

Yasser B Ruiz-Blanco

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

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687220

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docs citations

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times ranked

1183
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Effect of Organic Solvents on the Structure and Activity of a Minimal Lipase. <i>Journal of Organic Chemistry</i> , 2022, 87, 1669-1678. | 1.7 | 10 |
| 2 | The role of DNA nanostructures in the catalytic properties of an allosterically regulated protease. <i>Science Advances</i> , 2022, 8, eabk0425. | 4.7 | 16 |
| 3 | Selective Disruption of Survivin's Protein-Protein Interactions: A Supramolecular Approach Based on Guanidiniocarbonylpyrrole. <i>ChemBioChem</i> , 2022, , e202100618. | 1.3 | 3 |
| 4 | Computational Design of Inhibitors Targeting the Catalytic \hat{F}^2 Subunit of Escherichia coli FOF1-ATP Synthase. <i>Antibiotics</i> , 2022, 11, 557. | 1.5 | 3 |
| 5 | PPI-Affinity: A Web Tool for the Prediction and Optimization of Protein-Protein and Protein-Protein Binding Affinity. <i>Journal of Proteome Research</i> , 2022, 21, 1829-1841. | 1.8 | 24 |
| 6 | Engineering protein fragments via evolutionary and protein-protein interaction algorithms: <i>de novo</i> design of peptide inhibitors for F ₁ O ₁ -ATP synthase. <i>FEBS Letters</i> , 2021, 595, 183-194. | 1.3 | 3 |
| 7 | Specific inhibition of the Survivin-CRM1 interaction by peptide-modified molecular tweezers. <i>Nature Communications</i> , 2021, 12, 1505. | 5.8 | 18 |
| 8 | Alpha-1 antitrypsin inhibits TMPRSS2 protease activity and SARS-CoV-2 infection. <i>Nature Communications</i> , 2021, 12, 1726. | 5.8 | 86 |
| 9 | Inhibition of Staphylococcus aureus biofilm-forming functional amyloid by molecular tweezers. <i>Cell Chemical Biology</i> , 2021, 28, 1310-1320.e5. | 2.5 | 15 |
| 10 | Adoption of a Turn Conformation Drives the Binding Affinity of p53 C-Terminal Domain Peptides to 14-3-3 β . <i>ACS Chemical Biology</i> , 2020, 15, 262-271. | 1.6 | 10 |
| 11 | Peptide and peptide-based inhibitors of SARS-CoV-2 entry. <i>Advanced Drug Delivery Reviews</i> , 2020, 167, 47-65. | 6.6 | 132 |
| 12 | Proteome-wide Prediction of Lysine Methylation Leads to Identification of H2BK43 Methylation and Outlines the Potential Methyllysine Proteome. <i>Cell Reports</i> , 2020, 32, 107896. | 2.9 | 17 |
| 13 | Respiratory \hat{A}^2 -Microglobulin exerts pH dependent antimicrobial activity. <i>Virulence</i> , 2020, 11, 1402-1414. | 1.8 | 9 |
| 14 | Supramolecular Mechanism of Viral Envelope Disruption by Molecular Tweezers. <i>Journal of the American Chemical Society</i> , 2020, 142, 17024-17038. | 6.6 | 31 |
| 15 | CL-FEP: An End-State Free Energy Perturbation Approach. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 1396-1410. | 2.3 | 8 |
| 16 | A Placenta Derived C-Terminal Fragment of \hat{F}^2 -Hemoglobin With Combined Antibacterial and Antiviral Activity. <i>Frontiers in Microbiology</i> , 2020, 11, 508. | 1.5 | 23 |
| 17 | Control of TLR7-mediated type I IFN signaling in pDCs through CXCR4 engagement-A new target for lupus treatment. <i>Science Advances</i> , 2019, 5, eaav9019. | 4.7 | 34 |
| 18 | <i>ProtDCal</i> -Suite: A web server for the numerical codification and functional analysis of proteins. <i>Protein Science</i> , 2019, 28, 1734-1743. | 3.1 | 19 |

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|----|---|-----|-----------|
| 19 | Multivalent Ligands with Tailor-Made Anion Binding Motif as Stabilizers of Protein-Protein Interactions. <i>ChemBioChem</i> , 2019, 20, 2921-2926. | 1.3 | 13 |
| 20 | PPI-Detect: A support vector machine model for sequence-based prediction of protein-protein interactions. <i>Journal of Computational Chemistry</i> , 2019, 40, 1233-1242. | 1.5 | 54 |
| 21 | Mono- and Bivalent 14-3-3 Inhibitors for Characterizing Supramolecular Lysine Wrapping of Oligoethylene Glycol (OEG) Moieties in Proteins. <i>Chemistry - A European Journal</i> , 2018, 24, 13807-13814. | 1.7 | 6 |
| 22 | Novel extended sequons of human N-glycosylation sites improve the precision of qualitative predictions: an alignment-free study of pattern recognition using ProtD-Cal protein features. <i>Amino Acids</i> , 2017, 49, 317-325. | 1.2 | 10 |
| 23 | Unveiled electric profiles within hydrogen bonds suggest DNA base pairs with similar bond strengths. <i>PLoS ONE</i> , 2017, 12, e0185638. | 1.1 | 5 |
| 24 | Exploring general-purpose protein features for distinguishing enzymes and non-enzymes within the twilight zone. <i>BMC Bioinformatics</i> , 2017, 18, 349. | 1.2 | 10 |
| 25 | Orthotropic Piezoelectricity in 2D Nanocellulose. <i>Scientific Reports</i> , 2016, 6, 34616. | 1.6 | 32 |
| 26 | ProtD-Cal: A program to compute general-purpose-numerical descriptors for sequences and 3D-structures of proteins. <i>BMC Bioinformatics</i> , 2015, 16, 162. | 1.2 | 58 |
| 27 | Optical and mechanical properties of nanofibrillated cellulose: Toward a robust platform for next-generation green technologies. <i>Carbohydrate Polymers</i> , 2015, 126, 40-46. | 5.1 | 45 |
| 28 | A Hooke's law-based approach to protein folding rate. <i>Journal of Theoretical Biology</i> , 2015, 364, 407-417. | 0.8 | 9 |
| 29 | A physics-based scoring function for protein structural decoys: Dynamic testing on targets of CASP-ROLL. <i>Chemical Physics Letters</i> , 2014, 610-611, 135-140. | 1.2 | 7 |
| 30 | Global stability of protein folding from an empirical free energy function. <i>Journal of Theoretical Biology</i> , 2013, 321, 44-53. | 0.8 | 13 |
| 31 | STUDY BASED ON ELECTRONIC DESCRIPTORS OF THE DIASTEREOSELECTIVE AZA-DIELS-ALDER CYCLOADDITION OF [(1R)-10-(N,N-DIETHYLSULFAMOYL)ISOBORNYL] 2H-AZIRINE-3-CARBOXYLATE TO E,E-1,4-DIACETOXY-1,3-BUTADIENE. <i>Journal of the Chilean Chemical Society</i> , 2013, 58, 2243-2247. | 0.5 | 1 |
| 32 | New set of 2D/3D thermodynamic indices for proteins. A formalism based on Molten Globule theory. <i>Physics Procedia</i> , 2010, 8, 63-72. | 1.2 | 8 |
| 33 | Quantitative structure activity relationship of α -like peptides as aspartic proteinase inhibitors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 859-869. | 1.5 | 10 |