

# Bashkim Kokona

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

679  
citations

623734

14  
h-index

552781

26  
g-index

29  
all docs

29  
docs citations

29  
times ranked

963  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Helix Propensity of Highly Fluorinated Amino Acids. <i>Journal of the American Chemical Society</i> , 2006, 128, 15556-15557.   | 13.7 | 104       |
| 2  | A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.  | 2.5  | 71        |
| 3  | Self-Assembly of Peptide Porphyrin Complexes: Toward the Development of Smart Biomaterials. <i>Journal of the American Chemical Society</i> , 2006, 128, 4166-4167.   | 13.7 | 67        |
| 4  | Effect of Highly Fluorinated Amino Acids on Protein Stability at a Solvent-Exposed Position on an Internal Strand of Protein G B1 Domain. <i>Journal of the American Chemical Society</i> , 2009, 131, 13192-13193. | 13.7 | 64        |
| 5  | Self Assembly of Coiled-Coil Peptide~Porphyrin Complexes. <i>Biomacromolecules</i> , 2009, 10, 1454-1459.   | 5.4  | 49        |
| 6  | Role of the Coiled-Coil Structural Motif in Polyglutamine Aggregation. <i>Biochemistry</i> , 2014, 53, 6738-6746.   | 2.5  | 35        |
| 7  | Structure, Regulation, and Inhibition of the Quorum-Sensing Signal Integrator LuxO. <i>PLoS Biology</i> , 2016, 14, e1002464.   | 5.6  | 32        |
| 8  | Single Amino Acid Mutations Alter the Distribution of Human Porphobilinogen Synthase Quaternary Structure Isoforms (Morpheins). <i>Journal of Biological Chemistry</i> , 2006, 281, 6682-6690.                      | 3.4  | 28        |
| 9  | Characterization of Mesoscale Coiled-Coil Peptide~Porphyrin Complexes. <i>Biomacromolecules</i> , 2011, 12, 4196-4203.  | 5.4  | 27        |
| 10 | Crystal Structure of a Glycyl Radical Enzyme from <i>Archaeoglobus fulgidus</i> . <i>Journal of Molecular Biology</i> , 2006, 357, 221-235.   | 4.2  | 23        |
| 11 | Probing the Oligomeric Assemblies of Pea Porphobilinogen Synthase by Analytical Ultracentrifugation. <i>Biochemistry</i> , 2008, 47, 10649-10656.   | 2.5  | 21        |
| 12 | Design of a heterotetrameric coiled coil. <i>Protein Science</i> , 2009, 18, 329-336.   | 7.6  | 21        |
| 13 | Polyglutamine fibrils are formed using a simple designed hairpin model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1971-1979.  | 2.6  | 15        |
| 14 | Uncovering protein~protein interactions through a team-based undergraduate biochemistry course. <i>PLoS Biology</i> , 2017, 15, e2003145.   | 5.6  | 15        |
| 15 | Probing the selectivity of $\beta^2$ -hydroxylation reactions in non-ribosomal peptide synthesis using analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2016, 495, 42-51.                           | 2.4  | 13        |
| 16 | Roles of singleton tryptophan motifs in COPI coat stability and vesicle tethering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24031-24040.                 | 7.1  | 13        |
| 17 | Effect of Helical Flanking Sequences on the Morphology of Polyglutamine-Containing Fibrils. <i>Biochemistry</i> , 2014, 53, 6747-6753.  | 2.5  | 12        |
| 18 | The Plasmid-Encoded Regulator Activates Factors Conferring Lysozyme Resistance on Enteropathogenic <i>Escherichia coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2009, 75, 275-280.              | 3.1  | 11        |

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|----|---|-----|-----------|
| 19 | Self-association motifs in the enteroaggregative <i>Escherichia coli</i> heat-resistant agglutinin 1. <i>Microbiology</i> (United Kingdom), 2016, 162, 1091-1102.   | 1.8 | 11        |
| 20 | Quantitative atomic force microscopy image analysis of unusual filaments formed by the <i>Acanthamoeba castellanii</i> myosin II rod domain. <i>Analytical Biochemistry</i> , 2005, 346, 189-200.   | 2.4 | 10        |
| 21 | Studying polyglutamine aggregation in <i>Caenorhabditis elegans</i> using an analytical ultracentrifuge equipped with fluorescence detection. <i>Protein Science</i> , 2016, 25, 605-617.   | 7.6 | 10        |
| 22 | The effect of divalent cations on the thermostability of type II polyketide synthase acyl carrier proteins. <i>AIChE Journal</i> , 2018, 64, 4308-4318.   | 3.6 | 9         |
| 23 | Widening the bottleneck: Heterologous expression, purification, and characterization of the <i>Ktedonobacter racemifer</i> minimal type II polyketide synthase in <i>Escherichia coli</i> . <i>Bioorganic and Medicinal Chemistry</i> , 2020, 28, 115686. | 3.0 | 7         |
| 24 | Testing the Role of Charge and Structure on the Stability of Peptide-Porphyrin Complexes. <i>Biomacromolecules</i> , 2014, 15, 4544-4550.   | 5.4 | 6         |
| 25 | Sedimentation Velocity Analysis with Fluorescence Detection of Mutant Huntingtin Exon 1 Aggregation in <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> . <i>Biochemistry</i> , 2017, 56, 4676-4688.                                      | 2.5 | 4         |
| 26 | Effect of helix length on the stability of the lac repressor antiparallel coiled coil. <i>Biopolymers</i> , 2015, 104, 395-404.   | 2.4 | 1         |
| 27 | Aggregation Profiling of C9orf72 Dipeptide Repeat Proteins Transgenically Expressed in <i>Drosophila melanogaster</i> Using an Analytical Ultracentrifuge Equipped with Fluorescence Detection. <i>Methods in Molecular Biology</i> , 2019, 2039, 81-90.  | 0.9 | 0         |
| 28 | Size Analysis of C9orf72 Dipeptide Repeat Proteins Expressed in <i>Drosophila melanogaster</i> Using Semidenaturing Detergent Agarose Gel Electrophoresis. <i>Methods in Molecular Biology</i> , 2019, 2039, 91-101.                                      | 0.9 | 0         |
| 29 | The Placement of Vibrational Probe Labeled Substrates to the Phosphopantetheine Arm of the <i>E. coli</i> Acyl Carrier Protein for Site Specific Vibrational Spectroscopy. <i>Biophysical Journal</i> , 2019, 116, 485a-486a.                             | 0.5 | 0         |