## Bengt Göran Karlsson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3267651/publications.pdf

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51 2,204 26 46 papers citations h-index 51 51 2280

51 51 51 2280 all docs docs citations times ranked citing authors

| #  | Article  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | The structure of the complex of plastocyanin and cytochrome f, determined by paramagnetic NMR and restrained rigid-body molecular dynamics. Structure, 1998, 6, 323-335.   | 3.3  | 307       |
| 2  | Raman Spectroscopy as an Indicator of Cu-S Bond Length in Type 1 and Type 2 Copper Cysteinate Proteins. Journal of the American Chemical Society, 1994, 116, 11489-11498.  | 13.7 | 155       |
| 3  | Reduction potentials and their pH dependence in site-directed-mutant forms of azurin from Pseudomonas aeruginosa. FEBS Journal, 1993, 212, 289-296.  | 0.2  | 152       |
| 4  | Reorganization Energy of Blue Copper:Â Effects of Temperature and Driving Force on the Rates of Electron Transfer in Ruthenium- and Osmium-Modified Azurins. Journal of the American Chemical Society, 1997, 119, 9921-9922. | 13.7 | 141       |
| 5  | Using NMR metabolomics to identify responses of an environmental estrogen in blood plasma of fish. Aquatic Toxicology, 2006, 78, 341-349.  | 4.0  | 116       |
| 6  | Expression of the blue copper protein azurin from Pseudomonas aeruginosain Escherichia coli. FEBS Letters, 1989, 246, 211-217.   | 2.8  | 105       |
| 7  | Cassette mutagenesis of Met121 in azurin from Pseudomonas aeruginosa. Protein Engineering, Design and Selection, 1991, 4, 343-349.   | 2.1  | 96        |
| 8  | Structural Information through NMR Hyperfine Shifts in Blue Copper Proteins. Journal of the American Chemical Society, 2000, 122, 3701-3707.   | 13.7 | 95        |
| 9  | Reduction potentials of blue and purple copper proteins in their unfolded states: a closer look at rack-induced coordination. Journal of Biological Inorganic Chemistry, 1998, 3, 367-370.                                   | 2.6  | 83        |
| 10 | Rack-induced bonding in blue copper proteins: Spectroscopic properties and reduction potential of the azurin mutant Met-121 â†' Leu. FEBS Letters, 1989, 253, 99-102.  | 2.8  | 73        |
| 11 | The effect of redox state on the folding free energy of azurin. Journal of Biological Inorganic Chemistry, 1997, 2, 368-371.   | 2.6  | 69        |
| 12 | Optimized in vitro and in vivo expression of proteorhodopsin: A seven-transmembrane proton pump. Protein Expression and Purification, 2008, 58, 103-113.   | 1.3  | 55        |
| 13 | Highly Efficient NMR Assignment of Intrinsically Disordered Proteins: Application to B- and T Cell Receptor Domains. PLoS ONE, 2013, 8, e62947.  | 2.5  | 44        |
| 14 | <scp><i>GREM</i></scp> <i>1</i> <ah< a=""> and <scp>POLE</scp> variants in hereditary colorectal cancer syndromes. Genes Chromosomes and Cancer, 2016, 55, 95-106.</ah<>   | 2.8  | 40        |
| 15 | NMR Analysis of the Transient Complex between Membrane Photosystem I and Soluble Cytochrome c6. Journal of Biological Chemistry, 2005, 280, 7925-7931.   | 3.4  | 37        |
| 16 | Effects of Codon Usage and Vectorâ€"Host Combinations on the Expression of Spinach Plastocyanin inEscherichia coli. Protein Expression and Purification, 1997, 11, 17-25.  | 1.3  | 36        |
| 17 | Aromatic Residues May Enhance Intramolecular Electron Transfer in Azurin. Journal of the American Chemical Society, 1997, 119, 5453-5454.  | 13.7 | 35        |
| 18 | X-ray absorption spectroscopy of folded and unfolded copper(I) azurin. Inorganica Chimica Acta, 2000, 297, 278-282.  | 2.4  | 35        |

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|----|--|-----|-----------|
| 19 | The structural gene for cytochromec551fromPseudomonas aeruginosa. FEBS Letters, 1990, 259, 230-232.  | 2.8 | 34        |
| 20 | Expression screening of membrane proteins with cell-free protein synthesis. Protein Expression and Purification, 2012, 82, 218-225.  | 1.3 | 34        |
| 21 | NMR detection of multiple transitions to low-populated states in azurin. Protein Science, 2003, 12, 56-65.   | 7.6 | 32        |
| 22 | X-ray Structure of Domain I of the Proton-pumping Membrane Protein Transhydrogenase from Escherichia coli. Journal of Molecular Biology, 2005, 352, 299-312.   | 4.2 | 32        |
| 23 | Mutant Met121Ala ofPseudomonas aeruginosaAzurin and Its Azide Derivative: Crystal Structures and Spectral Properties. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 950-958.         | 2.5 | 30        |
| 24 | Identification and quantification of even and odd chained 5-n alkylresorcinols, branched chain-alkylresorcinols and methylalkylresorcinols in Quinoa (Chenopodium quinoa). Food Chemistry, 2017, 220, 344-351. | 8.2 | 30        |
| 25 | Novel Findings in Swedish Patients With MYH-Associated Polyposis: Mutation Detection and Clinical Characterization. Clinical Gastroenterology and Hepatology, 2006, 4, 499-506.                                | 4.4 | 29        |
| 26 | Structure of Metal Site in Azurin, Met 121 Mutants of Azurin, and Stellacyanin Investigated by 111m Cd Perturbed Angular Correlation (PAC). Journal of Biological Chemistry, 1995, 270, 573-580.               | 3.4 | 28        |
| 27 | NMR characterization of the NADP(H)-binding domain of Escherichia colitranshydrogenase: sequential assignment and global fold. FEBS Letters, 1999, 458, 180-184.   | 2.8 | 24        |
| 28 | Metabolic profiles from two different breakfast meals characterized by 1 H NMR-based metabolomics. Food Chemistry, 2017, 231, 267-274.   | 8.2 | 23        |
| 29 | Effects of a Novel Disulfide Bond and Engineered Electrostatic Interactions on the Thermostability of Azurinâ€. Biochemistry, 2004, 43, 12563-12574.   | 2.5 | 20        |
| 30 | NMR studies on the 46-kDa dimeric protein, 3,4-dihydroxy-2-butanone 4-phosphate synthase, using 2H, 13C, and 15N-labelling. FEBS Journal, 1999, 261, 57-65.  | 0.2 | 19        |
| 31 | Apo-azurin folds via an intermediate that resembles the molten-globule. Protein Science, 2009, 13, 2628-2638.  | 7.6 | 19        |
| 32 | Structure of the azurin mutant nickel–Trp48Met fromPseudomonas aeruginosaat 2.2 à resolution. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 711-717.                                 | 2.5 | 17        |
| 33 | Reconstitution of the Anti-Apoptotic Bcl-2 Protein into Lipid Membranes and Biophysical Evidence for Its Detergent-Driven Association with the Pro-Apoptotic Bax Protein. PLoS ONE, 2013, 8, e61452.           | 2.5 | 16        |
| 34 | The binding of TIA-1 to RNA C-rich sequences is driven by its C-terminal RRM domain. RNA Biology, 2014, 11, 766-776.   | 3.1 | 16        |
| 35 | Serum nuclear magnetic resonance-based metabolomics and outcome in diffuse large B-cell lymphoma patients – a pilot study. Leukemia and Lymphoma, 2016, 57, 1814-1822.   | 1.3 | 16        |
| 36 | RNA Binding of T-cell Intracellular Antigen-1 (TIA-1) C-terminal RNA Recognition Motif Is Modified by pH Conditions. Journal of Biological Chemistry, 2013, 288, 25986-25994.                                  | 3.4 | 15        |

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|----|---|-----|-----------|
| 37 | Expression and purification of full-length anti-apoptotic Bcl-2 using cell-free protein synthesis. Protein Expression and Purification, 2011, 77, 220-223.  | 1.3 | 12        |
| 38 | Redox-sensitive loops D and E regulate NADP(H) binding in domain III and domain I-domain III interactions in proton-translocating Escherichia coli transhydrogenase. FEBS Journal, 2002, 269, 4505-4515.    | 0.2 | 11        |
| 39 | Probing the influence on folding behavior of structurally conserved core residues in P. aeruginosa apo-azurin. Protein Science, 2009, 13, 2706-2715.  | 7.6 | 10        |
| 40 | NMR Spectroscopic Analysis to Evaluate the Quality of Insulin: Concentration, Variability, and Excipient Content. Journal of Diabetes Science and Technology, 2020, 14, 180-184.                            | 2.2 | 10        |
| 41 | Surface interactions in the complex between cytochrome f and the E43Q/D44N and E59K/E60Q plastocyanin double mutants as determined by 1H-NMR chemical shift analysis. Protein Science, 2001, 10, 2623-2626. | 7.6 | 10        |
| 42 | Sequential assignment and secondary structure analysis of the NADP(H)-binding domain of Escherichia coli transhydrogenase. Journal of Biomolecular NMR, 1999, 14, 295-296.                                  | 2.8 | 8         |
| 43 | Structure of Pseudomonas aeruginosai zinc azurin mutant Asn47Asp at 2.4 Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 1993, 49, 449-457.                                      | 2.5 | 6         |
| 44 | Investigation of the copper binding sites in the Menkes disease protein, ATP7A. Journal of Inherited Metabolic Disease, 1998, 21, 195-198.  | 3.6 | 5         |
| 45 | Occurrence, overexpression and partial purification of the protein (majastridin) corresponding to the URF6 gene of the Rhodobacter blasticus atp operon. FEBS Journal, 1998, 255, 87-92.                    | 0.2 | 5         |
| 46 | Structure of the N $\hat{a}\in \mathbb{R}$ erminal domain of the metalloprotease P rt V from V ibrio cholerae. Protein Science, 2015, 24, 2076-2080.  | 7.6 | 4         |
| 47 | Combined Solution―and Magic Angle Spinning NMR Reveals Regions of Distinct Dynamics in Amyloid β<br>Protofibrils. ChemistrySelect, 2016, 1, 5850-5853.  | 1.5 | 4         |
| 48 | High-affinity recognition of the human C-reactive protein independent of phosphocholine. Organic and Biomolecular Chemistry, 2017, 15, 4644-4654.   | 2.8 | 4         |
| 49 | Backbone resonance assignment of Staphylococcal Enterotoxin H. Biomolecular NMR Assignments, 2010, 4, 1-4.  | 0.8 | 3         |
| 50 | Crystallization and preliminary crystallographic data for the azurin mutant End-121 fromPseudomonas aeruginosa. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 37-39.              | 2.5 | 2         |
| 51 | Solution structure of the calmodulin-like C-terminal domain of Entamoeba $\hat{l}$ ±-actinin2. Proteins: Structure, Function and Bioinformatics, 2016, 84, 461-466.   | 2.6 | 2         |