

Norbert Sträter

List of Publications by Year in descending order

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114
papers

7,419
citations

94433

37
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56724

83
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122
all docs

122
docs citations

122
times ranked

8017
citing authors

#	ARTICLE	IF	CITATIONS
1	Recent Advances in Zinc Enzymology. <i>Chemical Reviews</i> , 1996, 96, 2375-2434.	47.7	1,323
2	Cellular function and molecular structure of ecto-nucleotidases. <i>Purinergic Signalling</i> , 2012, 8, 437-502.	2.2	850
3	Two-Metal Ion Catalysis in Enzymatic Acyl- and Phosphoryl-Transfer Reactions. <i>Angewandte Chemie International Edition in English</i> , 1996, 35, 2024-2055.	4.4	595
4	Mechanism of Fe(III) \leftrightarrow Zn(II) Purple Acid Phosphatase Based on Crystal Structures. <i>Journal of Molecular Biology</i> , 1996, 259, 737-748.	4.2	342
5	Insect-Derived Proline-Rich Antimicrobial Peptides Kill Bacteria by Inhibiting Bacterial Protein Translation at the 70S Ribosome. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 12236-12239.	13.8	195
6	Structural and functional studies on a thermostable polyethylene terephthalate degrading hydrolase from <i>Thermobifida fusca</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7815-7823.	3.6	191
7	Crystal Structure of the Human Ecto-5'-Nucleotidase (CD73): Insights into the Regulation of Purinergic Signaling. <i>Structure</i> , 2012, 20, 2161-2173.	3.3	164
8	Ecto-5'-nucleotidase: Structure function relationships. <i>Purinergic Signalling</i> , 2006, 2, 343-350.	2.2	159
9	Transition State Analog L-Leucinephosphonic Acid Bound to Bovine Lens Leucine Aminopeptidase: X-ray Structure at 1.65 Å Resolution in a New Crystal Form. <i>Biochemistry</i> , 1995, 34, 9200-9210.	2.5	146
10	Vaspin inhibits kallikrein 7 by serpin mechanism. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 2569-2583.	5.4	125
11	Crystal structure of the plasmid maintenance system Δ : Functional mechanism of toxin Δ and inactivation by Δ 2 complex formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1661-1666.	7.1	119
12	X-ray structure of aminopeptidase A from <i>Escherichia coli</i> and a model for the nucleoprotein complex in Xer site-specific recombination. <i>EMBO Journal</i> , 1999, 18, 4513-4522.	7.8	114
13	X-ray structure of the <i>Escherichia coli</i> periplasmic 5'-nucleotidase containing a dimetal catalytic site. , 1999, 6, 448-453.		111
14	$\hat{1}\pm, \hat{1}^2$ -Methylene-ADP (AOPCP) Derivatives and Analogues: Development of Potent and Selective ecto-5'-Nucleotidase (CD73) Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 6248-6263.	6.4	110
15	The X-ray Crystal Structure of Human $\hat{1}^2$ -Hexosaminidase B Provides New Insights into Sandhoff Disease. <i>Journal of Molecular Biology</i> , 2003, 328, 669-681.	4.2	109
16	Structural Studies on the Forward and Reverse Binding Modes of Peptides to the Chaperone DnaK. <i>Journal of Molecular Biology</i> , 2013, 425, 2463-2479.	4.2	104
17	Enzymatische Acyl- und Phosphoryltransferreaktionen unter Beteiligung von zwei Metallionen. <i>Angewandte Chemie</i> , 1996, 108, 2158-2191.	2.0	103
18	A bicarbonate ion as a general base in the mechanism of peptide hydrolysis by dizinc leucine aminopeptidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 11151-11155.	7.1	100

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19	Crystal structure of amyloamylase from <i>Thermus aquaticus</i> , a glycosyltransferase catalysing the production of large cyclic glucans. <i>Journal of Molecular Biology</i> , 2000, 296, 873-886.	4.2	96
20	Mechanism of hydrolysis of phosphate esters by the dimetal center of 5'-nucleotidase based on crystal structures. <i>Journal of Molecular Biology</i> , 2001, 309, 239-254.	4.2	96
21	Api88 Is a Novel Antibacterial Designer Peptide To Treat Systemic Infections with Multidrug-Resistant Gram-Negative Pathogens. <i>ACS Chemical Biology</i> , 2012, 7, 1281-1291.	3.4	94
22	Mechanisms of catalysis and allosteric regulation of yeast chorismate mutase from crystal structures. <i>Structure</i> , 1997, 5, 1437-1452.	3.3	93
23	Structural relationship between the mammalian Fe(III)-Fe(II) and the Fe(III)-Zn(II) plant purple acid phosphatases. <i>FEBS Letters</i> , 1995, 367, 56-60.	2.8	88
24	Calcium-sensing receptor-mediated NLRP3 inflammasome response to calciprotein particles drives inflammation in rheumatoid arthritis. <i>Nature Communications</i> , 2020, 11, 4243.	12.8	79
25	Rational Design of Oncocin Derivatives with Superior Protease Stabilities and Antibacterial Activities Based on the High-Resolution Structure of the Oncocin-DnaK Complex. <i>ChemBioChem</i> , 2011, 12, 874-876.	2.6	77
26	Crystal Structures of Recombinant Human Purple Acid Phosphatase With and Without an Inhibitory Conformation of the Repression Loop. <i>Journal of Molecular Biology</i> , 2005, 351, 233-246.	4.2	73
27	Crystallographic Evidence for a Domain Motion in Rat Nucleoside Triphosphate Diphosphohydrolase (NTPDase) 1. <i>Journal of Molecular Biology</i> , 2012, 415, 288-306.	4.2	73
28	Structural insight into signal conversion and inactivation by NTPDase2 in purinergic signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6882-6887.	7.1	71
29	Low Carbon Footprint Recycling of Post-Consumer PET Plastic with a Metagenomic Polyester Hydrolase. <i>ChemSusChem</i> , 2022, 15, .	6.8	70
30	Structure and allosteric regulation of eukaryotic 6-phosphofructokinases. <i>Biological Chemistry</i> , 2013, 394, 977-993.	2.5	58
31	Crystal Structure of <i>Thermotoga maritima</i> β -Glucosidase AglA Defines a New Clan of NAD ⁺ -dependent Glycosidases. <i>Journal of Biological Chemistry</i> , 2003, 278, 19151-19158.	3.4	56
32	Discovery of AB680: A Potent and Selective Inhibitor of CD73. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 11448-11468.	6.4	52
33	<i>E. coli</i> 5'-nucleotidase undergoes a hinge-bending domain rotation resembling a ball-and-socket motion. <i>Journal of Molecular Biology</i> , 2001, 309, 255-266.	4.2	50
34	Crystal structure of the T state of allosteric yeast chorismate mutase and comparison with the R state.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 3330-3334.	7.1	46
35	Surface supercharged human enteropeptidase light chain shows improved solubility and refolding yield. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 261-268.	2.1	45
36	Crystallographic Snapshots along the Reaction Pathway of Nucleoside Triphosphate Diphosphohydrolases. <i>Structure</i> , 2013, 21, 1460-1475.	3.3	44

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37	X-ray structure of acarbose bound to amylomaltase from <i>Thermus aquaticus</i> . <i>FEBS Journal</i> , 2000, 267, 6903-6913.	0.2	43
38	Amylose recognition and ring-size determination of amylomaltase. <i>Science Advances</i> , 2017, 3, e1601386.	10.3	42
39	A glutamate residue in the catalytic center of the yeast chorismate mutase restricts enzyme activity to acidic conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 8491-8496.	7.1	38
40	2-Substituted β -Methylene-ADP Derivatives: Potent Competitive Ecto-5'-nucleotidase (CD73) Inhibitors with Variable Binding Modes. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 2941-2957.	6.4	37
41	Characterization of Rat NTPDase1, -2, and -3 Ectodomains Refolded from Bacterial Inclusion Bodies. <i>Biochemistry</i> , 2007, 46, 11945-11956.	2.5	34
42	Discovery of Potent and Selective Non-Nucleotide Small Molecule Inhibitors of CD73. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 3935-3955.	6.4	34
43	X-Ray Crystal Structure Guides the Way to Subnanomolar Competitive Ecto-5'-Nucleotidase (CD73) Inhibitors for Cancer Immunotherapy. <i>Advanced Therapeutics</i> , 2019, 2, 1900075.	3.2	33
44	Crystal structure and spectroscopic characterization of cesium vanadium sulfate $\text{CsV}(\text{SO}_4)_2$. Evidence for an electronic Raman transition. <i>Inorganic Chemistry</i> , 1993, 32, 4714-4720.	4.0	30
45	A Large Hinge Bending Domain Rotation Is Necessary for the Catalytic Function of <i>Escherichia coli</i> 5'-Nucleotidase. <i>Biochemistry</i> , 2005, 44, 2244-2252.	2.5	30
46	Reinforced HNA Backbone Hydration in the Crystal Structure of a Decameric HNA/RNA Hybrid. <i>Journal of the American Chemical Society</i> , 2005, 127, 2937-2943.	13.7	30
47	Structural Identification of DnaK Binding Sites within Bovine and Sheep Bactenecin Bac7. <i>Protein and Peptide Letters</i> , 2014, 21, 407-412.	0.9	30
48	Crystallization and preliminary crystallographic data of purple acid phosphatase from red kidney bean. <i>Journal of Molecular Biology</i> , 1992, 224, 511-513.	4.2	27
49	Identification of residues important for NAD ⁺ binding by the <i>Thermotoga maritima</i> β -glucosidase AglA, a member of glycoside hydrolase family 4. <i>FEBS Letters</i> , 2002, 517, 267-271.	2.8	26
50	Crystal Structure of Hexokinase K1Hxk1 of <i>Kluyveromyces lactis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 41019-41033.	3.4	26
51	Functional Linkage of Adenine Nucleotide Binding Sites in Mammalian Muscle 6-Phosphofructokinase. <i>Journal of Biological Chemistry</i> , 2012, 287, 17546-17553.	3.4	25
52	Structures of <i>Legionella pneumophila</i> NTPDase1 in complex with polyoxometallates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1147-1154.	2.5	25
53	Crystal structure of NTPDase2 in complex with the sulfoanthraquinone inhibitor PSB-071. <i>Journal of Structural Biology</i> , 2014, 185, 336-341.	2.8	25
54	Trapping a 96° domain rotation in two distinct conformations by engineered disulfide bridges. <i>Protein Science</i> , 2004, 13, 1811-1822.	7.6	24

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55	Cosubstrate-induced dynamics of D-3-hydroxybutyrate dehydrogenase from <i>Pseudomonas putida</i> . FEBS Journal, 2007, 274, 5767-5779.	4.7	24
56	Structural Basis of the Stereospecificity of Bacterial B12-dependent 2-Hydroxyisobutyryl-CoA Mutase. Journal of Biological Chemistry, 2015, 290, 9727-9737.	3.4	23
57	Functional impact of intramolecular cleavage and dissociation of adhesion G protein-coupled receptor GPR133 (ADGRD1) on canonical signaling. Journal of Biological Chemistry, 2021, 296, 100798.	3.4	23
58	Crystal structure of human platelet phosphofructokinase-1 locked in an activated conformation. Biochemical Journal, 2015, 469, 421-432.	3.7	22
59	Structural Insight into Activation Mechanism of Toxoplasma gondii Nucleoside Triphosphate Diphosphohydrolases by Disulfide Reduction*. Journal of Biological Chemistry, 2012, 287, 3051-3066.	3.4	21
60	Proline-rich Antimicrobial Peptides Optimized for Binding to Escherichia coli Chaperone DnaK. Protein and Peptide Letters, 2016, 23, 1061-1071.	0.9	21
61	Crystallization and preliminary X-ray diffraction studies of the σ^{70} addiction system encoded by Streptococcus pyogenes plasmid pSM19035. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 745-747.	2.5	19
62	An Artificial Imine Reductase based on the Ribonuclease...S Scaffold. ChemCatChem, 2014, 6, 736-740.	3.7	19
63	Characterization of the Domain Orientations of E. coli 5'-Nucleotidase by Fitting an Ensemble of Conformers to DEER Distance Distributions. Structure, 2016, 24, 43-56.	3.3	19
64	Structure and function of the abasic site specificity pocket of an AP endonuclease from Archaeoglobus fulgidus. DNA Repair, 2009, 8, 219-231.	2.8	18
65	Active-Site Mobility Revealed by the Crystal Structure of Arylmalonate Decarboxylase from Bordetella bronchiseptica. Journal of Molecular Biology, 2008, 377, 386-394.	4.2	17
66	A unique serpin P1 ² glutamate and a conserved β -sheet C arginine are key residues for activity, protease recognition and stability of serpinA12 (vaspin). Biochemical Journal, 2015, 470, 357-367.	3.7	17
67	Surface-Binding Peptide Facilitates Electricity-Driven NADPH-Free Cytochrome P450 Catalysis. ChemCatChem, 2018, 10, 525-530.	3.7	17
68	Discovery of Potent and Selective Methylene phosphonic Acid CD73 Inhibitors. Journal of Medicinal Chemistry, 2021, 64, 845-860.	6.4	17
69	X-ray structure of acarbose bound to amyloamylase from Thermus aquaticus. Implications for the synthesis of large cyclic glucans. FEBS Journal, 2000, 267, 6903-6913.	0.2	17
70	Understanding the Structural Basis of Adhesion GPCR Functions. Handbook of Experimental Pharmacology, 2016, 234, 67-82.	1.8	16
71	Structure of DNA helicase RepA in complex with sulfate at 1.95-Å resolution implicates structural changes to an 'open' form. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 815-822.	2.5	14
72	Molecular architecture and structural basis of allosteric regulation of eukaryotic phosphofructokinases. FASEB Journal, 2011, 25, 89-98.	0.5	14

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73	Basic Residues of Î²-Sheet A Contribute to Heparin Binding and Activation of Vaspin (Serpina12). Journal of Biological Chemistry, 2017, 292, 994-1004.	3.4	14
74	Kallikrein-related peptidase 14 is the second KLK protease targeted by the serpin vaspin. Biological Chemistry, 2018, 399, 1079-1084.	2.5	14
75	Ribosomal Targeting Sites of Antimicrobial Peptides Api137 and Onc112 Are Conserved among Pathogens Indicating New Lead Structures To Develop Novel Broad-Spectrum Antibiotics. ChemBioChem, 2020, 21, 2628-2634.	2.6	14
76	Crystal structure of a supercharged variant of the human enteropeptidase light chain. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1907-1910.	2.6	13
77	Contribution of the two domains of <i>E. coli</i> 5'-nucleotidase to substrate specificity and catalysis. FEBS Letters, 2013, 587, 460-466.	2.8	13
78	New crystal forms of NTPDase1 from the bacterium <i>Legionella pneumophila</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 257-262.	0.7	13
79	Fluorine-Containing 6,7-Dialkoxybiaryl-Based Inhibitors for Phosphodiesterase...: Synthesis and in vitro Evaluation of Inhibitory Potency, Selectivity, and Metabolism. ChemMedChem, 2014, 9, 1476-1487.	3.2	13
80	Glycosylation of human vaspin (SERPINA12) and its impact on serpin activity, heparin binding and thermal stability. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1188-1194.	2.3	12
81	Structures of 2-Hydroxyisobutyric Acid-CoA Ligase Reveal Determinants of Substrate Specificity and Describe a Multi-Conformational Catalytic Cycle. Journal of Molecular Biology, 2019, 431, 2747-2761.	4.2	12
82	Expression and purification of the ligand-binding domain of peroxisome proliferator-activated receptor alpha (PPAR α). Protein Expression and Purification, 2008, 62, 185-189.	1.3	10
83	Protein surface charge of trypsinogen changes its activation pattern. BMC Biotechnology, 2014, 14, 109.	3.3	10
84	Recombinant expression of a unique chloromuconolactone dehalogenase ClcF from <i>Rhodococcus opacus</i> 1CP and identification of catalytically relevant residues by mutational analysis. Archives of Biochemistry and Biophysics, 2012, 526, 69-77.	3.0	9
85	The crystal structure of <i>Toxoplasma gondii</i> nucleoside triphosphate diphosphohydrolase 1 represents a conformational intermediate in the reductive activation mechanism of the tetrameric enzyme. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1271-1276.	2.6	9
86	Localization and orientation of heavy-atom cluster compounds in protein crystals using molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 284-297.	2.5	9
87	Crystal structure and substrate binding mode of ectonucleotide phosphodiesterase/pyrophosphatase-3 (NPP3). Scientific Reports, 2018, 8, 10874.	3.3	9
88	Leucyl aminopeptidase (animal). , 2004, , 896-901.		9
89	Regulatory Function of Hexokinase 2 in Glucose Signaling in <i>Saccharomyces cerevisiae</i> . Journal of Biological Chemistry, 2016, 291, 16477.	3.4	8
90	Structural Studies on the Inhibitory Binding Mode of Aromatic Coumarinic Esters to Human Kallikrein-Related Peptidase 7. Journal of Medicinal Chemistry, 2020, 63, 5723-5733.	6.4	8

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91	Substrate binding modes of purine and pyrimidine nucleotides to human ecto-5â€²-nucleotidase (CD73) and inhibition by their bisphosphonic acid derivatives. <i>Purinergic Signalling</i> , 2021, 17, 693-704.	2.2	8
92	Crystal structure of cleaved vaspin (serpinA12). <i>Biological Chemistry</i> , 2016, 397, 111-123.	2.5	7
93	RNase T1 Variant RV Cleaves Single-Stranded RNA after Purines Due to Specific Recognition by the Asn46 Side Chain Amide. <i>Biochemistry</i> , 2004, 43, 2854-2862.	2.5	6
94	Crystallization and preliminary X-ray analysis of the open form of human ecto-5â€²-nucleotidase (CD73). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1545-1549.	0.7	6
95	Analysis of a rare functional truncating mutation rs61757459 in vaspin (SERPINA12) on circulating vaspin levels. <i>Journal of Molecular Medicine</i> , 2013, 91, 1285-1292.	3.9	6
96	In vivo phosphorylation and in vitro autophosphorylation-inactivation of <i>Kluyveromyces lactis</i> hexokinase K1Hxk1. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 313-318.	2.1	6
97	Crystal structure and catalytic mechanism of chloromuconolactone dehalogenase <sc>ClcF</sc> from <i>Rhodococcus opacus</i> 1 <sc>CP</sc>. <i>Molecular Microbiology</i> , 2013, 88, 254-267.	2.5	6
98	Membrane Phospholipids and Polyphosphates as Cofactors and Binding Molecules of SERPINA12 (vaspin). <i>Molecules</i> , 2020, 25, 1992.	3.8	6
99	The ATP/ADP Substrate Specificity Switch between <i>Toxoplasma gondii</i> NTPDase1 and NTPDase3 is Caused by an Altered Mode of Binding of the Substrate Base. <i>ChemBioChem</i> , 2013, 14, 2292-2300.	2.6	5
100	Leucyl Aminopeptidase (Animal). , 2013, , 1465-1470.		5
101	Crystallization and preliminary crystallographic analysis of human muscle phosphofructokinase, the main regulator of glycolysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 578-582.	0.8	5
102	Structure-Activity Relationship of 3-Methylcytidine-5â€²-Î±,Î²-methylenediphosphates as CD73 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 2409-2433.	6.4	5
103	X-Ray Structure Analysis of Methane Monooxygenase: An Important Step toward Understanding the Oxidation of Methane in Biological Systems. <i>Angewandte Chemie International Edition in English</i> , 1994, 33, 841-843.	4.4	4
104	Röntgenstrukturanalyse der Methan-Monooxygenase: ein wichtiger Beitrag zum Verständnis der Oxidation von Methan in biologischen Systemen. <i>Angewandte Chemie</i> , 1994, 106, 889-891.	2.0	3
105	Crystallization and preliminary characterization of chloromuconolactone dehalogenase from <i>Rhodococcus opacus</i> 1CP. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 591-595.	0.7	3
106	Crystal Structure of Apo- and Metalated Thiolate containing RNase S as Structural Basis for the Design of Artificial Metalloenzymes by Peptide-Protein Complementation. <i>Zeitschrift Fur Anorganische Und Allgemeine Chemie</i> , 2013, 639, 2395-2400.	1.2	3
107	Mono-ADP-ribosylation sites of human CD73 inhibit its adenosine-generating enzymatic activity. <i>Purinergic Signalling</i> , 2022, 18, 115-121.	2.2	3
108	Yeast chorismate and other allosteric enzymes. <i>Pure and Applied Chemistry</i> , 1998, 70, 527-531.	1.9	2

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109	Crystallization and preliminary X-ray characterization of two thermostable DNA nucleases. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1290-1293.	0.7	2
110	Crystallization and preliminary X-ray diffraction studies of hexokinase KIHxk1 from Kluyveromyces lactis. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 430-433.	0.7	2
111	Crystallization of ectonucleotide phosphodiesterase/pyrophosphatase-3 and orientation of the SMB domains in the full-length ectodomain. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 696-703.	0.8	2
112	Posttranslational Incorporation of Noncanonical Amino Acids in the RNase S System by Semisynthetic Protein Assembly. Methods in Molecular Biology, 2014, 1216, 71-87.	0.9	1
113	Biochemie und Molekularbiologie 2003. Nachrichten Aus Der Chemie, 2004, 52, 292-305.	0.0	0
114	Structure activity relationship of 3-methylcytidine-5-phosphate, 2-methylenediphosphates as CD73 inhibitors. FASEB Journal, 2022, 36, .	0.5	0