

Anders Liljas

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

78
papers

5,197
citations

37
h-index

72
g-index

87
ext. papers

5,492
ext. citations

8.4
avg, IF

5.15
L-index

#	Paper	IF	Citations
78	Crystallography of the past and in the future. <i>Crystallography Reviews</i> , 2020 , 26, 101-112	1.3	
77	An enzyme in disguise. <i>IUCrJ</i> , 2020 , 7, 144-145	4.7	2
76	Perspectives on the Classical Enzyme Carbonic Anhydrase and the Search for Inhibitors. <i>Biophysical Journal</i> , 2020 , 119, 1275-1280	2.9	9
75	Carbonic anhydrase under pressure. <i>IUCrJ</i> , 2018 , 5, 4-5	4.7	5
74	The enigmatic ribosomal stalk. <i>Quarterly Reviews of Biophysics</i> , 2018 , 51, e12	7	15
73	A recent intermezzo at the Ribosome Club. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	8
72	Labor pains in the early days of the Nobel Committee for Chemistry. <i>Structural Chemistry</i> , 2017 , 28, 555-561	5.6	6
71	Deep sequencing reveals global patterns of mRNA recruitment during translation initiation. <i>Scientific Reports</i> , 2016 , 6, 30170	4.9	4
70	Protein Crystallography from the Perspective of Technology Developments. <i>Crystallography Reviews</i> , 2015 , 21, 122-153	1.3	26
69	A new system for naming ribosomal proteins. <i>Current Opinion in Structural Biology</i> , 2014 , 24, 165-9	8.1	365
68	From a Grain of Salt to the Ribosome. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2014 ,	0.5	2
67	Background to the Nobel Prize to the Braggs. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013 , 69, 10-5		3
66	Comment on "The Mechanism for Activation of GTP Hydrolysis on the Ribosome". <i>Science</i> , 2011 , 333, 37-37	33.3	37
65	The ribosome story: An overview of structural studies of protein synthesis on the ribosome. <i>Crystallography Reviews</i> , 2011 , 17, 205-223	1.3	1
64	Comment on "The mechanism for activation of GTP hydrolysis on the ribosome". <i>Science</i> , 2011 , 333, 37; author reply 37	33.3	28
63	Biochemistry. Leaps in translational elongation. <i>Science</i> , 2009 , 326, 677-8	33.3	4
62	Biochemistry. Getting close to termination. <i>Science</i> , 2008 , 322, 863-5	33.3	0

61	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, 468-79	6.5	100
60	Deepening ribosomal insights. <i>ACS Chemical Biology</i> , 2006 , 1, 567-9	4.9	4
59	On the complementarity of methods in structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 941-5		1
58	Yeast ribosomal P0 protein has two separate binding sites for P1/P2 proteins. <i>Molecular Microbiology</i> , 2006 , 60, 386-400	4.1	68
57	Structural insights into fusidic acid resistance and sensitivity in EF-G. <i>Journal of Molecular Biology</i> , 2005 , 348, 939-49	6.5	53
56	Francis Crick (8 June 1916--28 July 2004): a memoir. <i>FEBS Letters</i> , 2005 , 579, 852-4	3.8	0
55	Crystal structure of a mutant elongation factor G trapped with a GTP analogue. <i>FEBS Letters</i> , 2005 , 579, 4492-7	3.8	61
54	Is tRNA binding or tRNA mimicry mandatory for translation factors?. <i>Current Protein and Peptide Science</i> , 2002 , 3, 133-41	2.8	8
53	Post-termination complex disassembly by ribosome recycling factor, a functional tRNA mimic. <i>EMBO Journal</i> , 2002 , 21, 2272-81	13	86
52	L22 ribosomal protein and effect of its mutation on ribosome resistance to erythromycin. <i>Journal of Molecular Biology</i> , 2002 , 322, 635-44	6.5	38
51	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, 968-76		32
50	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, 1150-2		1
49	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, 28774-8	5.4	20
48	Archaeal ribosomal protein L1: the structure provides new insights into RNA binding of the L1 protein family. <i>Structure</i> , 2000 , 8, 363-71	5.2	29
47	Structure of a mutant EF-G reveals domain III and possibly the fusidic acid binding site. <i>Journal of Molecular Biology</i> , 2000 , 303, 593-603	6.5	128
46	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, 257-61	2	5
45	A wheel invented three times. The molecular structures of the three carbonic anhydrases. <i>EMBO Reports</i> , 2000 , 1, 16-7	6.5	49
44	Crystallization and preliminary X-ray analysis of <i>Thermotoga maritima</i> ribosome recycling factor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 2049-50		4

43	Crystal structure of Thermotoga maritima ribosome recycling factor: a tRNA mimic. <i>Science</i> , 1999 , 286, 2349-52	33.3	160
42	N-terminal domain, residues 1-91, of ribosomal protein TL5 from <i>Thermus thermophilus</i> binds specifically and strongly to the region of 5S rRNA containing loop E. <i>FEBS Letters</i> , 1999 , 451, 51-5	3.8	12
41	Protein biosynthesis: structural studies of the elongation cycle. <i>FEBS Letters</i> , 1998 , 430, 95-9	3.8	21
40	Crystal structure of ribosomal protein S8 from <i>Thermus thermophilus</i> reveals a high degree of structural conservation of a specific RNA binding site. <i>Journal of Molecular Biology</i> , 1998 , 279, 233-44	6.5	28
39	Preliminary NMR studies of <i>Thermus thermophilus</i> ribosomal protein S19 overproduced in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1997 , 415, 155-9	3.8	2
38	The dynamic structure of EF-G studied by fusidic acid resistance and internal revertants. <i>Journal of Molecular Biology</i> , 1996 , 258, 420-32	6.5	62
37	Imprinting through molecular mimicry. Protein synthesis. <i>Current Biology</i> , 1996 , 6, 247-9	6.3	29
36	The structure of elongation factor G in complex with GDP: conformational flexibility and nucleotide exchange. <i>Structure</i> , 1996 , 4, 555-65	5.2	126
35	Crystallographic studies of elongation factor G. <i>Biochemistry and Cell Biology</i> , 1995 , 73, 1209-16	3.6	19
34	Ribosomal protein L22 from <i>Thermus thermophilus</i> : sequencing, overexpression and crystallisation. <i>FEBS Letters</i> , 1995 , 369, 229-32	3.8	6
33	Inhibition and catalysis of carbonic anhydrase. Recent crystallographic analyses. <i>FEBS Journal</i> , 1994 , 219, 1-10		18
32	Crystal structure of catechol O-methyltransferase. <i>Nature</i> , 1994 , 368, 354-8	50.4	385
31	Inhibition and catalysis of carbonic anhydrase. <i>FEBS Journal</i> , 1994 , 219, 1-10		115
30	Modification of a metal ligand in carbonic anhydrase: crystal structure of His94-->Glu human isozyme II. <i>FEBS Letters</i> , 1994 , 352, 137-40	3.8	5
29	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	6.5	32
28	Crystallographic analysis of Thr-200-->His human carbonic anhydrase II and its complex with the substrate, HCO ₃ ⁻ . <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 15, 80-7	4.2	85
27	Metal poison inhibition of carbonic anhydrase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 15, 177-82	4.2	42
26	Refined structure of bovine carbonic anhydrase III at 2.0 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 16, 29-42	4.2	102

25	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	4.2	58
24	Refined structure of the aminobenzamide complex of human carbonic anhydrase II at 1.9 A and sulphamide modelling of bovine carbonic anhydrase III. <i>International Journal of Biological Macromolecules</i> , 1993 , 15, 97-100	7.9	48
23	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, 1192-204	6.5	462
22	Crystallization and preliminary X-ray investigation of a recombinant form of rat catechol O-methyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 11, 233-6	4.2	19
21	Comparative biochemistry and biophysics of ribosomal proteins. <i>International Review of Cytology</i> , 1991 , 124, 103-36		72
20	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 Escherichia coli. <i>Journal of Molecular Biology</i> , 1990 , 213, 275-88	6.5	126
19	Refined structure of the acetazolamide complex of human carbonic anhydrase II at 1.9 A. <i>International Journal of Biological Macromolecules</i> , 1990 , 12, 342-4	7.9	86
18	Structural comparison of the prokaryotic ribosomal proteins L7/L12 and L30. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988 , 3, 243-51	4.2	22
17	Refined structure of human carbonic anhydrase II at 2.0 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988 , 4, 274-82	4.2	465
16	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, 283-93	4.2	167
15	The structure and dynamics of ribosomal protein L12. <i>Biochimie</i> , 1987 , 69, 1043-7	4.6	44
14	Structure of the C-terminal domain of the ribosomal protein L7/L12 from Escherichia coli at 1.7 A. <i>Journal of Molecular Biology</i> , 1987 , 195, 555-79	6.5	186
13	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, 237-9		
12	True identity of a diffraction pattern attributed to valyl tRNA. <i>Nature</i> , 1983 , 303, 195-6	50.4	6
11	Structural studies of ribosomes. <i>Progress in Biophysics and Molecular Biology</i> , 1982 , 40, 161-228	4.7	136
10	Crystal structure of a ribosomal component at 2.6 A resolution. <i>Nature</i> , 1980 , 286, 824-6	50.4	109
9	The stoichiometry and reconstitution of a stable protein complex from Escherichia coli ribosomes. <i>FEBS Letters</i> , 1979 , 98, 139-44	3.8	43
8	Isolation and crystallization of stable domains of the protein L7/L12 from Escherichia coli ribosomes. <i>FEBS Letters</i> , 1978 , 88, 300-4	3.8	30

7	Small-angle X-ray scattering and crosslinking study of the proteins L7/L12 from <i>Escherichia coli</i> ribosomes. <i>FEBS Letters</i> , 1976 , 66, 48-51	3.8	63
6	4 Lactate Dehydrogenase. <i>The Enzymes</i> , 1975 , 11, 191-292	2.3	225
5	Letter: Recognition of structural domains in globular proteins. <i>Journal of Molecular Biology</i> , 1974 , 85, 177-81	6.5	158
4	Atomic co-ordinates for dogfish M4 apo-lactate dehydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 1973 , 53, 46-51	3.4	37
3	Functional anion binding sites in dogfish M4 lactate dehydrogenase. <i>Journal of Molecular Biology</i> , 1973 , 76, 519-28	6.5	63
2	Letter: Molecular symmetry axes and subunit interfaces in certain dehydrogenases. <i>Journal of Molecular Biology</i> , 1973 , 76, 533-7	6.5	86
1	The States, Conformational Dynamics, and Fusidic Acid-Resistant Mutants of Elongation Factor G359-365		1