of New Delhi Metallo-Î²-lactamase-1. ACS Medicinal Chemistry Letters, 2018, 9, 45-50.	1.3	38
31	In silico identification and experimental validation of hits active against KPC-2 Î²-lactamase. PLoS ONE, 2018, 13, e0203241.	1.1	9
32	Cleavage of the Glycoprotein of Arenaviruses. , 2018, , 47-70.		2
33	SOS response in bacteria: Inhibitory activity of lichen secondary metabolites against Escherichia coli RecA protein. Phytomedicine, 2017, 29, 11-18.	2.3	34
34	Catalysis and Structure of Zebrafish Urate Oxidase Provide Insights into the Origin of Hyperuricemia in Hominoids. Scientific Reports, 2016, 6, 38302.	1.6	21
35	Mechanism of Folding and Activation of Subtilisin Kexin Isozyme-1 (SKI-1)/Site-1 Protease (S1P). Journal of Biological Chemistry, 2016, 291, 2055-2066.	1.6	13
36	The Structure and Function of a Microbial Allantoin Racemase Reveal the Origin and Conservation of a Catalytic Mechanism. Biochemistry, 2016, 55, 6421-6432.	1.2	7

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37	Stability data of FlgD from Helicobacter pylori and structural comparison with other homologs. Data in Brief, 2016, 7, 493-501.	0.5	1
38	Crystal structure of truncated FlgD from the human pathogen Helicobacter pylori. Journal of Structural Biology, 2016, 194, 147-155.	1.3	7
39	Structure and Stability of FlgD from the Pathogenic 26695 Strain of Helicobacter pylori. Croatica Chemica Acta, 2016, 89, 1-7.	0.1	1
40	Structural basis for double cofactor specificity in a new formate dehydrogenase from the acidobacterium Granulicella mallensis MP5ACTX8. Applied Microbiology and Biotechnology, 2015, 99, 9541-9554.	1.7	39
41	The EF-Hand Ca²⁺ Binding Protein MICU Choreographs Mitochondrial Ca²⁺ Dynamics in Arabidopsis. Plant Cell, 2015, 27, 3190-3212.	3.1	103
42	Structural Insights into Complexes of Glucose-Regulated Protein94 (Grp94) with Human Immunoglobulin G. Relevance for Grp94-IgG Complexes that Form In Vivo in Pathological Conditions. PLoS ONE, 2014, 9, e86198.	1.1	13
43	Structural and functional aspects of the<i>Helicobacter pylori</i>secretome. World Journal of Gastroenterology, 2014, 20, 1402.	1.4	33
44	Zymogen Activation and Subcellular Activity of Subtilisin Kexin Isozyme 1/Site 1 Protease. Journal of Biological Chemistry, 2014, 289, 35743-35756.	1.6	18
45	Crystal structure of the secreted protein HP1454 from the human pathogen <i>Helicobacter pylori</i>. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2868-2873.	1.5	2
46	<scp><i>H</i></scp><i>elicobacter pylori</i> periplasmic receptor <scp>CeuE</scp> (<scp>HP</scp>1561) modulates its nickel affinity via organic metallophores. Molecular Microbiology, 2014, 91, 724-735.	1.2	35
47	DJ-1 Is a Copper Chaperone Acting on SOD1 Activation. Journal of Biological Chemistry, 2014, 289, 10887-10899.	1.6	76
48	Structural evidence for native state stabilization of a conformationally labile amyloidogenic transthyretin variant by fibrillogenesis inhibitors. FEBS Letters, 2013, 587, 2325-2331.	1.3	21
49	Differential Recognition of Old World and New World Arenavirus Envelope Glycoproteins by Subtilisin Kexin Isozyme 1 (SKI-1)/Site 1 Protease (S1P). Journal of Virology, 2013, 87, 6406-6414.	1.5	18
50	Protein HP1028 from the human pathogen<i>Helicobacter pylori</i>belongs to the lipocalin family. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1387-1394.	2.5	3
51	Biochemical Analysis of the Interactions between the Proteins Involved in the [FeFe]-Hydrogenase Maturation Process. Journal of Biological Chemistry, 2012, 287, 36544-36555.	1.6	33
52	The [4Feâ€“4S]-cluster coordination of [FeFe]-hydrogenase maturation protein HydF as revealed by EPR and HYSCORE spectroscopies. Biochimica Et Biophysica Acta - Bioenergetics, 2012, 1817, 2149-2157.	0.5	38
53	Crystal structure of sarcoplasmic reticulum Ca2+-ATPase (SERCA) from bovine muscle. Journal of Structural Biology, 2012, 178, 38-44.	1.3	35
54	Bicyclic Peptide Inhibitor Reveals Large Contact Interface with a Protease Target. ACS Chemical Biology, 2012, 7, 817-821.	1.6	156

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55	Structural analysis of trimeric phospholipase A₂ neurotoxin from the Australian taipan snake venom. FEBS Journal, 2012, 279, 3121-3135.	2.2	23
56	Aluminum, copper, iron and zinc differentially alter amyloid-AÎ²1â€“42 aggregation and toxicity. International Journal of Biochemistry and Cell Biology, 2011, 43, 877-885.	1.2	147
57	The crystal structure of ADP-L-glycero-D-manno-heptose-6-epimerase (HP0859) from Helicobacter pylori. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1641-1647.	1.1	4
58	Probing the Evolution of Hydroxyisourate Hydrolase into Transthyretin through Active-Site Redesign. Journal of Molecular Biology, 2011, 409, 504-512.	2.0	15
59	Structural and functional aspects of unique type IV secretory components in the <i>Helicobacterâ€ƒpylori cag</i>â€pathogenicity island. FEBS Journal, 2011, 278, 1223-1231.	2.2	32
60	Structure of the uncomplexed<i>Neisseria meningitidis</i>factor H-binding protein fHbp (rLP2086). Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 531-535.	0.7	33
61	Crystal Structure of HydF Scaffold Protein Provides Insights into [FeFe]-Hydrogenase Maturation. Journal of Biological Chemistry, 2011, 286, 43944-43950.	1.6	32
62	The Structure of Helicobacter pylori HP0310 Reveals an Atypical Peptidoglycan Deacetylase. PLoS ONE, 2011, 6, e19207.	1.1	19
63	Functional and structural aspects of <i>helicobacter pylori</i> acidic stress response factors. IUBMB Life, 2010, 62, 715-723.	1.5	19
64	Functional and structural aspects of helicobacter pylori acidic stress response factors. IUBMB Life, 2010, 62, spcone-spcone.	1.5	0
65	<i>Helicobacterâ€ƒpylori</i> acidic stress response factor HP1286 is a YceI homolog with new binding specificity. FEBS Journal, 2010, 277, 1896-1905.	2.2	26
66	An aminotransferase branch point connects purine catabolism to amino acid recycling. Nature Chemical Biology, 2010, 6, 801-806.	3.9	26
67	Amyloidogenic Potential of Transthyretin Variants. Journal of Biological Chemistry, 2009, 284, 25832-25841.	1.6	44
68	Structural and mutational analysis of TenA protein (HP1287) from the <i>Helicobacterâ€ƒpylori</i> thiamin salvage pathway â€“ evidence of a different substrate specificity. FEBS Journal, 2009, 276, 6227-6235.	2.2	12
69	The Helicobacter pylori CagD (HP0545, Cag24) Protein Is Essential for CagA Translocation and Maximal Induction of Interleukin-8 Secretion. Journal of Molecular Biology, 2009, 386, 204-217.	2.0	33
70	Vertebrate 5-Hydroxyisourate Hydrolase Identification, Function, Structure, and Evolutionary Relationship with Transthyretin. , 2009, , 95-108.		2
71	Structural and enzymatic characterization of HP0496, a YbgC thioesterase from <i>Helicobacter pylori</i>. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1212-1221.	1.5	30
72	The crystal structure of the superoxide dismutase from Helicobacter pylori reveals a structured C-terminal extension. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1601-1606.	1.1	18

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73	Structural and mutational analyses of proteinâ€“protein interactions between transthyretin and retinolâ€binding protein. FEBS Journal, 2008, 275, 5841-5854.	2.2	34
74	Potential pathogenic role of Î²-amyloid1â€“42â€“aluminum complex in Alzheimer's disease. International Journal of Biochemistry and Cell Biology, 2008, 40, 731-746.	1.2	79
75	Logical Identification of an Allantoinase Analog (puuE) Recruited from Polysaccharide Deacetylases. Journal of Biological Chemistry, 2008, 283, 23295-23304.	1.6	62
76	Multiple Binding Sites for Substrates and Modulators of Semicarbazide-Sensitive Amine Oxidases: Kinetic Consequences. Molecular Pharmacology, 2008, 73, 525-538.	1.0	40
77	The Structure of 2-Oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline Decarboxylase Provides Insights into the Mechanism of Uric Acid Degradation. Journal of Biological Chemistry, 2007, 282, 18182-18189.	1.6	46
78	Acidic pH-induced Conformational Changes in Amyloidogenic Mutant Transthyretin. Journal of Molecular Biology, 2007, 366, 711-719.	2.0	38
79	The ATPâ€Binding Site of Protein Kinase CK2 Holds a Positive Electrostatic Area and Conserved Water Molecules. ChemBioChem, 2007, 8, 1804-1809.	1.3	98
80	The crystal structure of CagS from the <i>Helicobacter pylori</i> pathogenicity island. Proteins: Structure, Function and Bioinformatics, 2007, 69, 440-443.	1.5	10
81	Structural biology of Helicobacter pylori type IV secretion system. Microbial Cell Factories, 2006, 5, P45.	1.9	1
82	Structure of Zebra fish HIUase: Insights into Evolution of an Enzyme to a Hormone Transporter. Journal of Molecular Biology, 2006, 363, 1-9.	2.0	52
83	Crystal structure of alkyl hydroperoxide-reductase (AhpC) from Helicobacter pylori. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1753, 240-246.	1.1	29
84	Crystal Structure of CagZ, a Protein from the Helicobacter pylori Pathogenicity Island that Encodes for a Type IV Secretion System. Journal of Molecular Biology, 2004, 340, 881-889.	2.0	21