

# Timothy C Umland

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

982  
citations

759055

12  
h-index

580701

25  
g-index

25  
all docs

25  
docs citations

25  
times ranked

1606  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | The K1 Capsular Polysaccharide of <i>Acinetobacter baumannii</i> Strain 307-0294 Is a Major Virulence Factor. <i>Infection and Immunity</i> , 2010, 78, 3993-4000.  | 1.0 | 271       |
| 2  | Severe Acute Respiratory Syndrome Coronavirus nsp9 Dimerization Is Essential for Efficient Viral Growth. <i>Journal of Virology</i> , 2009, 83, 3007-3018.  | 1.5 | 101       |
| 3  | Penicillin-Binding Protein 7/8 Contributes to the Survival of <i>Acinetobacter baumannii</i> In Vitro and In Vivo. <i>Journal of Infectious Diseases</i> , 2009, 199, 513-521.  | 1.9 | 91        |
| 4  | The Response Regulator BfmR Is a Potential Drug Target for <i>Acinetobacter baumannii</i> . <i>MSphere</i> , 2016, 1, .   | 1.3 | 91        |
| 5  | Structural Basis of DNA Bridging by Barrier-to-Autointegration Factor. <i>Biochemistry</i> , 2000, 39, 9130-9138.   | 1.2 | 79        |
| 6  | A New Crystal Structure of Deoxyhypusine Synthase Reveals the Configuration of the Active Enzyme and of an Enzyme-NAD <sup>+</sup> -Inhibitor Ternary Complex. <i>Journal of Biological Chemistry</i> , 2004, 279, 28697-28705.   | 1.6 | 70        |
| 7  | <i>In Vivo</i> -Validated Essential Genes Identified in <i>Acinetobacter baumannii</i> by Using Human Ascites Overlap Poorly with Essential Genes Detected on Laboratory Media. <i>MBio</i> , 2012, 3, .  | 1.8 | 66        |
| 8  | Structure of a human Clara cell phospholipid-binding protein-ligand complex at 1.9 Å... resolution. <i>Nature Structural Biology</i> , 1994, 1, 538-545.  | 9.7 | 65        |
| 9  | Identification of Key Amino Acids Responsible for the Substantially Higher Affinities of Human Type 1 3 $\beta$ -Hydroxysteroid Dehydrogenase/Isomerase (3 $\beta$ -HSD1) for Substrates, Coenzymes, and Inhibitors Relative to Human 3 $\beta$ -HSD2. <i>Journal of Biological Chemistry</i> , 2005, 280, 21321-21328.               | 1.6 | 28        |
| 10 | Influenza A polymerase subunit PB2 possesses overlapping binding sites for polymerase subunit PB1 and human MAVS proteins. <i>Virus Research</i> , 2013, 172, 75-80.  | 1.1 | 20        |
| 11 | Conformational stability changes of the amino terminal domain of enzyme I of the <i>Escherichia coli</i> phosphoenolpyruvate: sugar phosphotransferase system produced by substituting alanine or glutamate for the active-site histidine 189: Implications for phosphorylation effects. <i>Protein Science</i> , 2000, 9, 1085-1094. | 3.1 | 15        |
| 12 | Rational proteomics V: Structure-based mutagenesis has revealed key residues responsible for substrate recognition and catalysis by the dehydrogenase and isomerase activities in human 3 $\beta$ -hydroxysteroid dehydrogenase/isomerase type 1. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2006, 101, 50-60.    | 1.2 | 15        |
| 13 | Crystal structure of 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase from the ESKAPE pathogen <i>Acinetobacter baumannii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 179-187.   | 0.4 | 11        |
| 14 | The Higher Affinity of Human Type 1 3 $\beta$ -Hydroxysteroid Dehydrogenase (3 $\beta$ -HSD1) for Substrate and Inhibitor Steroids Relative to Human 3 $\beta$ -HSD2 is Validated in MCF7 Tumor Cells and Related to Subunit Interactions. <i>Endocrine Research</i> , 2004, 30, 935-941.   | 0.6 | 10        |
| 15 | Divergent evolution of a Rossmann fold and identification of its oldest surviving ancestor. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 280.  | 0.1 | 9         |
| 16 | <i>De Novo</i> Pyrimidine Biosynthesis Connects Cell Integrity to Amphotericin B Susceptibility in <i>Cryptococcus neoformans</i> . <i>MSphere</i> , 2016, 1, .   | 1.3 | 9         |
| 17 | Crystallization and preliminary X-ray analysis of tetanus neurotoxin C fragment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 273-275.   | 2.5 | 8         |
| 18 | Structure of shikimate kinase, an <i>in vivo</i> essential metabolic enzyme in the nosocomial pathogen <i>Acinetobacter baumannii</i> , in complex with shikimate. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1736-1744.   | 2.5 | 7         |

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|----|---|-----|-----------|
| 19 | Accuracy of secondary structure and solvent accessibility predictions for a clostridial neurotoxin C-fragment. <i>The Protein Journal</i> , 1998, 17, 311-318.  | 1.1 | 5         |
| 20 | Crystallization and X-ray diffraction analysis of the $\beta$ -ketoacyl-acyl carrier protein reductase FabG from <i>Aquifex aeolicus</i> VF5. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 106-109. | 0.7 | 3         |
| 21 | Re-evaluating the approach to drug target discovery in multidrug-resistant Gram-negative bacilli. <i>Future Microbiology</i> , 2014, 9, 1113-1116.  | 1.0 | 3         |
| 22 | Expression, purification and characterization of recombinant severe acute respiratory syndrome coronavirus non-structural protein 1. <i>Protein Expression and Purification</i> , 2007, 52, 249-257.  | 0.6 | 2         |
| 23 | Twixt form and function. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 919-922.   | 3.6 | 1         |
| 24 | The short-chain oxidoreductase Q9HYA2 from <i>Pseudomonas aeruginosa</i> PAO1 contains an atypical catalytic center. <i>Protein Science</i> , 2010, 19, 1097-1103.  | 3.1 | 1         |
| 25 | Sequence fingerprint and structural analysis of the SCOR enzyme A3DFK9 from <i>Clostridium thermocellum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 603-613.  | 1.5 | 1         |