# Dimitrios Morikis

List of Publications by Year
in descending order

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| 137 | 4,195 | 117625 | 133252 |
|---|---|---|---|
| papers | citations | 34 h-index | 59 g-index |

| 181 | 181 | 181 | 3606 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Resonance Raman investigations of site-directed mutants of myoglobin: effects of distal histidine replacement. Biochemistry, 1989, 28, 4791-4800. | 2.5 | 197 |
| 2 | The molecular basis for protein kinase A anchoring revealed by solution NMR. Nature Structural Biology, 1999, 6, 222-227. | 9.7 | 181 |
| 3 | A novel mechanism of PKA anchoring revealed by solution structures of anchoring complexes. EMBO Journal, 2001, 20, 1651-1662. | 7.8 | 179 |
| 4 | Spectroscopic studies of myoglobin at low pH: heme structure and ligation. Biochemistry, 1991, 30, 1227-1237. | 2.5 | 162 |
| 5 | Endosidin2 targets conserved exocyst complex subunit EXO70 to inhibit exocytosis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E41-50. | 7.1 | 129 |
| 6 | Adaptation of inorganic quantum dots for stable molecular beacons. Sensors and Actuators B: Chemical, 2004, 102, 315-319. | 7.8 | 128 |
| 7 | Alteration of sperm whale myoglobin heme axial ligation by site-directed mutagenesis. Biochemistry, 1990, 29, 9783-9791. | 2.5 | 121 |
| 8 | A Gain-of-Function Mutation ofArabidopsisLipid Transfer Protein 5 Disturbs Pollen Tube Tip Growth and Fertilization Â. Plant Cell, 2010, 21, 3902-3914. | 6.6 | 106 |
| 9 | Binding Kinetics, Structure-Activity Relationship, and Biotransformation of the Complement Inhibitor Compstatin. Journal of Immunology, 2000, 165, 2491-2499. | 0.8 | 105 |
| 10 | Solution structure of Compstatin, a potent complement inhibitor. Protein Science, 1998, 7, 619-627. | 7.6 | 87 |
| 11 | Integrated Computational and Experimental Approach for Lead Optimization and Design of Compstatin Variants with Improved Activity. Journal of the American Chemical Society, 2003, 125, 8422-8423. | 13.7 | 85 |
| 12 | Compstatin, a peptide inhibitor of complement, exhibits species-specific binding to complement component C3. Molecular Immunology, 2003, 39, 557-566. | 2.2 | 81 |
| 13 | Alteration of heme axial ligands by site-directed mutagenesis: a cytochrome becomes a catalytic demethylase. Journal of the American Chemical Society, 1987, 109, 7896-7897. | 13.7 | 77 |
| 14 | A multifaceted study of stigma/style cysteine-rich adhesin (SCA)-like Arabidopsis lipid transfer proteins (LTPs) suggests diversified roles for these LTPs in plant growth and reproduction. Journal of Experimental Botany, 2010, 61, 4277-4290. | 4.8 | 74 |
| 15 | Electrostatic Modeling Predicts the Activities of Orthopoxvirus Complement Control Proteins. Journal of Immunology, 2005, 174, 2143-2151. | 0.8 | 73 |
| 16 | ADF/Cofilin Binds Phosphoinositides in a Multivalent Manner to Act as a PIP2-Density Sensor. Biophysical Journal, 2010, 98, 2327-2336. | 0.5 | 73 |
| 17 | Design and NMR Characterization of Active Analogues of Compstatin Containing Non-Natural Amino Acids. Journal of Medicinal Chemistry, 2005, 48, 274-286. | 6.4 | 68 |
| 18 | Discovery of functionally selective C5aR2 ligands: novel modulators of C5a signalling. Immunology and Cell Biology, 2016, 94, 787-795. | 2.3 | 68 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | The iron-histidine mode of myoglobin revisited: resonance Raman studies of isotopically labeled Escherichia coli-expressed myoglobin. Journal of the American Chemical Society, 1991, 113, 9655-9660. | 13.7 | 61 |
| 20 | NMR evidence for multiple conformations in a highly helical model peptide. Biochemistry, 1993, 32, 13089-13097. | 2.5 | 61 |
| 21 | Related Proteinâ€"Protein Interaction Modules Present Drastically Different Surface Topographies Despite A Conserved Helical Platform. Journal of Molecular Biology, 2003, 330, 1117-1129. | 4.2 | 57 |
| 22 | Conformational interconversion in protein crystals. Journal of Molecular Biology, 1992, 224, 207-215. | 4.2 | 56 |
| 23 | Design of Peptide Analogues with Improved Activity Using a Novel de Novo Protein Design Approach. Industrial & Engineering Chemistry Research, 2004, 43, 3817-3826. | 3.7 | 56 |
| 24 | Complement. Immunologic Research, 2003, 27, 367-385. | 2.9 | 53 |
| 25 | Electrostatic Clustering and Free Energy Calculations Provide a Foundation for Protein Design and Optimization. Annals of Biomedical Engineering, 2011, 39, 1252-1263. | 2.5 | 53 |
| 26 | The Structural Basis of Compstatin Activity Examined by Structure-Function-based Design of Peptide Analogs and NMR. Journal of Biological Chemistry, 2002, 277, 14942-14953. | 3.4 | 50 |
| 27 | Structural aspects and design of low-molecular-mass complement inhibitors. Biochemical Society Transactions, 2002, 30, 1026-1036. | 3.4 | 49 |
| 28 | The Electrostatic Nature of C3d-Complement Receptor 2 Association. Journal of Immunology, 2004, 172, 7537-7547. | 0.8 | 48 |
| 29 | Immunophysical Properties and Prediction of Activities for Vaccinia Virus Complement Control Protein and Smallpox Inhibitor of Complement Enzymes Using Molecular Dynamics and Electrostatics. Biophysical Journal, 2006, 90, 3106-3119. | 0.5 | 47 |
| 30 | Toward Full-Sequence De Novo Protein Design with Flexible Templates for Human Beta-Defensin-2. Biophysical Journal, 2008, 94, 584-599. | 0.5 | 45 |
| 31 | Quantitative Modeling of the Alternative Pathway of the Complement System. PLoS ONE, 2016, 11, e0152337. | 2.5 | 42 |
| 32 | Studies of Structure-Activity Relations of Complement Inhibitor Compstatin. Journal of Immunology, 2003, 171, 1881-1890. | 0.8 | 39 |
| 33 | An evaluation of poisson-boltzmann electrostatic free energy calculations through comparison with experimental mutagenesis data. Biopolymers, 2011, 95, n/a-n/a. | 2.4 | 37 |
| 34 | Resonance Raman scattering as a probe of electron-nuclear coupling: applications to heme proteins. The Journal of Physical Chemistry, 1991, 95, 3391-3398. | 2.9 | 36 |
| 35 | Improvement of the anti-C3 activity of compstatin using rational and combinatorial approaches. Biochemical Society Transactions, 2004, 32, 28-32. | 3.4 | 34 |
| 36 | Species specificity of the complement inhibitor compstatin investigated by allâ€atom molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2655-2667. | 2.6 | 34 |

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| 37 | Molecular Dynamics in Drug Design: New Generations of Compstatin Analogs. Chemical Biology and Drug Design, 2012, 79, 703-718. | 3.2 | 34 |
| 38 | Two SCA (Stigma/Style Cysteine-rich Adhesin) Isoforms Show Structural Differences That Correlate with Their Levels of in Vitro Pollen Tube Adhesion Activity. Journal of Biological Chemistry, 2007, 282, 33845-33858. | 3.4 | 33 |
| 39 | Influence of Electrostatics on the Complement Regulatory Functions of Kaposica, the Complement Inhibitor of Kaposiâ€™s Sarcoma-Associated Herpesvirus. Journal of Immunology, 2010, 184, 1956-1967. | 0.8 | 33 |
| 40 | Contribution of Specific Amino Acid Changes in Penicillin Binding Protein 1 to Amoxicillin Resistance in Clinical Helicobacter pylori isolates. Antimicrobial Agents and Chemotherapy, 2011, 55, 101-109. | 3.2 | 33 |
| 41 | The Two Sides of Complement C3d: Evolution of Electrostatics in a Link between Innate and Adaptive Immunity. PLoS Computational Biology, 2012, 8, e1002840. | 3.2 | 32 |
| 42 | New Compstatin Variants through Two De Novo Protein Design Frameworks. Biophysical Journal, 2010, 98, 2337-2346. | 0.5 | 31 |
| 43 | De Novo Peptide Design with C3a Receptor Agonist and Antagonist Activities: Theoretical Predictions and Experimental Validation. Journal of Medicinal Chemistry, 2012, 55, 4159-4168. | 6.4 | 31 |
| 44 | Viral regulators of complement activation: Structure, function and evolution. Molecular Immunology, 2014, 61, 89-99. | 2.2 | 31 |
| 45 | Immunophysical Exploration of C3dâ€“CR2(CCP1-2) Interaction Using Molecular Dynamics and Electrostatics. Journal of Molecular Biology, 2007, 369, 567-583. | 4.2 | 30 |
| 46 | Physical methods for structure, dynamics and binding in immunological research. Trends in Immunology, 2004, 25, 700-707. | 6.8 | 29 |
| 47 | Synthetic small-molecule complement inhibitors. Current Opinion in Investigational Drugs, 2004, 5, 1164-73. | 2.3 | 28 |
| 48 | Development of a Quasi-Dynamic Pharmacophore Model for Anti-Complement Peptide Analogues. Journal of the American Chemical Society, 2005, 127, 10967-10976. | 13.7 | 26 |
| 49 | Molecular Analysis of the Interaction between Staphylococcal Virulence Factor Sbi-IV and Complement C3d. Biophysical Journal, 2014, 106, 1164-1173. | 0.5 | 26 |
| 50 | Resonance Raman studies of oriented chromophores: Metmyoglobin single crystals. Journal of Chemical Physics, 1989, 90, 3015-3032. | 3.0 | 25 |
| 51 | Is the rigid-body assumption reasonable?. Journal of Non-Crystalline Solids, 2011, 357, 707-716. | 3.1 | 25 |
| 52 | Automated computational framework for the analysis of electrostatic similarities of proteins. Biotechnology Progress, 2011, 27, 316-325. | 2.6 | 25 |
| 53 | Novel compstatin family peptides inhibit complement activation by drusen-like deposits in human retinal pigmented epithelial cell cultures. Experimental Eye Research, 2013, 116, 96-108. | 2.6 | 25 |
| 54 | Thermodynamic Studies on the Interaction of the Third Complement Component and Its Inhibitor, Compstatin. Journal of Biological Chemistry, 2004, 279, 54987-54995. | 3.4 | 24 |

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| 55 | 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. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3166-3179. | 2.6 | 24 |
| 56 | Exploring Protein-Protein and Protein-Ligand Interactions in the Immune System using Molecular Dynamics and Continuum Electrostatics. Current Physical Chemistry, 2012, 2, 324-343. | 0.2 | 24 |
| 57 | Conformational interconversion in compstatin probed with molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2003, 53, 130-141. | 2.6 | 23 |
| 58 | A computational model for the evaluation of complement system regulation under homeostasis, disease, and drug intervention. PLoS ONE, 2018, 13, e0198644. | 2.5 | 23 |
| 59 | Resonance Raman studies of myoglobin single crystals. Journal of the American Chemical Society, 1988, 110, 6341-6342. | 13.7 | 21 |
| 60 | Insights into the mechanism of C5aR inhibition by PMX53 via implicit solvent molecular dynamics simulations and docking. BMC Biophysics, 2014, 7, 5. | 4.4 | 21 |
| 61 | A theoretical view of the C3d:CR2 binding controversy. Molecular Immunology, 2015, 64, 112-122. | 2.2 | 21 |
| 62 | The effect of electrostatics on factor H function and related pathologies. Journal of Molecular Graphics and Modelling, 2011, 29, 1047-1055. | 2.4 | 20 |
| 63 | Complement Inhibition by Staphylococcus aureus: Electrostatics of C3dâ€“EfbC and C3dâ€“Ehp Association. Cellular and Molecular Bioengineering, 2012, 5, 32-43. | 2.1 | 20 |
| 64 | Hybrid flagellin as a T cell independent vaccine scaffold. BMC Biotechnology, 2015, 15, 71. | 3.3 | 20 |
| 65 | Characterization, Dynamics, and Mechanism of CXCR4 Antagonists on a Constitutively Active Mutant. Cell Chemical Biology, 2019, 26, 662-673.e7. | 5.2 | 20 |
| 66 | Insights into the Structure, Correlated Motions, and Electrostatic Properties of Two HIV-1 gp120 V3 Loops. PLoS ONE, 2012, 7, e49925. | 2.5 | 20 |
| 67 | Solvation effects in calculated electrostatic association free energies for the C3dâ€CR2 complex and comparison with experimental data. Biopolymers, 2010, 93, 509-519. | 2.4 | 19 |
| 68 | Clustering of HIV-1 Subtypes Based on gp120 V3 Loop electrostatic properties. BMC Biophysics, 2012, 5, 3. | 4.4 | 19 |
| 69 | Molecular thermodynamics for charged biomacromolecules. Fluid Phase Equilibria, 2006, 241, 317-333. | 2.5 | 18 |
| 70 | AESOP: A Python Library for Investigating Electrostatics in Protein Interactions. Biophysical Journal, 2017, 112, 1761-1766. | 0.5 | 18 |
| 71 | Hydrogen Exchange in the Carbon Monoxide Complex of Soybean Leghemoglobin. FEBS Journal, 1996, 237, 212-220. | 0.2 | 17 |
| 72 | New Compstatin Peptides Containing N-Terminal Extensions and Non-Natural Amino Acids Exhibit Potent Complement Inhibition and Improved Solubility Characteristics. Journal of Medicinal Chemistry, 2015, 58, 814-826. | 6.4 | 17 |

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| 73 | Energetic evaluation of binding modes in the <scp>C</scp>3d and Factor <scp>H</scp> (<scp>CCP</scp> 19â€20) complex. Protein Science, 2015, 24, 789-802. | 7.6 | 17 |
| 74 | Proton transfer dynamics of GART: The pH-dependent catalytic mechanism examined by electrostatic calculations. Protein Science, 2008, 10, 2379-2392. | 7.6 | 16 |
| 75 | Derivation of ligands for the complement C3a receptor from the C-terminus of C5a. European Journal of Pharmacology, 2014, 745, 176-181. | 3.5 | 16 |
| 76 | Detection of Side Chain Rearrangements Mediating the Motions of Transmembrane Helices in Molecular Dynamics Simulations of G Protein-Coupled Receptors. Computational and Structural Biotechnology Journal, 2017, 15, 131-137. | 4.1 | 16 |
| 77 | M13 bacteriophage spheroids as scaffolds for directed synthesis of spiky gold nanostructures. Nanoscale, 2018, 10, 13055-13063. | 5.6 | 16 |
| 78 | Applications of Molecular Dynamics Simulations in Immunology: A Useful Computational Method in Aiding Vaccine Design. Current Proteomics, 2006, 3, 259-270. | 0.3 | 15 |
| 79 | Native-state conformational dynamics of GART: A regulatory pH-dependent coil-helix transition examined by electrostatic calculations. Protein Science, 2008, 10, 2363-2378. | 7.6 | 15 |
| 80 | Electrostatic Steering Accelerates C3d:CR2 Association. Journal of Physical Chemistry B, 2016, 120, 8416-8423. | 2.6 | 15 |
| 81 | Virtual Screening of Chemical Compounds for Discovery of Complement C3 Ligands. ACS Omega, 2018, 3, 6427-6438. | 3.5 | 15 |
| 82 | Hydration of the partially folded peptide RN-24 studied by multidimensional NMR. Journal of Biomolecular NMR, 1995, 5, 353-6. | 2.8 | 14 |
| 83 | A New Generation of Potent Complement Inhibitors of the Compstatin Family. Chemical Biology and Drug Design, 2011, 77, 431-440. | 3.2 | 14 |
| 84 | Electrostatic modeling of peptides derived from the V3-loop of HIV-1 gp120: implications of the interaction with chemokine receptor CCR5. International Journal of Molecular Medicine, 2007, 19, 343-51. | 4.0 | 14 |
| 85 | Electrostatic properties of the structure of the docking and dimerization domain of protein kinase A IIÎ±. FEBS Journal, 2002, 269, 2040-2051. | 0.2 | 13 |
| 86 | Molecular Mechanism of Biased Ligand Conformational Changes in CC Chemokine Receptor 7. Journal of Chemical Information and Modeling, 2016, 56, 1808-1822. | 5.4 | 13 |
| 87 | Conformational analysis of compstatin analogues with molecular dynamics simulations in explicit water. Journal of Molecular Graphics and Modelling, 2007, 26, 571-580. | 2.4 | 12 |
| 88 | Dissecting Distinct Roles of NEDDylation E1 Ligase Heterodimer APPBP1 and UBA3 Reveals Potential Evolution Process for Activation of Ubiquitin-related Pathways. Scientific Reports, 2018, 8, 10108. | 3.3 | 12 |
| 89 | Determination of local ligand conformations in slowly tumbling proteins by homonuclear 2D and 3D NMR: application to heme propionates in leghemoglobin. Journal of the American Chemical Society, 1993, 115, 6238-6246. | 13.7 | 10 |
| 90 | 1H resonance assignments and secondary structure of the carbon monoxide complex of soybean leghemoglobin determined by homonuclear two-dimensional and three-dimensional NMR spectroscopy. FEBS Journal, 1994, 219, 611-626. | 0.2 | 10 |

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| 91 | From atoms to systems: a cross-disciplinary approach to complement-mediated functions*1. Molecular Immunology, 2004, 41, 153-164. | 2.2 | 10 |
| 92 | Structure-Based Integrative Computational and Experimental Approach for the Optimization of Drug Design. Lecture Notes in Computer Science, 2005, , 680-688. | 1.3 | 10 |
| 93 | Characterization of the interaction between peptides derived from the gp120/V3 domain of HIV-1 and the amino terminal of the chemokine receptor CCR5 by NMR spectroscopy and light scattering. Journal of Non-Crystalline Solids, 2006, 352, 4451-4458. | 3.1 | 10 |
| 94 | Discovery of Small Molecules for Fluorescent Detection of Complement Activation Product C3d. Journal of Medicinal Chemistry, 2015, 58, 9535-9545. | 6.4 | 10 |
| 95 | Complement Inhibitors Targeting C3, C4, and C5. , 0, , 75-112. | | 10 |
| 96 | Low pH myoglobin photoproducts. Biophysical Journal, 1992, 61, 1041-1044. | 0.5 | 9 |
| 97 | Electrostatic exploration of the C3dâ€“FH4 interaction using a computational alanine scan. Molecular Immunology, 2011, 48, 1844-1850. | 2.2 | 9 |
| 98 | An immunophysical study of the complement system: Examples for the pH dependence of protein binding and stability. Journal of Non-Crystalline Solids, 2006, 352, 4445-4450. | 3.1 | 8 |
| 99 | Structural study of Acâ€Pheâ€[Ornâ€Proâ€dChaâ€Trpâ€Arg], a potent C5a receptor antagonist, by NMR. Biopolymers, 2008, 90, 803-815. | 2.4 | 8 |
| 100 | Engineering pre-SUMO4 as efficient substrate of SENP2. Protein Engineering, Design and Selection, 2014, 27, 117-126. | 2.1 | 8 |
| 101 | Molecular Mechanisms of Macular Degeneration Associated with the Complement Factor H Y402H Mutation. Biophysical Journal, 2019, 116, 215-226. | 0.5 | 8 |
| 102 | The pH dependence of stability of the activation helix and the catalytic site of GART. Biophysical Chemistry, 2003, 105, 279-291. | 2.8 | 7 |
| 103 | pH Dependence of Stability of the 10th Human Fibronectin Type III Domain: A Computational Study. Biotechnology Progress, 2008, 24, 48-55. | 2.6 | 6 |
| 104 | Crosslinked flagella as a stabilized vaccine adjuvant scaffold. BMC Biotechnology, 2019, 19, 48. | 3.3 | 6 |
| 105 | Hybrid Inorganic-Organic Molecular Beacons. Sensor Letters, 2004, 2, 85-90. | 0.4 | 6 |
| 106 | Peptide redesign for inhibition of the complement system: Targeting age-related macular degeneration. Molecular Vision, 2016, 22, 1280-1290. | 1.1 | 6 |
| 107 | De novo protein design of agonists and antagonists of C5a receptors. Immunobiology, 2012, 217, 1162-1163. | 1.9 | 5 |
| 108 | Conformational heterogeneity in CCR7 undergoes transitions to specific states upon ligand binding. Journal of Molecular Graphics and Modelling, 2017, 74, 352-358. | 2.4 | 5 |

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| 109 | Ionic tethering contributes to the conformational stability and function of complement C3b. Molecular Immunology, 2017, 85, 137-147. | 2.2 | 5 |
| 110 | SPARC coordinates extracellular matrix remodeling and efficient recruitment to and migration of antigen-specific T cells in the brain following infection. Scientific Reports, 2021, 11, 4549. | 3.3 | 5 |
| 111 | Electrostatic modeling of peptides derived from the V3-loop of HIV-1 gp120: Implications of the interaction with chemokine receptor CCR5. International Journal of Molecular Medicine, 0, , . | 4.0 | 5 |
| 112 | Solution Structure of a Bent Î±-Helix<sup>,</sup>. Biochemistry, 2007, 46, 12959-12967. | 2.5 | 4 |
| 113 | Computational studies of CXCR1, the receptor of ILâ€8/CXCL8, using molecular dynamics and electrostatics. Biopolymers, 2008, 89, 52-61. | 2.4 | 4 |
| 114 | NMR evidence of chargeâ€dependent interaction between various PND V3 and CCR5 Nâ€terminal peptides. Biopolymers, 2009, 92, 94-109. | 2.4 | 4 |
| 115 | Immunophysical Evaluation of the Initiating Step in the Formation of the Membrane Attack Complex. Frontiers in Physics, 2018, 6, . | 2.1 | 4 |
| 116 | Systems Biology Modeling of the Complement System Under Immune Susceptible Pathogens. Frontiers in Physics, 2021, 9, . | 2.1 | 4 |
| 117 | Structure, Dynamics, Activity, and Function of Compstatin and Design of More Potent Analogues. , 2005, , 317-340. | | 4 |
| 118 | Electrostatic Similarity Determination Using Multiresolution Analysis. Molecular Informatics, 2011, 30, 733-746. | 2.5 | 3 |
| 119 | A Predictive Model for HIV Type 1 Coreceptor Selectivity. AIDS Research and Human Retroviruses, 2013, 29, 1386-1394. | 1.1 | 3 |
| 120 | Factor H-Inspired Design of Peptide Biomarkers of the Complement C3d Protein. ACS Medicinal Chemistry Letters, 2020, 11, 1054-1059. | 2.8 | 3 |
| 121 | Structure, Dynamics, Activity, and Function of Compstatin and Design of More Potent Analogues. , 2005, , 317-340. | | 3 |
| 122 | Exploring Protein-Protein and Protein-Ligand Interactions in the Immune System using Molecular Dynamics and Continuum Electrostatics. Current Physical Chemistry, 2012, 2, 324-343. | 0.2 | 2 |
| 123 | Structure of the Anaphylatoxins C3a and C5a. , 2005, , 161-178. | | 2 |
| 124 | Charge Discriminates Coreceptor Selectivity for HIV-1. Biophysical Journal, 2012, 102, 64a. | 0.5 | 1 |
| 125 | Electrostatic Interactions between Complement Regulator CD46(SCR1-2) and Adenovirus Ad11/Ad21 Fiber Protein Knob. Molecular Biology International, 2015, 2015, 1-15. | 1.7 | 1 |
| 126 | Interplay between Ionic Strength, Association Rates and Electrostatic Interaction in the C3d:CR2 Complex. Biophysical Journal, 2016, 110, 43a. | 0.5 | 1 |

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| 127 | Role of Electrostatic Hotspots in the Selectivity of Complement Control Proteins Toward Human and Bovine Complement Inhibition. Frontiers in Molecular Biosciences, 2021, 8, 618068. | 3.5 | 1 |
| 128 | Structure Calculations of Symmetric Dimers using Molecular Dynamics/Simulated Annealing and NMR Restraints: The Case of the RIIÎ± Subunit of Protein Kinase A. Nonconvex Optimization and Its Applications, 2000, , 141-156. | 0.1 | 1 |
| 129 | Overcoming the Key Challenges in De Novo Protein Design: Enhancing Computational Efficiency and Incorporating True Backbone Flexibility. , 2008, , 133-183. | | 1 |
| 130 | The Building Blocks of the Complement System. , 2005, , 1-18. | | 1 |
| 131 | Computational and Experimental Analysis of the Interactions Between C3 and Compstatin Family Peptides. Biophysical Journal, 2012, 102, 62a. | 0.5 | 0 |
| 132 | The Role of Electrostatics in the Function of Homologous Thioester Containing Proteins: Insights into the Evolution of the Complement C3d:Cr2 Interaction. Biophysical Journal, 2012, 102, 463a. | 0.5 | 0 |
| 133 | Ligand-Specific Conformational Changes in CCR7 Coupled to Selecting Different Signaling Pathways upon CCL19 And CCL21 Ligand Binding. Biophysical Journal, 2016, 110, 361a. | 0.5 | 0 |
| 134 | Synergy of Putative Binding Modes in the Factor H (CCP 19-20) and C3d Complex. Biophysical Journal, 2016, 110, 44a. | 0.5 | 0 |
| 135 | Editorial: ImmunoPhysics and ImmunoEngineering. Frontiers in Physics, 2020, 8, . | 2.1 | 0 |
| 136 | Structure of the Anaphylatoxins C3a and C5a. , 2005, , 161-177. | | 0 |
| 137 | Title is missing!. , 2012, 7, e49925. | | 0 |