

# Anders Liljas

## List of Publications by Year in descending order

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82  
papers

6,060  
citations

94415

37  
h-index

69246

77  
g-index

87  
all docs

87  
docs citations

87  
times ranked

4106  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | 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       |
| 2  | 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       |
| 3  | A new system for naming ribosomal proteins. <i>Current Opinion in Structural Biology</i> , 2014, 24, 165-169.  | 5.7  | 481       |
| 4  | 4 Lactate Dehydrogenase. <i>The Enzymes</i> , 1975, 11, 191-292.   | 1.7  | 444       |
| 5  | Crystal structure of catechol O-methyltransferase. <i>Nature</i> , 1994, 368, 354-358.   | 27.8 | 428       |
| 6  | 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       |
| 7  | Crystallographic studies of inhibitor binding sites in human carbonic anhydrase II: A pentacoordinated binding of the SCN <sup>-</sup> ion to the zinc at high pH. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 283-293. | 2.6  | 187       |
| 8  | Crystal Structure of <i>Thermotoga maritima</i> Ribosome Recycling Factor: A tRNA Mimic. <i>Science</i> , 1999, 286, 2349-2352.  | 12.6 | 184       |
| 9  | Recognition of structural domains in globular proteins. <i>Journal of Molecular Biology</i> , 1974, 85, 177-181.   | 4.2  | 176       |
| 10 | Structural studies of ribosomes. <i>Progress in Biophysics and Molecular Biology</i> , 1982, 40, 161-228.  | 2.9  | 157       |
| 11 | 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       |
| 12 | The structure of elongation factor G in complex with GDP: conformational flexibility and nucleotide exchange. <i>Structure</i> , 1996, 4, 555-565.   | 3.3  | 137       |
| 13 | Characterization of the binding sites of protein L11 and the L10.(L12) <sub>4</sub> 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       |
| 14 | Inhibition and catalysis of carbonic anhydrase. Recent crystallographic analyses. <i>FEBS Journal</i> , 1994, 219, 1-10.   | 0.2  | 125       |
| 15 | Crystal structure of a ribosomal component at 2.6 Å... resolution. <i>Nature</i> , 1980, 286, 824-826.   | 27.8 | 118       |
| 16 | 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       |
| 17 | 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       |
| 18 | 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        |

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|----|---|-----|-----------|
| 19 | Post-termination complex disassembly by ribosome recycling factor, a functional tRNA mimic. EMBO Journal, 2002, 21, 2272-2281.  | 7.8 | 97        |
| 20 | Molecular symmetry axes and subunit interfaces in certain dehydrogenases. Journal of Molecular Biology, 1973, 76, 533-537.  | 4.2 | 93        |
| 21 | Crystallographic analysis of Thr-200 $\hat{a}$ ' His human carbonic anhydrase II and its complex with the substrate, HCO <sub>3</sub> $\hat{a}$ ". Proteins: Structure, Function and Bioinformatics, 1993, 15, 80-87.       | 2.6 | 92        |
| 22 | Comparative Biochemistry and Biophysics of Ribosomal Proteins. International Review of Cytology, 1991, 124, 103-136.  | 6.2 | 84        |
| 23 | Yeast ribosomal P0 protein has two separate binding sites for P1/P2 proteins. Molecular Microbiology, 2006, 60, 386-400.  | 2.5 | 75        |
| 24 | Functional anion binding sites in dogfish M4 lactate dehydrogenase. Journal of Molecular Biology, 1973, 76, 519-528.  | 4.2 | 72        |
| 25 | 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        |
| 26 | 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        |
| 27 | Structural analysis of the zinc hydroxide-Thr-199-Glu-106 hydrogen-bond network in human carbonic anhydrase II. Proteins: Structure, Function and Bioinformatics, 1993, 17, 93-106.   | 2.6 | 65        |
| 28 | Crystal structure of a mutant elongation factor G trapped with a GTP analogue. FEBS Letters, 2005, 579, 4492-4497.  | 2.8 | 64        |
| 29 | Structural Insights into Fusidic Acid Resistance and Sensitivity in EF-G. Journal of Molecular Biology, 2005, 348, 939-949.   | 4.2 | 56        |
| 30 | A wheel invented three times. EMBO Reports, 2000, 1, 16-17.   | 4.5 | 54        |
| 31 | Refined structure of the aminobenzamide complex of human carbonic anhydrase II at 1.9Å...and sulphonamide modelling of bovine carbonic anhydrase III. International Journal of Biological Macromolecules, 1993, 15, 97-100. | 7.5 | 49        |
| 32 | The stoichiometry and reconstitution of a stable protein complex from escherichia coli ribosomes. FEBS Letters, 1979, 98, 139-144.  | 2.8 | 48        |
| 33 | L22 Ribosomal Protein and Effect of Its Mutation on Ribosome Resistance to Erythromycin. Journal of Molecular Biology, 2002, 322, 635-644.  | 4.2 | 48        |
| 34 | Metal poison inhibition of carbonic anhydrase. Proteins: Structure, Function and Bioinformatics, 1993, 15, 177-182.   | 2.6 | 47        |
| 35 | The structure and dynamics of ribosomal protein L12. Biochimie, 1987, 69, 1043-1047.  | 2.6 | 46        |
| 36 | Structure of ribosomal protein TL5 complexed with RNA provides new insights into the CTC family of stress proteins. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 968-976.                        | 2.5 | 38        |

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|----|---|------|-----------|
| 37 | Comment on "The Mechanism for Activation of GTP Hydrolysis on the Ribosome", Science, 2011, 333, 37-37.   | 12.6 | 38        |
| 38 | Atomic co-ordinates for dogfish M4 apo-lactate dehydrogenase. Biochemical and Biophysical Research Communications, 1973, 53, 46-51.   | 2.1  | 37        |
| 39 | Crystal Structure of the Complex between Human Carbonic Anhydrase II and the Aromatic Inhibitor 1,2,4-Triazole. Journal of Molecular Biology, 1993, 232, 9-14.  | 4.2  | 36        |
| 40 | Archaeal ribosomal protein L1: the structure provides new insights into RNA binding of the L1 protein family. Structure, 2000, 8, 363-371.  | 3.3  | 35        |
| 41 | Protein synthesis: Imprinting through molecular mimicry. Current Biology, 1996, 6, 247-249.   | 3.9  | 34        |
| 42 | Isolation and crystallization of stable domains of the protein L7/L12 from Escherichia coli ribosomes. FEBS Letters, 1978, 88, 300-304.   | 2.8  | 33        |
| 43 | Protein crystallography from the perspective of technology developments. Crystallography Reviews, 2015, 21, 122-153.  | 1.5  | 33        |
| 44 | Structural aspects of protein synthesis. Nature Structural Biology, 1997, 4, 767-771.   | 9.7  | 31        |
| 45 | 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        |
| 46 | Response to Comment on "The Mechanism for Activation of GTP Hydrolysis on the Ribosome", Science, 2011, 333, 37-37.   | 12.6 | 29        |
| 47 | The enigmatic ribosomal stalk. Quarterly Reviews of Biophysics, 2018, 51, e12.  | 5.7  | 27        |
| 48 | Structural comparison of the prokaryotic ribosomal proteins L7/L12 and L30. Proteins: Structure, Function and Bioinformatics, 1988, 3, 243-251.   | 2.6  | 25        |
| 49 | Inhibition and catalysis of carbonic anhydrase. , 1994, 219, 1-10.  |      | 24        |
| 50 | Mutations in the G-domain of Elongation Factor G from Thermus thermophilus Affect Both Its Interaction with GTP and Fusidic Acid. Journal of Biological Chemistry, 2001, 276, 28774-28778.                                  | 3.4  | 24        |
| 51 | Crystallization and preliminary X-ray investigation of a recombinant form of rat catecholO-methyltransferase. Proteins: Structure, Function and Bioinformatics, 1991, 11, 233-236.  | 2.6  | 22        |
| 52 | Protein biosynthesis: structural studies of the elongation cycle. FEBS Letters, 1998, 430, 95-99.   | 2.8  | 22        |
| 53 | Crystallographic studies of elongation factor G. Biochemistry and Cell Biology, 1995, 73, 1209-1216.  | 2.0  | 20        |
| 54 | Perspectives on the Classical Enzyme Carbonic Anhydrase and the Search for Inhibitors. Biophysical Journal, 2020, 119, 1275-1280.   | 0.5  | 18        |

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|----|---|------|-----------|
| 55 | 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, 51-55.                         | 2.8  | 15        |
| 56 | Deep sequencing reveals global patterns of mRNA recruitment during translation initiation. <i>Scientific Reports</i> , 2016, 6, 30170.  | 3.3  | 11        |
| 57 | A recent intermezzo at the Ribosome Club. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160185.  | 4.0  | 10        |
| 58 | Is tRNA Binding or tRNA Mimicry Mandatory for Translation Factors?. <i>Current Protein and Peptide Science</i> , 2002, 3, 133-141.  | 1.4  | 9         |
| 59 | Exit Biology: Battle for the Nascent Chain. <i>Structure</i> , 2008, 16, 498-500.   | 3.3  | 8         |
| 60 | Ribosomal protein L22 from <i>Thermus thermophilus</i> : sequencing overexpression and crystallisation. <i>FEBS Letters</i> , 1995, 369, 229-232.   | 2.8  | 7         |
| 61 | Carbonic anhydrase under pressure. <i>IUCr</i> , 2018, 5, 4-5.  | 2.2  | 7         |
| 62 | True identity of a diffraction pattern attributed to valyl tRNA. <i>Nature</i> , 1983, 303, 195-195.  | 27.8 | 6         |
| 63 | Labor pains in the early days of the Nobel Committee for Chemistry. <i>Structural Chemistry</i> , 2017, 28, 555-561.  | 2.0  | 6         |
| 64 | Modification of a metal ligand in carbonic anhydrase: Crystal structure of His94 → Glu human isozyme II. <i>FEBS Letters</i> , 1994, 352, 137-140.  | 2.8  | 5         |
| 65 | Crystallization and preliminary X-ray analysis of <i>Thermotoga maritima</i> ribosome recycling factor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 2049-2050.                                      | 2.5  | 5         |
| 66 | 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         |
| 67 | Deepening Ribosomal Insights. <i>ACS Chemical Biology</i> , 2006, 1, 567-569.   | 3.4  | 4         |
| 68 | Leaps in Translational Elongation. <i>Science</i> , 2009, 326, 677-678.   | 12.6 | 4         |
| 69 | Background to the Nobel Prize to the Braggs. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, 10-15.   | 0.3  | 4         |
| 70 | Preliminary NMR studies of <i>Thermus thermophilus</i> ribosomal protein S19 overproduced in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1997, 415, 155-159.  | 2.8  | 2         |
| 71 | On the complementarity of methods in structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 941-945.   | 2.5  | 2         |
| 72 | uL11, a central player in translation. <i>Cell Cycle</i> , 2016, 15, 1529-1530.   | 2.6  | 2         |

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|----|--|------|-----------|
| 73 | Comments to the Editor Due to the Response by the Supuran Group to Our Article. Biophysical Journal, 2021, 120, 182-183.   | 0.5  | 2         |
| 74 | An enzyme in disguise. IUCrJ, 2020, 7, 144-145.  | 2.2  | 2         |
| 75 | Crystals of a mutant form of ribosomal protein L22 rendering bacterial ribosomes resistant to erythromycin. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1150-1152. | 2.5  | 1         |
| 76 | Molecular Mechanisms in Biological Processes. FEBS Letters, 2005, 579, 851-851.  | 2.8  | 1         |
| 77 | Getting Close to Termination. Science, 2008, 322, 863-865.   | 12.6 | 1         |
| 78 | The ribosome story: An overview of structural studies of protein synthesis on the ribosome. Crystallography Reviews, 2011, 17, 205-223.  | 1.5  | 1         |
| 79 | Zooming in on eukaryotic translation initiation. Nature Structural and Molecular Biology, 2013, 20, 1141-1142.   | 8.2  | 1         |
| 80 | The States, Conformational Dynamics, and Fusidic Acid-Resistant Mutants of Elongation Factor G. , 0, , 359-365.  |      | 1         |
| 81 | Comments on: Polymorphism of serine-specific transfer ribonucleic acid. Influence of the temperature on the crystallization of serine-specific tRNA. FEBS Journal, 1984, 141, 237-239.         | 0.2  | 0         |
| 82 | Crystallography of the past and in the future. Crystallography Reviews, 2020, 26, 101-112.   | 1.5  | 0         |