

# Phanourios Tamamis

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56  
papers

1,103  
citations

20  
h-index

30  
g-index

61  
ext. papers

1,380  
ext. citations

5  
avg. IF

4.51  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 56 | Computational and Experimental Protocols to Study Cyclo-dihistidine Self- and Co-assembly: Minimalistic Bio-assemblies with Enhanced Fluorescence and Drug Encapsulation Properties.. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2405, 179-203 | 1.4  | 1         |
| 55 | Computational design of a Bwrapin <sup>W</sup> N-terminal domain with canonical and non-canonical amino acid modifications mimicking curcumin <sup>W</sup> proposed inhibitory function.. <i>Biophysical Chemistry</i> , <b>2022</b> , 286, 106805      | 3.5  | 0         |
| 54 | Montmorillonite clay-based sorbents decrease the bioavailability of per- and polyfluoroalkyl substances (PFAS) from soil and their translocation to plants. <i>Environmental Research</i> , <b>2021</b> , 205, 112433                                   | 7.9  | 3         |
| 53 | Protection of Oxygen-Sensitive Enzymes by Peptide Hydrogel. <i>ACS Nano</i> , <b>2021</b> , 15, 6530-6539   | 16.7 | 9         |
| 52 | Combining Experimental Isotherms, Minimalistic Simulations, and a Model to Understand and Predict Chemical Adsorption onto Montmorillonite Clays. <i>ACS Omega</i> , <b>2021</b> , 6, 14090-14103   | 3.9  | 2         |
| 51 | Self-Assembled Peptide Nano-Superstructure towards Enzyme Mimicking Hydrolysis. <i>Angewandte Chemie</i> , <b>2021</b> , 133, 17301-17307   | 3.6  | 1         |
| 50 | Self-Assembled Peptide Nano-Superstructure towards Enzyme Mimicking Hydrolysis. <i>Angewandte Chemie - International Edition</i> , <b>2021</b> , 60, 17164-17170  | 16.4 | 9         |
| 49 | Hydroxylated Chalcones as Aryl Hydrocarbon Receptor Agonists: Structure-Activity Effects. <i>Toxicological Sciences</i> , <b>2021</b> , 180, 148-159  | 4.4  | 0         |
| 48 | Enhanced adsorption of per- and polyfluoroalkyl substances (PFAS) by edible, nutrient-amended montmorillonite clays. <i>Water Research</i> , <b>2021</b> , 188, 116534  | 12.5 | 18        |
| 47 | EDTA-mimicking amino acid <sup>W</sup> metal ion coordination for multifunctional packings. <i>Journal of Materials Chemistry A</i> , <b>2021</b> , 9, 20385-20394  | 13   | 1         |
| 46 | High-Efficiency Fluorescence through Bioinspired Supramolecular Self-Assembly. <i>ACS Nano</i> , <b>2020</b> , 14, 2798-2807  | 16.7 | 22        |
| 45 | Enhanced Fluorescence for Bioassembly by Environment-Switching Doping of Metal Ions. <i>Advanced Functional Materials</i> , <b>2020</b> , 30, 1909614   | 15.6 | 24        |
| 44 | Computational evolution of an RNA-binding protein towards enhanced oxidized-RNA binding. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 137-152  | 6.8  | 2         |
| 43 | Amyloid Peptide Scaffolds Coordinate with Alzheimer <sup>W</sup> Disease Drugs. <i>Journal of Physical Chemistry B</i> , <b>2020</b> , 124, 487-503   | 3.4  | 4         |
| 42 | Molecular Mechanism for Attractant Signaling to DHMA by E. <sup>W</sup> coli Tsr. <i>Biophysical Journal</i> , <b>2020</b> , 118, 492-504   | 2.9  | 6         |
| 41 | Interactions between Curcumin Derivatives and Amyloid- <sup>W</sup> Fibrils: Insights from Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , <b>2020</b> , 60, 289-305  | 6.1  | 18        |
| 40 | Insights into the interactions of bisphenol and phthalate compounds with unamended and carnitine-amended montmorillonite clays. <i>Computers and Chemical Engineering</i> , <b>2020</b> , 143, 107063-107063  | 4.3  | 7         |

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|----|---|-----|----|
| 39 | Activation of COUP-TFI by a Novel Diindolylmethane Derivative. <i>Cells</i> , <b>2019</b> , 8,  | 7.9 | 6  |
| 38 | Designer Amyloid Cell-Penetrating Peptides for Potential Use as Gene Transfer Vehicles. <i>Biomolecules</i> , <b>2019</b> , 10,   | 5.9 | 10 |
| 37 | Self-Assembling Amyloid Sequences as Scaffolds for Material Design: A Case Study of Building Blocks Inspired From the Adenovirus Fiber Protein. <i>Macromolecular Symposia</i> , <b>2019</b> , 386, 1900005   | 0.8 | 1  |
| 36 | Isoflavones as Ah Receptor Agonists in Colon-Derived Cell Lines: Structure-Activity Relationships. <i>Chemical Research in Toxicology</i> , <b>2019</b> , 32, 2353-2364   | 4   | 16 |
| 35 | Montmorillonites Can Tightly Bind Glyphosate and Paraquat Reducing Toxin Exposures and Toxicity. <i>ACS Omega</i> , <b>2019</b> , 4, 17702-17713  | 3.9 | 17 |
| 34 | Molecular Modeling of Chemoreceptor:Ligand Interactions. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1729, 353-372  | 1.4 | 4  |
| 33 | A high-throughput and rapid computational method for screening of RNA post-transcriptional modifications that can be recognized by target proteins. <i>Methods</i> , <b>2018</b> , 143, 34-47   | 4.6 | 5  |
| 32 | Structure-Dependent Modulation of Aryl Hydrocarbon Receptor-Mediated Activities by Flavonoids. <i>Toxicological Sciences</i> , <b>2018</b> , 164, 205-217   | 4.4 | 48 |
| 31 | Elucidating the multi-targeted anti-amyloid activity and enhanced islet amyloid polypeptide binding of -wrapins. <i>Computers and Chemical Engineering</i> , <b>2018</b> , 116, 322-332   | 4   | 10 |
| 30 | Virtual Screening of Chemical Compounds for Discovery of Complement C3 Ligands. <i>ACS Omega</i> , <b>2018</b> , 3, 6427-6438   | 3.9 | 11 |
| 29 | An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , <b>2018</b> , 8, 9939   | 4.9 | 16 |
| 28 | Computational Design of Functional Amyloid Materials with Cesium Binding, Deposition, and Capture Properties. <i>Journal of Physical Chemistry B</i> , <b>2018</b> , 122, 7555-7568   | 3.4 | 10 |
| 27 | Princeton_TIGRESS 2.0: High refinement consistency and net gains through support vector machines and molecular dynamics in double-blind predictions during the CASP11 experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2017</b> , 85, 1078-1098 | 4.2 | 12 |
| 26 | Computational design of amyloid self-assembling peptides bearing aromatic residues and the cell adhesive motif Arg-Gly-Asp. <i>Molecular Systems Design and Engineering</i> , <b>2017</b> , 2, 321-335  | 4.6 | 12 |
| 25 | Self-Assembled Amyloid Peptides with Arg-Gly-Asp (RGD) Motifs As Scaffolds for Tissue Engineering. <i>ACS Biomaterials Science and Engineering</i> , <b>2017</b> , 3, 1404-1416   | 5.5 | 28 |
| 24 | Editorial Highlight: Microbial-Derived 1,4-Dihydroxy-2-naphthoic Acid and Related Compounds as Aryl Hydrocarbon Receptor Agonists/Antagonists: Structure-Activity Relationships and Receptor Modeling. <i>Toxicological Sciences</i> , <b>2017</b> , 155, 458-473       | 4.4 | 23 |
| 23 | Highly Accurate Structure-Based Prediction of HIV-1 Coreceptor Usage Suggests Intermolecular Interactions Driving Tropism. <i>PLoS ONE</i> , <b>2016</b> , 11, e0148974   | 3.7 | 21 |
| 22 | Uncovering the Binding and Specificity of Wrapins for Amyloid- $\beta$ and $\alpha$ -Synuclein. <i>Journal of Physical Chemistry B</i> , <b>2016</b> , 120, 12781-12794   | 3.4 | 19 |

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|----|---|-----|----|
| 21 | New compstatin peptides containing N-terminal extensions and non-natural amino acids exhibit potent complement inhibition and improved solubility characteristics. <i>Journal of Medicinal Chemistry</i> , <b>2015</b> , 58, 814-26   | 8.3 | 16 |
| 20 | Elucidating a key anti-HIV-1 and cancer-associated axis: the structure of CCL5 (Rantes) in complex with CCR5. <i>Scientific Reports</i> , <b>2014</b> , 4, 5447   | 4.9 | 32 |
| 19 | Princeton_TIGRESS: protein geometry refinement using simulations and support vector machines. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82, 794-814   | 4.2 | 21 |
| 18 | Forcefield_NCAA: ab initio charge parameters to aid in the discovery and design of therapeutic proteins and peptides with unnatural amino acids and their application to complement inhibitors of the compstatin family. <i>ACS Synthetic Biology</i> , <b>2014</b> , 3, 855-69 | 5.7 | 47 |
| 17 | Elucidating a key component of cancer metastasis: CXCL12 (SDF-1 $\beta$ ) binding to CXCR4. <i>Journal of Chemical Information and Modeling</i> , <b>2014</b> , 54, 1174-88   | 6.1 | 37 |
| 16 | Self-assembly of an aspartate-rich sequence from the adenovirus fiber shaft: insights from molecular dynamics simulations and experiments. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 1765-74  | 3.4 | 20 |
| 15 | Insights into the mechanism of C5aR inhibition by PMX53 via implicit solvent molecular dynamics simulations and docking. <i>BMC Biophysics</i> , <b>2014</b> , 7, 5   | 0   | 20 |
| 14 | Molecular recognition of CCR5 by an HIV-1 gp120 V3 loop. <i>PLoS ONE</i> , <b>2014</b> , 9, e95767  | 3.7 | 44 |
| 13 | Combination of theoretical and experimental approaches for the design and study of fibril-forming peptides. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1216, 53-70   | 1.4 | 15 |
| 12 | Molecular recognition of CXCR4 by a dual tropic HIV-1 gp120 V3 loop. <i>Biophysical Journal</i> , <b>2013</b> , 105, 1502-14  | 2.9 | 39 |
| 11 | Novel compstatin family peptides inhibit complement activation by drusen-like deposits in human retinal pigmented epithelial cell cultures. <i>Experimental Eye Research</i> , <b>2013</b> , 116, 96-108  | 3.7 | 23 |
| 10 | Molecular dynamics in drug design: new generations of compstatin analogs. <i>Chemical Biology and Drug Design</i> , <b>2012</b> , 79, 703-18  | 2.9 | 31 |
| 9  | Exploring Protein-Protein and Protein-Ligand Interactions in the Immune System using Molecular Dynamics and Continuum Electrostatics. <i>Current Physical Chemistry</i> , <b>2012</b> , 2, 324-343  | 0.5 | 16 |
| 8  | Insights into the structure, correlated motions, and electrostatic properties of two HIV-1 gp120 V3 loops. <i>PLoS ONE</i> , <b>2012</b> , 7, e49925  | 3.7 | 17 |
| 7  | Amyloid-like self-assembly of a dodecapeptide sequence from the adenovirus fiber shaft: Perspectives from molecular dynamics simulations. <i>Journal of Non-Crystalline Solids</i> , <b>2011</b> , 357, 717-722   | 3.9 | 16 |
| 6  | Design of a modified mouse protein with ligand binding properties of its human analog by molecular dynamics simulations: the case of C3 inhibition by compstatin. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 3166-79                           | 4.2 | 23 |
| 5  | UV resonance Raman study of TTR(105-115) structural evolution as a function of temperature. <i>Journal of Physical Chemistry B</i> , <b>2011</b> , 115, 4088-98   | 3.4 | 6  |
| 4  | Species specificity of the complement inhibitor compstatin investigated by all-atom molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 2655-67   | 4.2 | 32 |

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|---|---|-----|-----|
| 3 | Amyloid-like self-assembly of peptide sequences from the adenovirus fiber shaft: insights from molecular dynamics simulations. <i>Journal of Physical Chemistry B</i> , <b>2009</b> , 113, 15639-47 | 3.4 | 35  |
| 2 | Self-assembly of phenylalanine oligopeptides: insights from experiments and simulations. <i>Biophysical Journal</i> , <b>2009</b> , 96, 5020-9  | 2.9 | 187 |
| 1 | Conformational analysis of compstatin analogues with molecular dynamics simulations in explicit water. <i>Journal of Molecular Graphics and Modelling</i> , <b>2007</b> , 26, 571-80                | 2.8 | 11  |