

Stefano Benini

List of Publications by Year in descending order

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54
papers

2,397
citations

331670

21
h-index

206112

48
g-index

56
all docs

56
docs citations

56
times ranked

1991
citing authors

#	ARTICLE	IF	CITATIONS
1	A new proposal for urease mechanism based on the crystal structures of the native and inhibited enzyme from <i>Bacillus pasteurii</i> : why urea hydrolysis costs two nickels. <i>Structure</i> , 1999, 7, 205-216.	3.3	462
2	Chemistry of Ni ²⁺ in Urease: Sensing, Trafficking, and Catalysis. <i>Accounts of Chemical Research</i> , 2011, 44, 520-530.	15.6	224
3	The complex of <i>Bacillus pasteurii</i> urease with acetohydroxamate anion from X-ray data at 1.55 Å resolution. <i>Journal of Biological Inorganic Chemistry</i> , 2000, 5, 110-118.	2.6	169
4	Structural properties of the nickel ions in urease: novel insights into the catalytic and inhibition mechanisms. <i>Coordination Chemistry Reviews</i> , 1999, 190-192, 331-355.	18.8	147
5	Molecular Details of Urease Inhibition by Boric Acid: Insights into the Catalytic Mechanism. <i>Journal of the American Chemical Society</i> , 2004, 126, 3714-3715.	13.7	142
6	Structure-based rationalization of urease inhibition by phosphate: novel insights into the enzyme mechanism. <i>Journal of Biological Inorganic Chemistry</i> , 2001, 6, 778-790.	2.6	132
7	The complex of <i>Bacillus pasteurii</i> urease with β -mercaptoethanol from X-ray data at 1.65 Å resolution. <i>Journal of Biological Inorganic Chemistry</i> , 1998, 3, 268-273.	2.6	119
8	Urease from the soil bacterium <i>Bacillus pasteurii</i> : Immobilization on Ca-polygalacturonate. <i>Soil Biology and Biochemistry</i> , 1996, 28, 811-817.	8.8	92
9	The Structure of the Elusive Urease-Urea Complex Unveils the Mechanism of a Paradigmatic Nickel-Dependent Enzyme. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 7415-7419.	13.8	66
10	Crystal Structure of Oxidized <i>Bacillus pasteurii</i> Cytochrome c553 at 0.97 Å Resolution. <i>Biochemistry</i> , 2000, 39, 13115-13126.	2.5	59
11	Fluoride inhibition of <i>Sporosarcina pasteurii</i> urease: structure and thermodynamics. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 1243-1261.	2.6	58
12	Structural basis for DNA recognition and loading into a viral packaging motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 811-816.	7.1	57
13	The crystal structure of <i>Erwinia amylovora</i> levansucrase provides a snapshot of the products of sucrose hydrolysis trapped into the active site. <i>Journal of Structural Biology</i> , 2015, 191, 290-298.	2.8	56
14	<i>Bacillus pasteurii</i> urease: A heteropolymeric enzyme with a binuclear nickel active site. <i>Soil Biology and Biochemistry</i> , 1996, 28, 819-821.	8.8	55
15	The crystal structure of <i>Sporosarcina pasteurii</i> urease in a complex with citrate provides new hints for inhibitor design. <i>Journal of Biological Inorganic Chemistry</i> , 2013, 18, 391-399.	2.6	49
16	Biomolecular Characterization of the Levansucrase of <i>Erwinia amylovora</i> , a Promising Biocatalyst for the Synthesis of Fructooligosaccharides. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 12265-12273.	5.2	45
17	Kinetic and structural studies reveal a unique binding mode of sulfite to the nickel center in urease. <i>Journal of Inorganic Biochemistry</i> , 2016, 154, 42-49.	3.5	42
18	X-ray Absorption Spectroscopy Study of Native and Phenylphosphorodiamidate-Inhibited <i>Bacillus pasteurii</i> Urease. <i>FEBS Journal</i> , 1996, 239, 61-66.	0.2	31

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19	Modulation of <i>Bacillus pasteurii</i> cytochrome c 553 reduction potential by structural and solution parameters. <i>Journal of Biological Inorganic Chemistry</i> , 1998, 3, 371-382.	2.6	28
20	Holo-Ni ²⁺ - <i>Helicobacter pylori</i> NikR contains four square-planar nickel-binding sites at physiological pH. <i>Dalton Transactions</i> , 2011, 40, 7831.	3.3	28
21	A complete structural characterization of the desferrioxamine E biosynthetic pathway from the fire blight pathogen <i>Erwinia amylovora</i> . <i>Journal of Structural Biology</i> , 2018, 202, 236-249.	2.8	26
22	Crystallization and preliminary high-resolution X-ray diffraction analysis of native and β -mercaptoethanol-inhibited urease from <i>Bacillus pasteurii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 409-412.	2.5	21
23	Enzymatic synthesis of nucleobase-modified UDP-sugars: scope and limitations. <i>Carbohydrate Research</i> , 2015, 404, 17-25.	2.3	21
24	The Impact of pH on Catalytically Critical Protein Conformational Changes: The Case of the Urease, a Nickel Enzyme. <i>Chemistry - A European Journal</i> , 2019, 25, 12145-12158.	3.3	21
25	Conservation of <i>Erwinia amylovora</i> pathogenicity-relevant genes among <i>Erwinia</i> genomes. <i>Archives of Microbiology</i> , 2017, 199, 1335-1344.	2.2	17
26	An Unusual, His-dependent Family I Pyrophosphatase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 41819-41826.	3.4	16
27	Cloning, expression, purification, crystallization and preliminary X-ray analysis of <i>Erwinia amylovora</i> Lsc, a levansucrase from <i>Erwinia amylovora</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 570-573.	0.7	15
28	The Structure of Sucrose-Soaked Levansucrase Crystals from <i>Erwinia tasmaniensis</i> reveals a Binding Pocket for Levanbiose. <i>International Journal of Molecular Sciences</i> , 2020, 21, 83.	4.1	15
29	Glucose-1-phosphate uridylyltransferase from <i>Erwinia amylovora</i> : Activity, structure and substrate specificity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1348-1357.	2.3	13
30	Comparison of the Levansucrase from the epiphyte <i>Erwinia tasmaniensis</i> vs its homologue from the phytopathogen <i>Erwinia amylovora</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 127, 496-501.	7.5	13
31	Oxidized and Reduced [Fe ₂ Q ₂] (Q = S, Se) Cores of Spinach Ferredoxin: a Comparative Study Using 1H NMR Spectroscopy. <i>Inorganic Chemistry</i> , 1995, 34, 417-420.	4.0	12
32	Structure of <i>Rhodospirillum rubrum</i> high-potential iron-sulfur protein solved by MAD. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1582-1588.	2.5	12
33	The structure of <i>Erwinia amylovora</i> AvrRpt2 provides insight into protein maturation and induced resistance to fire blight by <i>Malus domestica</i> cv. 'Robusta'. <i>Journal of Structural Biology</i> , 2019, 206, 233-242.	2.8	12
34	Carbohydrate-Active Enzymes: Structure, Activity, and Reaction Products. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2727.	4.1	12
35	Cytochrome c-553 from the Alkalophilic Bacterium <i>Bacillus pasteurii</i> Has the Primary Structure Characteristics of a Lipoprotein. <i>Biochemical and Biophysical Research Communications</i> , 1999, 264, 380-387.	2.1	11
36	Two-wavelength MAD phasing: in search of the optimal choice of wavelengths. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1449-1458.	2.5	9

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37	Crystals of cytochrome c-553 from <i>Bacillus pasteurii</i> show diffraction to 0.97 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 28, 580-585.	2.6	8
38	High resolution crystal structure of <i>Rubrivivax gelatinosus</i> cytochrome c ₂ . <i>Journal of Inorganic Biochemistry</i> , 2008, 102, 1322-1328.	3.5	8
39	Characterization and 1.57 Å resolution structure of the key fire blight phosphatase AmsI from <i>Erwinia amylovora</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 903-910.	0.8	8
40	A genome-wide analysis of desferrioxamine mediated iron uptake in <i>Erwinia</i> spp. reveals genes exclusive of the Rosaceae infecting strains. <i>Scientific Reports</i> , 2019, 9, 2818.	3.3	8
41	Structure of the <i>Mycobacterium tuberculosis</i> soluble inorganic pyrophosphatase Rv3628 at pH 7.0. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 866-870.	0.7	7
42	Expression, purification, crystallization and preliminary X-ray analysis of glucose-1-phosphate uridylyltransferase (GalU) from <i>Erwinia amylovora</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1249-1251.	0.8	7
43	The Structure of the Elusive Urease “Urea Complex Unveils the Mechanism of a Paradigmatic Nickel-Dependent Enzyme. <i>Angewandte Chemie</i> , 2019, 131, 7493-7497.	2.0	7
44	The structural and functional characterization of <i>Malus domestica</i> double bond reductase MdDBR provides insights towards the identification of its substrates. <i>International Journal of Biological Macromolecules</i> , 2021, 171, 89-99.	7.5	6
45	Cyclic voltammetry and spectroelectrochemistry of cytochrome c ₈ from <i>Rubrivivax gelatinosus</i> . Implications in photosynthetic electron transfer. <i>Inorganica Chimica Acta</i> , 1997, 263, 379-384.	2.4	5
46	The 1.58 Å resolution structure of the DNA-binding domain of bacteriophage SF6 small terminase provides new hints on DNA binding. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 376-381.	0.7	5
47	Cloning, purification, crystallization and 1.57 Å resolution X-ray data analysis of AmsI, the tyrosine phosphatase controlling amylovoran biosynthesis in the plant pathogen <i>Erwinia amylovora</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1693-1696.	0.8	4
48	Structural and functional analysis of <i>Erwinia amylovora</i> SrlD. The first crystal structure of a sorbitol-6-phosphate 2-dehydrogenase. <i>Journal of Structural Biology</i> , 2018, 203, 109-119.	2.8	4
49	The crystal structure of <i>Erwinia amylovora</i> AmyR, a member of the YbjN protein family, shows similarity to type III secretion chaperones but suggests different cellular functions. <i>PLoS ONE</i> , 2017, 12, e0176049.	2.5	3
50	Purification, crystallization and preliminary X-ray analysis of an acetylxylan esterase from <i>Bacillus pumilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1906-1907.	2.5	2
51	Structural and functional characterization of proteins from the fire blight pathogen <i>Erwinia amylovora</i> . A review on the state of the art. <i>Journal of Plant Pathology</i> , 2021, 103, 51-63.	1.2	2
52	Urease. , 2013, , 2287-2292.		1
53	Crystallization and preliminary X-ray diffraction analysis of cytochrome c ₂ from <i>Rubrivivax gelatinosus</i> at 1.3 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 284-287.	2.5	0
54	The crystal structure of Rv2991 from <i>Mycobacterium tuberculosis</i> : An F420 binding protein with unknown function. <i>Journal of Structural Biology</i> , 2019, 206, 216-224.	2.8	0