Yasser B Ruiz-Blanco

List of Publications by Year
in descending order

33 papers	747 citations	687220 13 h-index	580701 25 g-index
34 all docs	34 docs citations	34 times ranked	1183 citing authors

#	Article	IF	Citations
1	Peptide and peptide-based inhibitors of SARS-CoV-2 entry. Advanced Drug Delivery Reviews, 2020, 167, 47-65.	6.6	132
2	Alpha-1 antitrypsin inhibits TMPRSS2 protease activity and SARS-CoV-2 infection. Nature Communications, 2021, 12, 1726.	5.8	86
3	ProtDCal: A program to compute general-purpose-numerical descriptors for sequences and 3D-structures of proteins. BMC Bioinformatics, 2015, 16, 162.	1.2	58
4	PPIâ€Detect: A support vector machine model for sequenceâ€based prediction of proteinâ€“protein interactions. Journal of Computational Chemistry, 2019, 40, 1233-1242.	1.5	54
5	Optical and mechanical properties of nanofibrillated cellulose: Toward a robust platform for next-generation green technologies. Carbohydrate Polymers, 2015, 126, 40-46.	5.1	45
6	Control of TLR7-mediated type I IFN signaling in pDCs through CXCR4 engagementâ€”A new target for lupus treatment. Science Advances, 2019, 5, eaav9019.	4.7	34
7	Orthotropic Piezoelectricity in 2D Nanocellulose. Scientific Reports, 2016, 6, 34616.	1.6	32
8	Supramolecular Mechanism of Viral Envelope Disruption by Molecular Tweezers. Journal of the American Chemical Society, 2020, 142, 17024-17038.	6.6	31
9	PPI-Affinity: A Web Tool for the Prediction and Optimization of Proteinâ€“Peptide and Proteinâ€“Protein Binding Affinity. Journal of Proteome Research, 2022, 21, 1829-1841.	1.8	24
10	A Placenta Derived C-Terminal Fragment of Î²-Hemoglobin With Combined Antibacterial and Antiviral Activity. Frontiers in Microbiology, 2020, 11, 508.	1.5	23
11	ProtDCalâ€Suite: A web server for the numerical codification and functional analysis of proteins. Protein Science, 2019, 28, 1734-1743.	3.1	19
12	Specific inhibition of the Survivinâ€“CRM1 interaction by peptide-modified molecular tweezers. Nature Communications, 2021, 12, 1505.	5.8	18
13	Proteome-wide Prediction of Lysine Methylation Leads to Identification of H2BK43 Methylation and Outlines the Potential Methyllysine Proteome. Cell Reports, 2020, 32, 107896.	2.9	17
14	The role of DNA nanostructures in the catalytic properties of an allosterically regulated protease. Science Advances, 2022, 8, eabk0425.	4.7	16
15	Inhibition of Staphylococcus aureus biofilm-forming functional amyloid by molecular tweezers. Cell Chemical Biology, 2021, 28, 1310-1320.e5.	2.5	15
16	Global stability of protein folding from an empirical free energy function. Journal of Theoretical Biology, 2013, 321, 44-53.	0.8	13
17	Multivalent Ligands with Tailorâ€Made Anion Binding Motif as Stabilizers of Proteinâ€“Protein Interactions. ChemBioChem, 2019, 20, 2921-2926.	1.3	13
18	Quantitative structure activity relationship of IA₃â€like peptides as aspartic proteinase inhibitors. Proteins: Structure, Function and Bioinformatics, 2009, 75, 859-869.	1.5	10

#	Article	IF	Citations
19	Novel â€œextended sequonsâ€•of human N-glycosylation sites improve the precision of qualitative predictions: an alignment-free study of pattern recognition using ProtDCal protein features. Amino Acids, 2017, 49, 317-325.	1.2	10
20	Exploring general-purpose protein features for distinguishing enzymes and non-enzymes within the twilight zone. BMC Bioinformatics, 2017, 18, 349.	1.2	10
21	Adoption of a Turn Conformation Drives the Binding Affinity of p53 C-Terminal Domain Peptides to 14-3-3Ïƒ. ACS Chemical Biology, 2020, 15, 262-271.	1.6	10
22	Effect of Organic Solvents on the Structure and Activity of a Minimal Lipase. Journal of Organic Chemistry, 2022, 87, 1669-1678.	1.7	10
23	A Hooke×³s law-based approach to protein folding rate. Journal of Theoretical Biology, 2015, 364, 407-417.	0.8	9
24	Respiratory ÃŸ-2-Microglobulin exerts pH dependent antimicrobial activity. Virulence, 2020, 11, 1402-1414.	1.8	9
25	New set of 2D/3D thermodynamic indices for proteins. A formalism based on â€œMolten Globuleâ€•theory. Physics Procedia, 2010, 8, 63-72.	1.2	8
26	CL-FEP: An End-State Free Energy Perturbation Approach. Journal of Chemical Theory and Computation, 2020, 16, 1396-1410.	2.3	8
27	A physics-based scoring function for protein structural decoys: Dynamic testing on targets of CASP-ROLL. Chemical Physics Letters, 2014, 610-611, 135-140.	1.2	7
28	Monoâ€•and Bivalent 14â€3â€3 Inhibitors for Characterizing Supramolecular â€œLysine Wrappingâ€•of Oligoethylene Glycol (OEG) Moieties in Proteins. Chemistry - A European Journal, 2018, 24, 13807-13814.	1.7	6
29	Unveiled electric profiles within hydrogen bonds suggest DNA base pairs with similar bond strengths. PLoS ONE, 2017, 12, e0185638.	1.1	5
30	Engineering protein fragments via evolutionary and proteinâ€“protein interaction algorithms: de novo design of peptide inhibitors for F_OF₁â€ATP synthase. FEBS Letters, 2021, 595, 183-194.	1.3	3
31	Selective Disruption of Survivin's Proteinâ€Protein Interactions: A Supramolecular Approach Based on Guanidiniocarbonylpyrrole. ChemBioChem, 2022, , e202100618.	1.3	3
32	Computational Design of Inhibitors Targeting the Catalytic Î² Subunit of Escherichia coli FOF1-ATP Synthase. Antibiotics, 2022, 11, 557.	1.5	3
33	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. Journal of the Chilean Chemical Society, 2013, 58, 2243-2247.	0.5	1