

# Lars-Göran Mårtensson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6053035/publications.pdf>

Version: 2024-02-01

24  
papers

656  
citations

623734

14  
h-index

610901

24  
g-index

24  
all docs

24  
docs citations

24  
times ranked

836  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | Pharmacogenetic studies of thiopurine methyltransferase genotype-phenotype concordance and effect of methotrexate on thiopurine metabolism. <i>Basic and Clinical Pharmacology and Toxicology</i> , 2021, 128, 52-65.   | 2.5 | 8         |
| 2  | Comprehensive study of thiopurine methyltransferase genotype, phenotype, and genotype-phenotype discrepancies in Sweden. <i>Biochemical Pharmacology</i> , 2019, 164, 263-272.  | 4.4 | 11        |
| 3  | Methylation of selenocysteine catalysed by thiopurine S-methyltransferase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 182-190.   | 2.4 | 13        |
| 4  | One amino acid makes a difference-Characterization of a new TPMT allele and the influence of SAM on TPMT stability. <i>Scientific Reports</i> , 2017, 7, 46428.   | 3.3 | 16        |
| 5  | In Vitro Protein Stability of Two Naturally Occurring Thiopurine S-Methyltransferase Variants: Biophysical Characterization of TPMT*6 and TPMT*8. <i>ACS Omega</i> , 2017, 2, 4991-4999.  | 3.5 | 5         |
| 6  | Robust and convenient analysis of protein thermal and chemical stability. <i>Protein Science</i> , 2015, 24, 2055-2062.   | 7.6 | 51        |
| 7  | Methotrexate binds to recombinant thiopurine S-methyltransferase and inhibits enzyme activity after high-dose infusions in childhood leukaemia. <i>European Journal of Clinical Pharmacology</i> , 2013, 69, 1641-1649.   | 1.9 | 21        |
| 8  | Structural Characteristics Determine the Cause of the Low Enzyme Activity of Two Thiopurine S-Methyltransferase Allelic Variants: A Biophysical Characterization of TPMT*2 and TPMT*5. <i>Biochemistry</i> , 2012, 51, 5912-5920.   | 2.5 | 7         |
| 9  | Characterization of a novel sequence variant, TPMT*28, in the human thiopurine methyltransferase gene. <i>Pharmacogenetics and Genomics</i> , 2010, 20, 700-707.  | 1.5 | 25        |
| 10 | Critical biophysical properties in the <i>Pseudomonas aeruginosa</i> efflux gene regulator MexR are targeted by mutations conferring multidrug resistance. <i>Protein Science</i> , 2010, 19, 680-692.  | 7.6 | 32        |
| 11 | A test of proposed rules for helix capping: Implications for protein design. <i>Protein Science</i> , 2009, 11, 516-521.  | 7.6 | 13        |
| 12 | Thermodynamic Interrogation of a Folding Disease. Mutant Mapping of Position 107 in Human Carbonic Anhydrase II Linked to Marble Brain Disease. <i>Biochemistry</i> , 2008, 47, 1288-1298.  | 2.5 | 7         |
| 13 | Redesign of human carbonic anhydrase II for increased esterase activity and specificity towards esters with long acyl chains. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1601-1606.   | 2.3 | 25        |
| 14 | Denaturant-Assisted Formation of a Stabilizing Disulfide Bridge from Engineered Cysteines in Nonideal Conformations. <i>Biochemistry</i> , 2005, 44, 3487-3493.   | 2.5 | 12        |
| 15 | Circumnavigating Misfolding Traps in the Energy Landscape through Protein Engineering: Suppression of Molten Globule and Aggregation in Carbonic Anhydrase. <i>Biochemistry</i> , 2004, 43, 6803-6807.  | 2.5 | 10        |
| 16 | Dramatic Stabilization of the Native State of Human Carbonic Anhydrase II by an Engineered Disulfide Bond. <i>Biochemistry</i> , 2002, 41, 15867-15875.   | 2.5 | 41        |
| 17 | High-Resolution Probing of Local Conformational Changes in Proteins by the Use of Multiple Labeling: Unfolding and Self-Assembly of Human Carbonic Anhydrase II Monitored by Spin, Fluorescent, and Chemical Reactivity Probes. <i>Biophysical Journal</i> , 2001, 80, 2867-2885. | 0.5 | 35        |
| 18 | Comparison of Electron Paramagnetic Resonance Methods to Determine Distances between Spin Labels on Human Carbonic Anhydrase II. <i>Biophysical Journal</i> , 2001, 80, 2886-2897.  | 0.5 | 74        |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | Subtle Differences in Dissociation Rates of Interactions between Destabilized Human Carbonic Anhydrase II Mutants and Immobilized Benzenesulfonamide Inhibitors Probed by a Surface Plasmon Resonance Biosensor. <i>Analytical Biochemistry</i> , 2001, 296, 188-196. | 2.4 | 15        |
| 20 | Adsorption of Human Carbonic Anhydrase II Variants to Silica Nanoparticles Occur Stepwise: Binding Is Followed by Successive Conformational Changes to a Molten-Globule-like State. <i>Langmuir</i> , 2000, 16, 8470-8479.  | 3.5 | 61        |
| 21 | Structural Mapping of an Aggregation Nucleation Site in a Molten Globule Intermediate. <i>Journal of Biological Chemistry</i> , 1999, 274, 32897-32903.   | 3.4 | 52        |
| 22 | Cis-trans isomerization is rate-determining in the reactivation of denatured human carbonic anhydrase II as evidenced by proline isomerase. <i>FEBS Letters</i> , 1992, 296, 90-94.   | 2.8 | 57        |
| 23 | Role of an evolutionarily invariant serine for the stability of human carbonic anhydrase II. <i>BBA - Proteins and Proteomics</i> , 1992, 1118, 179-186.  | 2.1 | 29        |
| 24 | Folding around the C-terminus of human carbonic anhydrase II Kinetic characterization by use of a chemically reactive SH-group introduced by protein engineering. <i>FEBS Letters</i> , 1991, 289, 117-122.   | 2.8 | 36        |