

Anders Liljas

List of Publications by Year in descending order

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82
papers

6,060
citations

94433

37
h-index

69250

77
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87
all docs

87
docs citations

87
times ranked

4106
citing authors

#	ARTICLE	IF	CITATIONS
1	Comments to the Editor Due to the Response by the Supuran Group to Our Article. <i>Biophysical Journal</i> , 2021, 120, 182-183.	0.5	2
2	Perspectives on the Classical Enzyme Carbonic Anhydrase and the Search for Inhibitors. <i>Biophysical Journal</i> , 2020, 119, 1275-1280.	0.5	18
3	Crystallography of the past and in the future. <i>Crystallography Reviews</i> , 2020, 26, 101-112.	1.5	0
4	An enzyme in disguise. <i>IUCrJ</i> , 2020, 7, 144-145.	2.2	2
5	The enigmatic ribosomal stalk. <i>Quarterly Reviews of Biophysics</i> , 2018, 51, e12.	5.7	27
6	Carbonic anhydrase under pressure. <i>IUCrJ</i> , 2018, 5, 4-5.	2.2	7
7	A recent intermezzo at the Ribosome Club. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160185.	4.0	10
8	Labor pains in the early days of the Nobel Committee for Chemistry. <i>Structural Chemistry</i> , 2017, 28, 555-561.	2.0	6
9	Deep sequencing reveals global patterns of mRNA recruitment during translation initiation. <i>Scientific Reports</i> , 2016, 6, 30170.	3.3	11
10	uL11, a central player in translation. <i>Cell Cycle</i> , 2016, 15, 1529-1530.	2.6	2
11	Protein crystallography from the perspective of technology developments. <i>Crystallography Reviews</i> , 2015, 21, 122-153.	1.5	33
12	A new system for naming ribosomal proteins. <i>Current Opinion in Structural Biology</i> , 2014, 24, 165-169.	5.7	481
13	Zooming in on eukaryotic translation initiation. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1141-1142.	8.2	1
14	Background to the Nobel Prize to the Braggs. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, 10-15.	0.3	4
15	Comment on "The Mechanism for Activation of GTP Hydrolysis on the Ribosome". <i>Science</i> , 2011, 333, 37-37.	12.6	38
16	The ribosome story: An overview of structural studies of protein synthesis on the ribosome. <i>Crystallography Reviews</i> , 2011, 17, 205-223.	1.5	1
17	Response to Comment on "The Mechanism for Activation of GTP Hydrolysis on the Ribosome". <i>Science</i> , 2011, 333, 37-37.	12.6	29
18	Leaps in Translational Elongation. <i>Science</i> , 2009, 326, 677-678.	12.6	4

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19	Exit Biology: Battle for the Nascent Chain. <i>Structure</i> , 2008, 16, 498-500.	3.3	8
20	Getting Close to Termination. <i>Science</i> , 2008, 322, 863-865.	12.6	1
21	The Ribosomal Stalk Binds to Translation Factors IF2, EF-Tu, EF-G and RF3 via a Conserved Region of the L12 C-terminal Domain. <i>Journal of Molecular Biology</i> , 2007, 365, 468-479.	4.2	114
22	Deepening Ribosomal Insights. <i>ACS Chemical Biology</i> , 2006, 1, 567-569.	3.4	4
23	On the complementarity of methods in structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 941-945.	2.5	2
24	Yeast ribosomal P0 protein has two separate binding sites for P1/P2 proteins. <i>Molecular Microbiology</i> , 2006, 60, 386-400.	2.5	75
25	Structural Insights into Fusidic Acid Resistance and Sensitivity in EF-G. <i>Journal of Molecular Biology</i> , 2005, 348, 939-949.	4.2	56
26	Molecular Mechanisms in Biological Processes. <i>FEBS Letters</i> , 2005, 579, 851-851.	2.8	1
27	Crystal structure of a mutant elongation factor G trapped with a GTP analogue. <i>FEBS Letters</i> , 2005, 579, 4492-4497.	2.8	64
28	L22 Ribosomal Protein and Effect of Its Mutation on Ribosome Resistance to Erythromycin. <i>Journal of Molecular Biology</i> , 2002, 322, 635-644.	4.2	48
29	Is tRNA Binding or tRNA Mimicry Mandatory for Translation Factors?. <i>Current Protein and Peptide Science</i> , 2002, 3, 133-141.	1.4	9
30	Post-termination complex disassembly by ribosome recycling factor, a functional tRNA mimic. <i>EMBO Journal</i> , 2002, 21, 2272-2281.	7.8	97
31	Structure of ribosomal protein TL5 complexed with RNA provides new insights into the CTC family of stress proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 968-976.	2.5	38
32	Crystals of a mutant form of ribosomal protein L22 rendering bacterial ribosomes resistant to erythromycin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1150-1152.	2.5	1
33	Mutations in the G-domain of Elongation Factor G from <i>Thermus thermophilus</i> Affect Both Its Interaction with GTP and Fusidic Acid. <i>Journal of Biological Chemistry</i> , 2001, 276, 28774-28778.	3.4	24
34	Archaeal ribosomal protein L1: the structure provides new insights into RNA binding of the L1 protein family. <i>Structure</i> , 2000, 8, 363-371.	3.3	35
35	Structure of a mutant EF-G reveals domain III and possibly the fusidic acid binding site 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 303, 593-603.	4.2	141
36	Extremely Thermostable Elongation Factor G from <i>Aquifex aeolicus</i> : Cloning, Expression, Purification, and Characterization in a Heterologous Translation System. <i>Protein Expression and Purification</i> , 2000, 18, 257-261.	1.3	5

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37	A wheel invented three times. EMBO Reports, 2000, 1, 16-17.	4.5	54
38	Crystallization and preliminary X-ray analysis of Thermotoga maritima ribosome recycling factor. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 2049-2050.	2.5	5
39	Crystal Structure of Thermotoga maritima Ribosome Recycling Factor: A tRNA Mimic. Science, 1999, 286, 2349-2352.	12.6	184
40	N-terminal domain, residues 1-91, of ribosomal protein TL5 from Thermus thermophilus binds specifically and strongly to the region of 5S rRNA containing loop E. FEBS Letters, 1999, 451, 51-55.	2.8	15
41	Protein biosynthesis: structural studies of the elongation cycle. FEBS Letters, 1998, 430, 95-99.	2.8	22
42	Crystal structure of ribosomal protein S8 from Thermus thermophilus reveals a high degree of structural conservation of a specific RNA binding site 1 Edited by K. Nagai. Journal of Molecular Biology, 1998, 279, 233-244.	4.2	29
43	Preliminary NMR studies of Thermus thermophilus ribosomal protein S19 overproduced in Escherichia coli. FEBS Letters, 1997, 415, 155-159.	2.8	2
44	Structural aspects of protein synthesis. Nature Structural Biology, 1997, 4, 767-771.	9.7	31
45	The Dynamic Structure of EF-G Studied by Fusidic Acid Resistance and Internal Revertants. Journal of Molecular Biology, 1996, 258, 420-432.	4.2	68
46	Protein synthesis: Imprinting through molecular mimicry. Current Biology, 1996, 6, 247-249.	3.9	34
47	The structure of elongation factor G in complex with GDP: conformational flexibility and nucleotide exchange. Structure, 1996, 4, 555-565.	3.3	137
48	Crystallographic studies of elongation factor G. Biochemistry and Cell Biology, 1995, 73, 1209-1216.	2.0	20
49	Ribosomal protein L22 from Thermus thermophilus: sequencing overexpression and crystallisation. FEBS Letters, 1995, 369, 229-232.	2.8	7
50	Inhibition and catalysis of carbonic anhydrase. , 1994, 219, 1-10.		24
51	Crystal structure of catechol O-methyltransferase. Nature, 1994, 368, 354-358.	27.8	428
52	Inhibition and catalysis of carbonic anhydrase. Recent crystallographic analyses. FEBS Journal, 1994, 219, 1-10.	0.2	125
53	Modification of a metal ligand in carbonic anhydrase: Crystal structure of His94 → Glu human isozyme II. FEBS Letters, 1994, 352, 137-140.	2.8	5
54	Crystallographic analysis of Thr-200 → His human carbonic anhydrase II and its complex with the substrate, HCO ₃ ²⁻ . Proteins: Structure, Function and Bioinformatics, 1993, 15, 80-87.	2.6	92

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55	Metal poison inhibition of carbonic anhydrase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 177-182.	2.6	47
56	Refined structure of bovine carbonic anhydrase III at 2.0 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 29-42.	2.6	111
57	Structural analysis of the zinc hydroxide-Thr-199-Glu-106 hydrogen-bond network in human carbonic anhydrase II. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 17, 93-106.	2.6	65
58	Refined structure of the aminobenzamide complex of human carbonic anhydrase II at 1.9 Å... and sulphonamide modelling of bovine carbonic anhydrase III. <i>International Journal of Biological Macromolecules</i> , 1993, 15, 97-100.	7.5	49
59	Crystal Structure of the Complex between Human Carbonic Anhydrase II and the Aromatic Inhibitor 1,2,4-Triazole. <i>Journal of Molecular Biology</i> , 1993, 232, 9-14.	4.2	36
60	Structure of native and apo carbonic anhydrase II and structure of some of its anion-ligand complexes. <i>Journal of Molecular Biology</i> , 1992, 227, 1192-1204.	4.2	502
61	Comparative Biochemistry and Biophysics of Ribosomal Proteins. <i>International Review of Cytology</i> , 1991, 124, 103-136.	6.2	84
62	Crystallization and preliminary X-ray investigation of a recombinant form of rat catecholO-methyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 11, 233-236.	2.6	22
63	Characterization of the binding sites of protein L11 and the L10.(L12) ₄ pentameric complex in the GTPase domain of 23 S ribosomal RNA from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1990, 213, 275-288.	4.2	134
64	Refined structure of the acetazolamide complex of human carbonic anhydrase II at 1.9 Å... <i>International Journal of Biological Macromolecules</i> , 1990, 12, 342-344.	7.5	99
65	Structural comparison of the prokaryotic ribosomal proteins L7/L12 and L30. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 3, 243-251.	2.6	25
66	Refined structure of human carbonic anhydrase II at 2.0 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 274-282.	2.6	516
67	Crystallographic studies of inhibitor binding sites in human carbonic anhydrase II: A pentacoordinated binding of the SCN ⁻ ion to the zinc at high pH. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 283-293.	2.6	187
68	The structure and dynamics of ribosomal protein L12. <i>Biochimie</i> , 1987, 69, 1043-1047.	2.6	46
69	Structure of the C-terminal domain of the ribosomal protein from <i>Escherichia coli</i> at 1.7 Å... <i>Journal of Molecular Biology</i> , 1987, 195, 555-579.	4.2	199
70	Comments on: Polymorphism of serine-specific transfer ribonucleic acid. Influence of the temperature on the crystallization of serine-specific tRNA. <i>FEBS Journal</i> , 1984, 141, 237-239.	0.2	0
71	True identity of a diffraction pattern attributed to valyl tRNA. <i>Nature</i> , 1983, 303, 195-195.	27.8	6
72	Structural studies of ribosomes. <i>Progress in Biophysics and Molecular Biology</i> , 1982, 40, 161-228.	2.9	157

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73	Crystal structure of a ribosomal component at 2.6 Å... resolution. Nature, 1980, 286, 824-826.	27.8	118
74	The stoichiometry and reconstitution of a stable protein complex from escherichia coli ribosomes. FEBS Letters, 1979, 98, 139-144.	2.8	48
75	Isolation and crystallization of stable domains of the protein L7/L12 from Escherichia coli ribosomes. FEBS Letters, 1978, 88, 300-304.	2.8	33
76	Small-angle X-ray scattering and crosslinking study of the proteins L7/L12 from Escherichia coli ribosomes. FEBS Letters, 1976, 66, 48-51.	2.8	70
77	4 Lactate Dehydrogenase. The Enzymes, 1975, 11, 191-292.	1.7	444
78	Recognition of structural domains in globular proteins. Journal of Molecular Biology, 1974, 85, 177-181.	4.2	176
79	Atomic co-ordinates for dogfish M4 apo-lactate dehydrogenase. Biochemical and Biophysical Research Communications, 1973, 53, 46-51.	2.1	37
80	Functional anion binding sites in dogfish M4 lactate dehydrogenase. Journal of Molecular Biology, 1973, 76, 519-528.	4.2	72
81	Molecular symmetry axes and subunit interfaces in certain dehydrogenases. Journal of Molecular Biology, 1973, 76, 533-537.	4.2	93
82	The States, Conformational Dynamics, and Fusidic Acid-Resistant Mutants of Elongation Factor G. , 0, , 359-365.		1